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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 121.918 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-8

Perfect score: 26

Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 270181610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	15.2	58.5	25	14	US-10-215-112-6804
8	15.2	58.5	25	14	US-10-215-112-6930
9	14.6	56.2	25	15	US-10-098-263B-27628
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11	14.4	55.4	25	15	US-10-098-263B-61172
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c 154	12.2	46.9	50	16	US-09-274-553D-3089	Sequence 3089, App	c 227	11.8	45.4	24	9	US-09-791-377-671	Sequence 671, App
c 155	12.2	46.9	50	16	US-10-062-188-150	Sequence 150, App	c 228	11.8	45.4	24	9	US-09-993-170-27	Sequence 27, Appl
c 156	12.2	46.9	50	16	US-10-062-188-166	Sequence 166, App	c 229	11.8	45.4	25	14	US-10-215-112-7142	Sequence 7142, App
c 157	12.2	46.9	50	16	US-10-062-188-181	Sequence 181, App	c 230	11.8	45.4	25	14	US-10-215-112-8317	Sequence 8317, App
c 158	12.2	46.9	50	16	US-10-062-188-196	Sequence 196, App	c 231	11.8	45.4	25	15	US-10-098-263B-7841	Sequence 7841, App

C 232	11.8	45.4	25	15	US-10-098-263B-22400	Sequence 22400, A	305	11.6	44.6	23	9	US-09-730-289B-13	Sequence 13, Appl
C 233	11.8	45.4	25	15	US-10-098-263B-27360	Sequence 27360, A	306	11.6	44.6	25	10	US-09-730-289B-1597	Sequence 1597, Ap
C 234	11.8	45.4	25	15	US-10-098-263B-54743	Sequence 54743, A	307	11.6	44.6	25	10	US-09-730-289B-1598	Sequence 1598, Ap
C 235	11.8	45.4	25	15	US-10-098-263B-54744	Sequence 54744, A	308	11.6	44.6	25	10	US-09-730-289B-3511	Sequence 3511, Ap
C 236	11.8	45.4	25	15	US-10-098-263B-61943	Sequence 61943, A	309	11.6	44.6	25	10	US-09-730-289B-3512	Sequence 3512, Ap
C 237	11.8	45.4	25	15	US-10-098-263B-61944	Sequence 61944, A	310	11.6	44.6	25	14	US-10-215-112-5342	Sequence 5342, Ap
C 238	11.8	45.4	25	15	US-10-098-263B-62605	Sequence 62605, A	311	11.6	44.6	25	14	US-10-215-112-6723	Sequence 6723, Ap
C 239	11.8	45.4	25	15	US-10-098-263B-67185	Sequence 67185, A	312	11.6	44.6	25	14	US-10-215-112-6995	Sequence 6995, Ap
C 240	11.8	45.4	25	15	US-10-098-263B-70501	Sequence 70501, A	313	11.6	44.6	25	15	US-10-098-263B-11852	Sequence 11852, A
C 241	11.8	45.4	25	15	US-10-098-263B-70502	Sequence 70502, A	314	11.6	44.6	25	15	US-10-098-263B-20003	Sequence 20003, A
C 242	11.8	45.4	25	15	US-10-098-263B-76465	Sequence 76465, A	315	11.6	44.6	25	15	US-10-098-263B-21356	Sequence 21356, A
C 243	11.8	45.4	25	15	US-10-098-263B-80456	Sequence 80456, A	316	11.6	44.6	25	15	US-10-098-263B-23350	Sequence 23350, A
C 244	11.8	45.4	25	15	US-10-098-263B-99054	Sequence 99054, A	317	11.6	44.6	25	15	US-10-098-263B-60813	Sequence 60813, A
C 245	11.8	45.4	25	15	US-10-098-263B-102627	Sequence 102627, A	318	11.6	44.6	25	15	US-10-098-263B-74615	Sequence 74615, A
C 246	11.8	45.4	25	15	US-10-098-263B-104409	Sequence 104409, A	319	11.6	44.6	25	15	US-10-098-263B-86303	Sequence 86303, A
C 247	11.8	45.4	25	15	US-10-098-263B-117508	Sequence 117508, A	320	11.6	44.6	25	15	US-10-098-263B-94238	Sequence 94238, A
C 248	11.8	45.4	25	15	US-10-098-263B-126634	Sequence 126634, A	321	11.6	44.6	25	15	US-10-098-263B-128874	Sequence 128874, A
C 249	11.8	45.4	25	17	US-10-759-602-42	Sequence 42, Appl	322	11.6	44.6	25	15	US-10-098-263B-94856	Sequence 94856, A
C 250	11.8	45.4	28	9	US-09-875-644-1	Sequence 1, Appl	323	11.6	44.6	25	15	US-10-098-263B-101248	Sequence 101248, A
C 251	11.8	45.4	28	9	US-09-231-235-46	Sequence 46, Appl	324	11.6	44.6	25	15	US-10-098-263B-111197	Sequence 111197, A
C 252	11.8	45.4	28	9	US-09-797-518A-46	Sequence 46, Appl	325	11.6	44.6	25	15	US-10-098-263B-121065	Sequence 121065, A
C 253	11.8	45.4	28	10	US-09-872-696A-46	Sequence 46, Appl	326	11.6	44.6	25	15	US-10-098-263B-121701	Sequence 121701, A
C 254	11.8	45.4	29	15	US-10-112-221A-20	Sequence 20, Appl	327	11.6	44.6	25	15	US-10-098-263B-128874	Sequence 128874, A
C 255	11.8	45.4	31	10	US-09-961-077-417	Sequence 417, Appl	328	11.6	44.6	25	15	US-10-098-263B-130366	Sequence 130366, A
C 256	11.8	45.4	31	15	US-10-148-521-9	Sequence 9, Appl	329	11.6	44.6	27	16	US-10-449-831A-165	Sequence 165, Appl
C 257	11.8	45.4	32	9	US-09-858-217-16	Sequence 16, Appl	330	11.6	44.6	27	17	US-10-414-533-22	Sequence 22, Appl
C 258	11.8	45.4	32	15	US-10-171-174A-16	Sequence 16, Appl	331	11.6	44.6	28	16	US-10-387-387-4	Sequence 4, Appl
C 259	11.8	45.4	32	17	US-10-759-602-45	Sequence 45, Appl	332	11.6	44.6	29	14	US-10-071-485-82	Sequence 82, Appl
C 260	11.8	45.4	36	10	US-09-906-179A-165	Sequence 165, Appl	333	11.6	44.6	30	15	US-10-336-840-35	Sequence 35, Appl
C 261	11.8	45.4	40	10	US-09-906-179A-160	Sequence 160, Appl	334	11.6	44.6	31	10	US-09-961-077-496	Sequence 496, Appl
C 262	11.8	45.4	40	14	US-10-135-965-75	Sequence 75, Appl	335	11.6	44.6	32	16	US-10-434-269-13	Sequence 13, Appl
C 263	11.8	45.4	40	14	US-10-071-485-6	Sequence 6, Appl	336	11.6	44.6	32	16	US-10-434-269-24	Sequence 24, Appl
C 264	11.8	45.4	40	16	US-10-035-833A-816	Sequence 816, Appl	337	11.6	44.6	33	14	US-10-025-222A-20	Sequence 20, Appl
C 265	11.8	45.4	40	16	US-10-035-833A-6758	Sequence 6758, Ap	338	11.6	44.6	33	17	US-10-477-376-8	Sequence 8, Appl
C 266	11.8	45.4	40	17	US-10-168-781A-10	Sequence 10, Appl	339	11.6	44.6	35	15	US-10-136-44A-25	Sequence 25, Appl
C 267	11.8	45.4	40	18	US-10-469-851-158	Sequence 158, Appl	340	11.6	44.6	35	17	US-10-354-805A-13	Sequence 13, Appl
C 268	11.8	45.4	41	16	US-10-035-833A-1534	Sequence 1534, Ap	341	11.6	44.6	37	9	US-09-864-785-1855	Sequence 1855, Ap
C 269	11.8	45.4	41	16	US-10-035-833A-4031	Sequence 4031, Ap	342	11.6	44.6	37	10	US-09-927-046-3768	Sequence 3768, Ap
C 270	11.8	45.4	42	17	US-10-451-793-28	Sequence 28, Appl	343	11.6	44.6	37	10	US-09-848-754A-5958	Sequence 5958, Ap
C 271	11.8	45.4	44	9	US-09-823-823-31	Sequence 31, Appl	344	11.6	44.6	37	10	US-09-848-754A-6364	Sequence 6364, Ap
C 272	11.8	45.4	44	9	US-09-823-823-31	Sequence 31, Appl	345	11.6	44.6	39	14	US-10-044-692-265	Sequence 265, Appl
C 273	11.8	45.4	45	10	US-09-860-474-229	Sequence 229, Appl	346	11.6	44.6	39	14	US-10-044-692-267	Sequence 267, Appl
C 274	11.8	45.4	45	15	US-10-409-565-229	Sequence 229, Appl	347	11.6	44.6	39	14	US-10-044-692-269	Sequence 269, Appl
C 275	11.8	45.4	45	15	US-10-148-521-2	Sequence 2, Appl	348	11.6	44.6	39	14	US-10-044-692-271	Sequence 271, Appl
C 276	11.8	45.4	47	16	US-10-349-143-162	Sequence 162, Appl	349	11.6	44.6	39	15	US-10-044-539-265	Sequence 265, Appl
C 277	11.8	45.4	48	9	US-09-795-006A-15	Sequence 15, Appl	350	11.6	44.6	39	15	US-10-044-539-267	Sequence 267, Appl
C 278	11.8	45.4	48	9	US-09-795-006A-35	Sequence 35, Appl	351	11.6	44.6	39	15	US-10-044-539-269	Sequence 269, Appl
C 279	11.8	45.4	48	15	US-10-295-798-11	Sequence 11, Appl	352	11.6	44.6	39	15	US-10-044-539-271	Sequence 271, Appl
C 280	11.8	45.4	48	15	US-10-295-798-12	Sequence 12, Appl	353	11.6	44.6	39	15	US-10-005-956-1361	Sequence 1361, Ap
C 281	11.8	45.4	48	15	US-10-295-798-13	Sequence 13, Appl	354	11.6	44.6	39	15	US-10-005-956-1373	Sequence 1373, Ap
C 282	11.8	45.4	48	15	US-10-295-798-14	Sequence 14, Appl	355	11.6	44.6	39	15	US-10-325-810-498	Sequence 498, Appl
C 283	11.8	45.4	48	15	US-10-295-798-17	Sequence 17, Appl	356	11.6	44.6	39	15	US-10-325-810-500	Sequence 500, Appl
C 284	11.8	45.4	48	15	US-10-295-798-21	Sequence 21, Appl	357	11.6	44.6	39	15	US-10-325-810-502	Sequence 502, Appl
C 285	11.8	45.4	48	15	US-10-295-798-22	Sequence 22, Appl	358	11.6	44.6	39	15	US-10-325-810-504	Sequence 504, Appl
C 286	11.8	45.4	48	15	US-10-295-798-26	Sequence 26, Appl	359	11.6	44.6	39	16	US-10-411-066-43	Sequence 43, Appl
C 287	11.8	45.4	48	15	US-10-295-798-32	Sequence 32, Appl	360	11.6	44.6	41	16	US-10-035-833A-3101	Sequence 3101, Ap
C 288	11.8	45.4	48	15	US-10-295-798-34	Sequence 34, Appl	361	11.6	44.6	41	16	US-10-035-833A-5612	Sequence 5612, Ap
C 289	11.8	45.4	48	15	US-10-295-798-35	Sequence 35, Appl	362	11.6	44.6	45	16	US-10-387-387-9	Sequence 9, Appl
C 290	11.8	45.4	48	17	US-10-771-395-40	Sequence 40, Appl	363	11.6	44.6	45	16	US-10-387-387-11	Sequence 11, Appl
C 291	11.8	45.4	49	9	US-09-728-918-6	Sequence 6, Appl	364	11.6	44.6	46	10	US-09-993-346-17	Sequence 17, Appl
C 292	11.8	45.4	49	14	US-10-058-151A-6	Sequence 6, Appl	365	11.6	44.6	47	16	US-10-349-143-2653	Sequence 2653, Ap
C 293	11.8	45.4	50	15	US-10-295-798-18	Sequence 18, Appl	366	11.6	44.6	50	9	US-09-938-842A-4843	Sequence 4843, Ap
C 294	11.8	45.4	50	16	US-10-131-827-1418	Sequence 1418, Ap	367	11.6	44.6	50	11	US-09-938-842A-4843	Sequence 4843, Ap
C 295	11.8	45.4	50	16	US-10-131-827-1798	Sequence 1798, Ap	368	11.6	44.6	50	16	US-10-131-827-6459	Sequence 6459, Ap
C 296	11.8	45.4	50	16	US-10-131-827-7588	Sequence 7588, Ap	369	11.6	44.6	50	16	US-10-131-827-6532	Sequence 6532, Ap
C 297	11.6	44.6	20	15	US-10-174-465-45	Sequence 45, Appl	370	11.6	44.6	50	16	US-10-131-827-6859	Sequence 6859, Ap
C 298	11.6	44.6	20	15	US-10-174-465-68	Sequence 68, Appl	371	11.6	44.6	50	16	US-10-131-827-6922	Sequence 6922, Ap
C 299	11.6	44.6	20	15	US-10-348-431-45	Sequence 45, Appl	372	11.6	44.6	50	16	US-10-131-827-7195	Sequence 7195, Ap
C 300	11.6	44.6	20	15	US-10-348-431-68	Sequence 68, Appl	373	11.6	44.6	50	17	US-10-335-181-9	Sequence 9, Appl
C 301	11.6	44.6	20	15	US-10-289-762-2900	Sequence 2900, Appl	374	11.6	44.6	50	17	US-10-335-181-10	Sequence 10, Appl
C 302	11.6	44.6	20	17	US-10-317-253-21	Sequence 21, Appl	375	11.4	43.8	20	16	US-10-289-762-3342	Sequence 3342, Ap
C 303	11.6	44.6	20	17	US-10-317-253-56	Sequence 56, Appl	376	11.4	43.8	21	14	US-10-190-279-26	Sequence 26, Appl
C 304	11.6	44.6	21	15	US-10-165-099-278	Sequence 278, Appl	377	11.4	43.8	21	15	US-10-340-123-9	Sequence 9, Appl

c 378	11.4	43.8	23	9	US-09-216-393-334	Sequence 334, App	c 451	11.4	43.8	50	16	US-10-131-827-477	Sequence 477, App
c 379	11.4	43.8	23	10	US-09-993-312-32	Sequence 32, Appl	c 452	11.4	43.8	50	16	US-10-131-827-2211	Sequence 2211, Ap
c 380	11.4	43.8	23	15	US-10-321-856-334	Sequence 334, App	c 453	11.4	43.8	50	16	US-10-131-827-3050	Sequence 3050, Ap
c 381	11.4	43.8	25	14	US-10-215-112-13064	Sequence 13064, A	c 454	11.4	43.8	50	16	US-10-131-827-3377	Sequence 3377, Ap
c 382	11.4	43.8	25	15	US-10-098-263B-10173	Sequence 10173, A	c 455	11.4	43.8	50	16	US-10-131-827-3854	Sequence 3854, Ap
c 383	11.4	43.8	25	15	US-10-098-263B-12237	Sequence 12237, A	c 456	11.4	43.8	50	16	US-10-131-827-6732	Sequence 6732, Ap
c 384	11.4	43.8	25	15	US-10-098-263B-26218	Sequence 26218, A	c 457	11.4	43.8	50	16	US-10-131-827-7122	Sequence 7122, Ap
c 385	11.4	43.8	25	15	US-10-098-263B-27374	Sequence 27374, A	c 458	11.4	43.8	50	16	US-10-131-827-7416	Sequence 7416, Ap
c 386	11.4	43.8	25	15	US-10-098-263B-30970	Sequence 30970, A	c 459	11.4	43.8	50	16	US-10-131-827-7495	Sequence 7495, Ap
c 387	11.4	43.8	25	15	US-10-098-263B-35358	Sequence 35358, A	c 460	11.4	43.8	50	16	US-10-131-827-8099	Sequence 8099, Ap
c 388	11.4	43.8	25	15	US-10-098-263B-38915	Sequence 38915, A	c 461	11.2	43.1	18	9	US-09-067-638B-32	Sequence 32, Appl
c 389	11.4	43.8	25	15	US-10-098-263B-39614	Sequence 39614, A	c 462	11.2	43.1	18	15	US-10-116-325-32	Sequence 32, Appl
c 390	11.4	43.8	25	15	US-10-098-263B-49152	Sequence 49152, A	c 463	11.2	43.1	18	15	US-10-388-263-32	Sequence 32, Appl
c 391	11.4	43.8	25	15	US-10-098-263B-49908	Sequence 49908, A	c 464	11.2	43.1	18	17	US-10-698-689-32	Sequence 196, Appl
c 392	11.4	43.8	25	15	US-10-098-263B-50273	Sequence 50273, A	c 465	11.2	43.1	18	17	US-10-698-689-196	Sequence 32, Appl
c 393	11.4	43.8	25	15	US-10-098-263B-50557	Sequence 50557, A	c 466	11.2	43.1	18	18	US-10-830-475-32	Sequence 17, Appl
c 394	11.4	43.8	25	15	US-10-098-263B-52926	Sequence 52926, A	c 467	11.2	43.1	20	15	US-10-286-927-17	Sequence 2584, Ap
c 395	11.4	43.8	25	15	US-10-098-263B-60773	Sequence 60773, A	c 468	11.2	43.1	20	16	US-10-289-762-2584	Sequence 6523, Ap
c 396	11.4	43.8	25	15	US-10-098-263B-66167	Sequence 66167, A	c 469	11.2	43.1	20	18	US-10-289-762-6523	Sequence 34, Appl
c 397	11.4	43.8	25	15	US-10-098-263B-72519	Sequence 72519, A	c 470	11.2	43.1	20	18	US-10-738-986-34	Sequence 450, App
c 398	11.4	43.8	25	15	US-10-098-263B-77424	Sequence 77424, A	c 471	11.2	43.1	20	18	US-10-712-795-450	Sequence 771, App
c 399	11.4	43.8	25	15	US-10-098-263B-85888	Sequence 85888, A	c 472	11.2	43.1	20	18	US-10-712-795-771	Sequence 9, Appl
c 400	11.4	43.8	25	15	US-10-098-263B-86849	Sequence 86849, A	c 473	11.2	43.1	21	15	US-10-286-927-9	Sequence 19102, A
c 401	11.4	43.8	25	15	US-10-098-263B-90726	Sequence 90726, A	c 474	11.2	43.1	21	18	US-10-786-720-19102	Sequence 19103, A
c 402	11.4	43.8	25	15	US-10-098-263B-93617	Sequence 93617, A	c 475	11.2	43.1	21	18	US-10-786-720-19103	Sequence 19104, A
c 403	11.4	43.8	25	15	US-10-098-263B-97194	Sequence 97194, A	c 476	11.2	43.1	21	18	US-10-786-720-19104	Sequence 19105, A
c 404	11.4	43.8	25	15	US-10-098-263B-98079	Sequence 98079, A	c 477	11.2	43.1	21	18	US-10-786-720-19105	Sequence 19106, A
c 405	11.4	43.8	25	15	US-10-098-263B-98080	Sequence 98080, A	c 478	11.2	43.1	21	18	US-10-786-720-19107	Sequence 19107, A
c 406	11.4	43.8	25	15	US-10-098-263B-107420	Sequence 107420, A	c 479	11.2	43.1	21	18	US-10-786-720-19107	Sequence 19564, A
c 407	11.4	43.8	25	15	US-10-098-263B-113394	Sequence 113394, A	c 480	11.2	43.1	21	18	US-10-786-720-19564	Sequence 19565, A
c 408	11.4	43.8	25	15	US-10-098-263B-115034	Sequence 115034, A	c 481	11.2	43.1	21	18	US-10-786-720-19565	Sequence 19566, A
c 409	11.4	43.8	25	15	US-10-098-263B-119065	Sequence 119065, A	c 482	11.2	43.1	21	18	US-10-786-720-19566	Sequence 13, Appl
c 410	11.4	43.8	25	15	US-10-098-263B-123299	Sequence 123299, A	c 483	11.2	43.1	22	16	US-10-300-369-13	Sequence 3290, Ap
c 411	11.4	43.8	25	15	US-10-098-263B-123299	Sequence 123299, A	c 484	11.2	43.1	22	10	US-09-940-185-3290	Sequence 264, App
c 412	11.4	43.8	25	15	US-10-098-263B-128519	Sequence 128519, A	c 485	11.2	43.1	25	10	US-09-92-665-264	Sequence 419, App
c 413	11.4	43.8	25	15	US-10-098-263B-128838	Sequence 128838, A	c 486	11.2	43.1	25	14	US-10-215-112-419	Sequence 724, App
c 414	11.4	43.8	25	17	US-10-717-597-2020	Sequence 2020, Ap	c 487	11.2	43.1	25	14	US-10-215-112-724	Sequence 5099, Ap
c 415	11.4	43.8	25	17	US-10-717-597-2602	Sequence 2602, Ap	c 488	11.2	43.1	25	14	US-10-215-112-5099	Sequence 5363, Ap
c 416	11.4	43.8	25	17	US-10-775-169-2954	Sequence 2954, Ap	c 489	11.2	43.1	25	14	US-10-215-112-5363	Sequence 5565, Ap
c 417	11.4	43.8	26	9	US-09-738-625-7025	Sequence 7025, Ap	c 490	11.2	43.1	25	14	US-10-215-112-5565	Sequence 8628, Ap
c 418	11.4	43.8	26	14	US-10-234-432-80	Sequence 80, Appl	c 491	11.2	43.1	25	14	US-10-215-112-8628	Sequence 11067, A
c 419	11.4	43.8	29	15	US-10-182-616-18	Sequence 18, Appl	c 492	11.2	43.1	25	14	US-10-215-112-11067	Sequence 12429, A
c 420	11.4	43.8	30	15	US-10-091-841-22	Sequence 22, Appl	c 493	11.2	43.1	25	14	US-10-215-112-12429	Sequence 14406, A
c 421	11.4	43.8	30	15	US-10-091-841-47	Sequence 47, Appl	c 494	11.2	43.1	25	14	US-10-215-112-14406	Sequence 14701, A
c 422	11.4	43.8	30	17	US-10-148-989A-7	Sequence 7, Appl	c 495	11.2	43.1	25	15	US-10-098-263B-4326	Sequence 4326, Ap
c 423	11.4	43.8	30	17	US-10-629-313-87	Sequence 87, Appl	c 496	11.2	43.1	25	15	US-10-098-263B-7253	Sequence 7253, Ap
c 424	11.4	43.8	31	13	US-10-004-832-4	Sequence 4, Appl	c 497	11.2	43.1	25	15	US-10-098-263B-7837	Sequence 7837, Ap
c 425	11.4	43.8	31	16	US-10-069-040-24	Sequence 24, Appl	c 498	11.2	43.1	25	15	US-10-098-263B-7837	Sequence 13371, A
c 426	11.4	43.8	32	8	US-08-970-266-2	Sequence 2, Appl	c 499	11.2	43.1	25	15	US-10-098-263B-13371	Sequence 33910, A
c 427	11.4	43.8	32	8	US-08-744-685-2	Sequence 2, Appl	c 500	11.2	43.1	25	15	US-10-098-263B-39910	Sequence 42795, A
c 428	11.4	43.8	32	14	US-10-068-851-14	Sequence 14, Appl	c 501	11.2	43.1	25	15	US-10-098-263B-42795	Sequence 44070, A
c 429	11.4	43.8	32	16	US-10-612-779-96	Sequence 96, Appl	c 502	11.2	43.1	25	15	US-10-098-263B-44070	Sequence 49726, A
c 430	11.4	43.8	33	14	US-10-179-046-33	Sequence 33, Appl	c 503	11.2	43.1	25	15	US-10-098-263B-49726	Sequence 53621, A
c 431	11.4	43.8	33	14	US-10-179-046-35	Sequence 35, Appl	c 504	11.2	43.1	25	15	US-10-098-263B-53621	Sequence 55566, A
c 432	11.4	43.8	34	9	US-09-862-847-4	Sequence 4, Appl	c 505	11.2	43.1	25	15	US-10-098-263B-55566	Sequence 55988, A
c 433	11.4	43.8	34	10	US-09-906-179A-171	Sequence 171, App	c 506	11.2	43.1	25	15	US-10-098-263B-55988	Sequence 61870, A
c 434	11.4	43.8	35	10	US-09-906-179A-168	Sequence 168, App	c 507	11.2	43.1	25	15	US-10-098-263B-61870	Sequence 63454, A
c 435	11.4	43.8	35	15	US-10-021-425-10	Sequence 10, Appl	c 508	11.2	43.1	25	15	US-10-098-263B-63454	Sequence 68477, A
c 436	11.4	43.8	35	16	US-10-422-366-55	Sequence 55, Appl	c 509	11.2	43.1	25	15	US-10-098-263B-68477	Sequence 70566, A
c 437	11.4	43.8	37	9	US-09-117-447-4	Sequence 4, Appl	c 510	11.2	43.1	25	15	US-10-098-263B-70566	Sequence 73666, A
c 438	11.4	43.8	38	10	US-09-776-474-1678	Sequence 1678, Ap	c 511	11.2	43.1	25	15	US-10-098-263B-73666	Sequence 83095, A
c 439	11.4	43.8	38	18	US-10-741-789A-41	Sequence 41, Appl	c 512	11.2	43.1	25	15	US-10-098-263B-85095	Sequence 85144, A
c 440	11.4	43.8	39	10	US-09-994-064-28	Sequence 28, Appl	c 513	11.2	43.1	25	15	US-10-098-263B-85144	Sequence 92804, A
c 441	11.4	43.8	39	11	US-09-993-777-28	Sequence 28, Appl	c 514	11.2	43.1	25	15	US-10-098-263B-92804	Sequence 94323, A
c 442	11.4	43.8	40	14	US-10-067-956-5	Sequence 5, Appl	c 515	11.2	43.1	25	15	US-10-098-263B-94323	Sequence 94334, A
c 443	11.4	43.8	40	16	US-10-447-839A-88	Sequence 88, Appl	c 516	11.2	43.1	25	15	US-10-098-263B-94334	Sequence 95247, A
c 444	11.4	43.8	41	16	US-10-035-833A-982	Sequence 982, App	c 517	11.2	43.1	25	15	US-10-098-263B-95247	Sequence 99385, A
c 445	11.4	43.8	41	16	US-10-035-833A-692	Sequence 692, App	c 518	11.2	43.1	25	15	US-10-098-263B-99385	Sequence 101327, A
c 446	11.4	43.8	42	15	US-10-200-381A-69	Sequence 69, Appl	c 519	11.2	43.1	25	15	US-10-098-263B-101327	Sequence 102581, A
c 447	11.4	43.8	44	10	US-09-832-899-6	Sequence 6, Appl	c 520	11.2	43.1	25	15	US-10-098-263B-102581	Sequence 103784, A
c 448	11.4	43.8	47	15	US-10-170-097-1086	Sequence 1086, Ap	c 521	11.2	43.1	25	15	US-10-098-263B-103784	Sequence 108251, A
c 449	11.4	43.8	47	16	US-10-349-143-1052	Sequence 1052, Ap	c 522	11.2	43.1	25	15	US-10-098-263B-108251	
c 450	11.4	43.8	50	16	US-10-131-827-467	Sequence 467, App	c 523	11.2	43.1	25	15		

524	11.2	43.1	25	15	US-10-098-263B-108252	Sequence 108252,	c 597	11.2	43.1	45	9	US-09-999-832A-50	Sequence 50, Appl
525	11.2	43.1	25	15	US-10-098-263B-108598	Sequence 108598,	c 598	11.2	43.1	45	10	US-09-978-189-50	Sequence 50, Appl
526	11.2	43.1	25	15	US-10-098-263B-114646	Sequence 114646,	c 599	11.2	43.1	45	10	US-09-978-608A-50	Sequence 50, Appl
527	11.2	43.1	25	15	US-10-098-263B-116700	Sequence 116700,	c 600	11.2	43.1	45	10	US-09-978-585A-50	Sequence 50, Appl
528	11.2	43.1	25	15	US-10-098-263B-120734	Sequence 120734,	c 601	11.2	43.1	45	10	US-09-978-191A-50	Sequence 50, Appl
529	11.2	43.1	25	15	US-10-098-263B-121916	Sequence 121916,	c 602	11.2	43.1	45	10	US-09-978-403A-50	Sequence 50, Appl
530	11.2	43.1	25	15	US-10-032-585-4307	Sequence 4307, Ap	c 603	11.2	43.1	45	10	US-09-978-568A-50	Sequence 50, Appl
531	11.2	43.1	25	17	US-10-775-169-2041	Sequence 2041, Ap	c 604	11.2	43.1	45	10	US-09-999-833A-50	Sequence 50, Appl
532	11.2	43.1	25	17	US-10-775-169-2042	Sequence 2042, Ap	c 605	11.2	43.1	45	10	US-09-981-915A-50	Sequence 50, Appl
533	11.2	43.1	25	17	US-10-775-169-4567	Sequence 4567, Ap	c 606	11.2	43.1	45	10	US-09-978-824-50	Sequence 50, Appl
534	11.2	43.1	25	17	US-10-775-169-4568	Sequence 4568, Ap	c 607	11.2	43.1	45	10	US-09-918-585A-50	Sequence 50, Appl
535	11.2	43.1	27	15	US-10-436-826-67	Sequence 67, Appl	c 608	11.2	43.1	45	10	US-09-999-834A-50	Sequence 50, Appl
536	11.2	43.1	27	16	US-10-312-503A-36	Sequence 36, Appl	c 609	11.2	43.1	45	10	US-09-978-423A-50	Sequence 50, Appl
537	11.2	43.1	27	16	US-10-312-503A-40	Sequence 40, Appl	c 610	11.2	43.1	45	10	US-09-978-192A-50	Sequence 50, Appl
538	11.2	43.1	28	9	US-09-944-411-19	Sequence 19, Appl	c 611	11.2	43.1	45	10	US-09-999-830A-50	Sequence 50, Appl
539	11.2	43.1	28	9	US-09-759-352-17	Sequence 17, Appl	c 612	11.2	43.1	45	10	US-09-978-757A-50	Sequence 50, Appl
540	11.2	43.1	28	9	US-09-887-880-24	Sequence 24, Appl	c 613	11.2	43.1	45	10	US-09-978-187B-50	Sequence 50, Appl
541	11.2	43.1	28	15	US-10-260-516-19	Sequence 19, Appl	c 614	11.2	43.1	45	10	US-09-978-643A-50	Sequence 50, Appl
542	11.2	43.1	28	15	US-10-360-123A-26	Sequence 26, Appl	c 615	11.2	43.1	45	10	US-09-978-175A-50	Sequence 50, Appl
543	11.2	43.1	28	15	US-10-360-123A-32	Sequence 32, Appl	c 616	11.2	43.1	45	10	US-09-978-298A-50	Sequence 50, Appl
544	11.2	43.1	28	15	US-10-360-123A-33	Sequence 33, Appl	c 617	11.2	43.1	45	10	US-09-978-188A-50	Sequence 50, Appl
545	11.2	43.1	28	17	US-10-220-481-341	Sequence 341, App	c 618	11.2	43.1	45	10	US-09-978-681A-50	Sequence 50, Appl
546	11.2	43.1	29	9	US-09-863-040-43	Sequence 43, Appl	c 619	11.2	43.1	45	10	US-09-978-194A-50	Sequence 50, Appl
547	11.2	43.1	29	10	US-09-069-228-5	Sequence 5, Appli	c 620	11.2	43.1	45	10	US-09-999-829A-50	Sequence 50, Appl
548	11.2	43.1	29	15	US-10-454-210-43	Sequence 43, Appl	c 621	11.2	43.1	45	10	US-09-978-299A-50	Sequence 50, Appl
549	11.2	43.1	29	18	US-10-849-518-5	Sequence 5, Appli	c 622	11.2	43.1	45	10	US-09-978-544A-50	Sequence 50, Appl
550	11.2	43.1	30	16	US-10-632-117-3	Sequence 3, Appli	c 623	11.2	43.1	45	10	US-09-978-665A-50	Sequence 50, Appl
551	11.2	43.1	31	9	US-09-738-599-13	Sequence 13, Appl	c 624	11.2	43.1	45	10	US-09-978-802A-50	Sequence 50, Appl
552	11.2	43.1	31	10	US-09-961-077-284	Sequence 284, App	c 625	11.2	43.1	45	11	US-09-999-831A-50	Sequence 50, Appl
553	11.2	43.1	32	9	US-09-887-880-25	Sequence 25, Appl	c 626	11.2	43.1	45	14	US-10-017-081A-50	Sequence 50, Appl
554	11.2	43.1	32	15	US-10-314-861-20	Sequence 20, Appl	c 627	11.2	43.1	45	14	US-10-167-749-50	Sequence 50, Appl
555	11.2	43.1	33	17	US-10-479-787-24	Sequence 24, Appl	c 628	11.2	43.1	45	14	US-10-013-921A-50	Sequence 50, Appl
556	11.2	43.1	34	14	US-10-071-485-95	Sequence 95, Appl	c 629	11.2	43.1	45	14	US-10-013-922A-50	Sequence 50, Appl
557	11.2	43.1	34	16	US-10-607-631-27	Sequence 27, Appl	c 630	11.2	43.1	45	14	US-10-016-177A-50	Sequence 50, Appl
558	11.2	43.1	34	16	US-10-607-631-28	Sequence 28, Appl	c 631	11.2	43.1	45	15	US-10-166-709A-50	Sequence 50, Appl
559	11.2	43.1	35	15	US-10-456-097-4	Sequence 4, Appli	c 632	11.2	43.1	45	15	US-10-143-031A-50	Sequence 50, Appl
560	11.2	43.1	36	9	US-09-887-880-18	Sequence 18, Appl	c 633	11.2	43.1	45	15	US-10-143-030A-50	Sequence 50, Appl
561	11.2	43.1	36	9	US-09-887-880-19	Sequence 19, Appl	c 634	11.2	43.1	45	15	US-10-002-967A-50	Sequence 50, Appl
562	11.2	43.1	36	9	US-09-887-880-20	Sequence 20, Appl	c 635	11.2	43.1	45	15	US-10-017-083A-50	Sequence 50, Appl
563	11.2	43.1	36	9	US-09-887-880-21	Sequence 21, Appl	c 636	11.2	43.1	45	15	US-10-145-128A-50	Sequence 50, Appl
564	11.2	43.1	36	9	US-09-887-880-26	Sequence 26, Appl	c 637	11.2	43.1	45	15	US-10-017-191A-50	Sequence 50, Appl
565	11.2	43.1	36	9	US-09-887-880-29	Sequence 29, Appl	c 638	11.2	43.1	45	15	US-10-143-029A-50	Sequence 50, Appl
566	11.2	43.1	36	9	US-09-887-880-30	Sequence 30, Appl	c 639	11.2	43.1	45	15	US-10-143-028A-50	Sequence 50, Appl
567	11.2	43.1	37	15	US-10-267-217-21	Sequence 21, Appl	c 640	11.2	43.1	45	15	US-10-145-089A-50	Sequence 50, Appl
568	11.2	43.1	38	9	US-09-874-389-14	Sequence 14, Appl	c 641	11.2	43.1	45	15	US-10-165-067A-50	Sequence 50, Appl
569	11.2	43.1	38	9	US-09-874-389-15	Sequence 15, Appl	c 642	11.2	43.1	45	15	US-10-145-017A-50	Sequence 50, Appl
570	11.2	43.1	38	10	US-09-921-650-14	Sequence 14, Appl	c 643	11.2	43.1	45	15	US-10-164-728A-50	Sequence 50, Appl
571	11.2	43.1	38	10	US-09-921-650-15	Sequence 15, Appl	c 644	11.2	43.1	45	15	US-10-013-926A-50	Sequence 50, Appl
572	11.2	43.1	38	11	US-09-241-347-14	Sequence 14, Appl	c 645	11.2	43.1	45	15	US-10-165-247A-50	Sequence 50, Appl
573	11.2	43.1	38	11	US-09-241-347-15	Sequence 15, Appl	c 646	11.2	43.1	45	15	US-10-145-124A-50	Sequence 50, Appl
574	11.2	43.1	38	14	US-10-032-393-66	Sequence 66, Appl	c 647	11.2	43.1	45	15	US-10-160-502A-50	Sequence 50, Appl
575	11.2	43.1	38	15	US-10-301-516-11	Sequence 11, Appl	c 648	11.2	43.1	45	15	US-10-145-087A-50	Sequence 50, Appl
576	11.2	43.1	38	15	US-10-301-516-12	Sequence 12, Appl	c 649	11.2	43.1	45	15	US-10-017-086A-50	Sequence 50, Appl
577	11.2	43.1	38	15	US-10-326-671-55	Sequence 55, Appl	c 650	11.2	43.1	45	15	US-10-164-829A-50	Sequence 50, Appl
578	11.2	43.1	40	9	US-09-245-802-6	Sequence 6, Appli	c 651	11.2	43.1	45	15	US-10-164-929A-50	Sequence 50, Appl
579	11.2	43.1	40	9	US-09-245-802-55	Sequence 55, Appl	c 652	11.2	43.1	45	15	US-10-013-922A-50	Sequence 50, Appl
580	11.2	43.1	40	9	US-09-887-880-23	Sequence 23, Appl	c 653	11.2	43.1	45	15	US-10-020-445A-50	Sequence 50, Appl
581	11.2	43.1	40	9	US-09-887-880-27	Sequence 27, Appl	c 654	11.2	43.1	45	15	US-10-013-924A-50	Sequence 50, Appl
582	11.2	43.1	41	16	US-10-035-833A-3207	Sequence 3207, Ap	c 655	11.2	43.1	45	15	US-10-017-084A-50	Sequence 50, Appl
583	11.2	43.1	42	9	US-09-929-962-2	Sequence 2, Appli	c 656	11.2	43.1	45	15	US-10-145-016A-50	Sequence 50, Appl
584	11.2	43.1	42	9	US-10-210-747-2	Sequence 2, Appli	c 657	11.2	43.1	45	15	US-10-145-088A-50	Sequence 50, Appl
585	11.2	43.1	42	14	US-10-171-452A-6	Sequence 6, Appli	c 658	11.2	43.1	45	15	US-10-145-092A-50	Sequence 50, Appl
586	11.2	43.1	42	15	US-10-300-068-2	Sequence 2, Appli	c 659	11.2	43.1	45	15	US-10-145-129A-50	Sequence 50, Appl
587	11.2	43.1	42	15	US-10-353-708-6	Sequence 6, Appli	c 660	11.2	43.1	45	15	US-10-165-038A-50	Sequence 50, Appl
588	11.2	43.1	42	17	US-10-731-984-40	Sequence 40, Appl	c 661	11.2	43.1	45	15	US-10-165-353A-50	Sequence 50, Appl
589	11.2	43.1	43	15	US-10-032-585-1841	Sequence 1841, Ap	c 662	11.2	43.1	45	15	US-10-167-600-50	Sequence 50, Appl
590	11.2	43.1	43	15	US-09-887-880-28	Sequence 28, Appl	c 663	11.2	43.1	45	15	US-10-170-481A-50	Sequence 50, Appl
591	11.2	43.1	44	9	US-10-300-369-18	Sequence 18, Appl	c 664	11.2	43.1	45	15	US-10-172-039A-50	Sequence 50, Appl
592	11.2	43.1	44	16	US-10-300-369-20	Sequence 20, Appl	c 665	11.2	43.1	45	15	US-10-210-028-50	Sequence 50, Appl
593	11.2	43.1	44	16	US-09-978-295A-50	Sequence 50, Appl	c 666	11.2	43.1	45	15	US-10-017-085A-50	Sequence 50, Appl
594	11.2	43.1	45	9	US-09-978-637-50	Sequence 50, Appl	c 667	11.2	43.1	45	15	US-10-013-916A-50	Sequence 50, Appl
595	11.2	43.1	45	9	US-09-978-637-50	Sequence 50, Appl	c 668	11.2	43.1	45	15	US-10-143-026B-50	Sequence 50, Appl
596	11.2	43.1	45	9	US-09-978-192A-50	Sequence 50, Appl	c 669	11.2	43.1	45	15	US-10-013-918A-50	Sequence 50, Appl

c 670	11.2	43.1	45	15	US-10-162-521A-50	Sequence 50, Appl	c 743	11	42.3	25	15	US-10-098-263B-73998	Sequence 73998, A
c 671	11.2	43.1	45	15	US-10-013-928A-50	Sequence 50, Appl	744	11	42.3	25	15	US-10-098-263B-76628	Sequence 76628, A
c 672	11.2	43.1	45	15	US-10-162-522A-50	Sequence 50, Appl	745	11	42.3	25	15	US-10-098-263B-83147	Sequence 83147, A
c 673	11.2	43.1	45	15	US-10-013-923A-50	Sequence 50, Appl	746	11	42.3	25	15	US-10-098-263B-86661	Sequence 86661, A
c 674	11.2	43.1	45	15	US-10-013-925A-50	Sequence 50, Appl	747	11	42.3	25	15	US-10-098-263B-86662	Sequence 86662, A
c 675	11.2	43.1	45	15	US-10-013-927A-50	Sequence 50, Appl	748	11	42.3	25	15	US-10-098-263B-88074	Sequence 88074, A
c 676	11.2	43.1	45	16	US-10-013-929A-50	Sequence 50, Appl	749	11	42.3	25	15	US-10-098-263B-88074	Sequence 88074, A
c 677	11.2	43.1	45	16	US-10-013-931A-50	Sequence 50, Appl	750	11	42.3	25	15	US-10-098-263B-90994	Sequence 90994, A
c 678	11.2	43.1	45	16	US-10-013-920A-50	Sequence 50, Appl	751	11	42.3	25	15	US-10-098-263B-93974	Sequence 93974, A
c 679	11.2	43.1	45	16	US-10-164-749A-50	Sequence 50, Appl	752	11	42.3	25	15	US-10-098-263B-105219	Sequence 105219, A
c 680	11.2	43.1	45	16	US-10-013-917A-50	Sequence 50, Appl	753	11	42.3	25	15	US-10-098-263B-105220	Sequence 105220, A
c 681	11.2	43.1	45	18	US-10-152-388B-50	Sequence 50, Appl	754	11	42.3	25	15	US-10-098-263B-107565	Sequence 107565, A
c 682	11.2	43.1	46	17	US-10-466-939B-10	Sequence 10, Appl	755	11	42.3	25	15	US-10-098-263B-108201	Sequence 108201, A
c 683	11.2	43.1	47	15	US-10-198-235-179	Sequence 179, Appl	756	11	42.3	25	15	US-10-098-263B-111737	Sequence 111737, A
c 684	11.2	43.1	47	16	US-10-349-143-65	Sequence 65, Appl	757	11	42.3	25	15	US-10-098-263B-115326	Sequence 115326, A
c 685	11.2	43.1	47	16	US-10-349-143-1443	Sequence 1443, Appl	758	11	42.3	25	15	US-10-098-263B-123583	Sequence 123583, A
c 686	11.2	43.1	48	9	US-09-788-209A-14	Sequence 14, Appl	759	11	42.3	25	15	US-10-098-263B-123584	Sequence 123584, A
c 687	11.2	43.1	48	10	US-09-938-439-14	Sequence 14, Appl	760	11	42.3	25	15	US-10-098-263B-125100	Sequence 125100, A
c 688	11.2	43.1	48	10	US-09-938-433-14	Sequence 14, Appl	761	11	42.3	25	15	US-10-098-263B-126225	Sequence 126225, A
c 689	11.2	43.1	48	16	US-10-466-641-22	Sequence 22, Appl	762	11	42.3	25	15	US-10-098-263B-129368	Sequence 129368, A
c 690	11.2	43.1	50	8	US-08-781-986A-2020	Sequence 2020, Appl	763	11	42.3	25	15	US-10-098-263B-129568	Sequence 129568, A
c 691	11.2	43.1	50	9	US-09-504-231A-2990	Sequence 2990, Appl	764	11	42.3	25	15	US-10-303-161-41	Sequence 41, Appl
c 692	11.2	43.1	50	9	US-09-504-231A-3044	Sequence 3044, Appl	765	11	42.3	25	15	US-10-303-118-41	Sequence 41, Appl
c 693	11.2	43.1	50	9	US-09-274-553D-2990	Sequence 2990, Appl	766	11	42.3	25	15	US-10-303-128-41	Sequence 41, Appl
c 694	11.2	43.1	50	9	US-09-274-553D-3044	Sequence 3044, Appl	767	11	42.3	25	15	US-10-303-134-41	Sequence 41, Appl
c 695	11.2	43.1	50	15	US-10-402-365-15	Sequence 15, Appl	768	11	42.3	25	15	US-10-303-162-41	Sequence 41, Appl
c 696	11.2	43.1	50	16	US-10-131-827-821	Sequence 821, Appl	769	11	42.3	25	15	US-10-084-839-3420	Sequence 3420, Appl
c 697	11.2	43.1	50	16	US-10-131-827-5618	Sequence 5618, Appl	770	11	42.3	25	17	US-10-735-419-41	Sequence 41, Appl
c 698	11.2	43.1	50	16	US-10-329-624-2020	Sequence 2020, Appl	771	11	42.3	25	18	US-10-820-536-41	Sequence 41, Appl
c 699	11	42.3	19	10	US-09-995-793A-51	Sequence 51, Appl	772	11	42.3	25	18	US-10-845-408-41	Sequence 41, Appl
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c 701	11	42.3	20	16	US-10-289-762-4777	Sequence 4777, Appl	774	11	42.3	25	18	US-10-846-219-41	Sequence 41, Appl
c 702	11	42.3	20	17	US-10-317-278-22	Sequence 22, Appl	775	11	42.3	26	13	US-10-051-481-1	Sequence 1, Appl
c 703	11	42.3	20	17	US-10-317-278-55	Sequence 55, Appl	776	11	42.3	27	13	US-10-037-677-13	Sequence 13, Appl
c 704	11	42.3	20	17	US-10-619-739-1366	Sequence 1366, Appl	777	11	42.3	27	15	US-10-291-634-8	Sequence 8, Appl
c 705	11	42.3	21	14	US-10-001-254-60	Sequence 60, Appl	778	11	42.3	27	15	US-10-099-322-280	Sequence 280, Appl
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c 710	11	42.3	24	10	US-09-940-185-933	Sequence 933, Appl	783	11	42.3	28	13	US-10-027-348-4	Sequence 4, Appl
c 711	11	42.3	24	10	US-09-940-185-2814	Sequence 2814, Appl	784	11	42.3	28	13	US-10-027-348-8	Sequence 8, Appl
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; CURRENT FILING DATE: 2002-08-08
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
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RESULT 6
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; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3516

Query Match      58.5%; Score 15.2; DB 14; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  7  TCGCAGATCGGTACCTCAAT 26
    ||||| ||||| ||||| ||||| |||||
Db  22  TCACAGACAGGTACCTCAAT 3

RESULT 7
US-10-215-112-6804/c
; Sequence 6804, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6804
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6804

Query Match      58.5%; Score 15.2; DB 14; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  7  TCGCAGATCGGTACCTCAAT 26
    ||||| ||||| ||||| ||||| |||||
Db  21  TCACAGACAGGTACCTCAAT 2

RESULT 8
US-10-215-112-6930/c
; Sequence 6930, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6930
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6930

Query Match      58.5%; Score 15.2; DB 14; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  7  TCGCAGATCGGTACCTCAAT 26
    ||||| ||||| ||||| ||||| |||||
Db  21  TCACAGACTCGGTACCTCAAT 2

RESULT 9
US-10-098-263B-27628/c
; Sequence 27628, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
```

; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-27628

Query Match 56.2%; Score 14.6; DB 15; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCTTTCCGAGATCGGTACTCT 23
DB 23 TCTTTCCGAGATCGGTACTCT 3

RESULT 10
US-10-215-112-6384/c
; Sequence 6384, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6384
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6384.

Query Match 55.4%; Score 14.4; DB 14; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.6e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCTTTCCGAGATCGGTACTCTAA 25
DB 24 GTCTTTCCGAGATCGGTACTCTGA 1

RESULT 11
US-10-098-263B-61172
; Sequence 61172, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61172
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-61172

Query Match 55.4%; Score 14.4; DB 15; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCGCAGATCGGTACTCT 22
DB 1 TCGTAGATCGGTACTCT 16

RESULT 12
US-09-884-465A-37/c
; Sequence 37, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-37

Query Match 55.4%; Score 14.4; DB 10; Length 40;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TCTTTCCGAGATCGGTACTCTCAAT 26
DB 37 TTTTCCAGATAGGTACTTCCAT 14

RESULT 13
US-10-215-112-5215/c
; Sequence 5215, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5215
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-5215

Query Match 54.6%; Score 14.2; DB 14; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 TCGCAGATCGGTACTCTCA 25
DB 19 TCACAGACAGGTACTCTCA 1

```

; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 42442
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-42442

Query Match      53.8%; Score 14; DB 15; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GTCTTTTCGAGATCGGTACTCT 23
Db 22 GTCGTTTCACAGGTCGGGAATCT 1

RESULT 17
US-10-098-263B-126762/c
; Sequence 126762, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 126762
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-126762

Query Match      53.8%; Score 14; DB 15; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGTCTTTTCGAGATCGGTACTCT 22
Db 23 CGTTTTCGACAGGTGTATCT 2

RESULT 18
US-10-170-097-998/c
; Sequence 998, Application US/10170097
; Publication No. US20030228582A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267

```

; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 998
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-482-145 : polymorphic base A or G
US-10-170-097-998

Query Match 53.8%; Score 14; DB 15; Length 47;
Best Local Similarity 70.8%; Pred. No. 7.3e+03;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACCTCAA 25
Db 43 GTCCTTCGAGATCGGTACCTCAA 20

RESULT 19

US-09-940-185-1626/c
; Sequence 1626, Application US/09940185
; Publication No. US2003009639A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1626
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-1626

Query Match 53.1%; Score 13.8; DB 10; Length 24;
Best Local Similarity 88.2%; Pred. No. 9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CAGATCGGTACCTCAAT 26
Db 22 CAGATCGGTACCTCAAT 6

RESULT 20

US-10-403-232-67/c
; Sequence 67, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: Patentin version 3.2

; SEQ ID NO 67
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-403-232-67

Query Match 53.1%; Score 13.8; DB 15; Length 32;
Best Local Similarity 88.2%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTCGCAGATCGGTACCT 22
Db 26 TTCGCAGCTTGGTACCT 10

RESULT 21

US-10-403-232-71/c
; Sequence 71, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 71
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-403-232-71

Query Match 53.1%; Score 13.8; DB 15; Length 32;
Best Local Similarity 88.2%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTCGCAGATCGGTACCT 22
Db 26 TTCGCAGCTTGGTACCT 10

RESULT 22

US-10-131-827-1645
; Sequence 1645, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 50661200120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1645
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-131-827-1645
; Sequence 1645, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 50661200120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1645
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-131-827-1645

Query Match 53.1%; Score 13.8; DB 16; Length 50;
Best Local Similarity 72.0%; Pred. No. 9.2e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GTCTTCGAGATCGGTACCTCAAT 26
Db 4 GTCTCAAGGGTATCGGTACCTCAAT 28

RESULT 23

US-10-215-112-3642/c

; Sequence 3642, Application US/10215112

; Publication No. US20030082596A1

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; TITLE OF INVENTION: Method of Genetic Analysis of Probes:

; FILE OF INVENTION: Test3

; FILE REFERENCE: 3119

; CURRENT APPLICATION NUMBER: US/10/215,112

; CURRENT FILING DATE: 2002-08-08

; NUMBER OF SEQ ID NOS: 14936

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3642

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-3642

Query Match 52.3%; Score 13.6; DB 14; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26

Db 22 TCACAGACAGTACCTCAAT 3

RESULT 24

US-09-965-101-41

; Sequence 41, Application US/09965101

; Publication No. US20040186067A1

; GENERAL INFORMATION:

; APPLICANT: Davis, Heather L.

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Schorr, Joachim

; APPLICANT: Wu, Tong

; TITLE OF INVENTION: Vectors and Methods for Immunization or

; FILE OF INVENTION: Therapeutic Protocols

; FILE REFERENCE: C1039/7057 (HCL/MAT)

; CURRENT APPLICATION NUMBER: US/09/965,101

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: US 09/082,649

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: US 60/047,233

; PRIOR FILING DATE: 1997-05-20

; PRIOR APPLICATION NUMBER: US 60/047,209

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 41

; LENGTH: 34

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic oligonucleotide

US-09-965-101-41

Query Match 52.3%; Score 13.6; DB 11; Length 34;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26

Db 10 TCGCAGATCGATACCAGGAT 29

RESULT 25

US-10-160-670A-5/c

; Sequence 5, Application US/10160670A

; Publication No. US20030224066A1

; GENERAL INFORMATION:

; APPLICANT: National Yang-Ming University

; APPLICANT: Wu, Rong-Tsun

; TITLE OF INVENTION: Polysaccharide Extract of Dioscorea Sp. and an Orally Active

; FILE OF INVENTION: Pharmaceutical Composition Comprising the Same

; FILE REFERENCE: 1111-4070

; CURRENT APPLICATION NUMBER: US/10/160,670A

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-160-670A-5

Query Match 51.5%; Score 13.4; DB 15; Length 24;

Best Local Similarity 73.9%; Pred. No. 1.4e+04;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGAGATCGGTACCTCA 24

Db 24 GTCTTTCGAGAGAGAACTTCA 2

RESULT 26

US-09-180-394-3/c

; Sequence 3, Application US/09180394

; Patent No. US20020115206A1

; GENERAL INFORMATION:

; APPLICANT: M. Sawada

; TITLE OF INVENTION: ESTABLISHED CELL LINE OF MICROGLIA

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Peter F. Corless

; STREET: Dikey, Bronstein, Roberts & Cushman, LLP 130 Water St.

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-4280

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/180,394

; FILING DATE: 1998-11-05

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP98/00949

; FILING DATE: 1998-03-05

; ATTORNEY/AGENT INFORMATION:

; NAME: Peter F. Corless

; REGISTRATION NUMBER: 33,860

; REFERENCE/DOCKET NUMBER: 1526-48781

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)-523-3400

; TELEFAX: (617)-523-6440

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

```
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
US-09-180-394-3

Query Match
Best Local Similarity 51.5%; Score 13.4; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACTTCA 24
Db 24 GTCCTTCGAGAGAGGAAGTCTCA 2

RESULT 27
US-09-848-986-3/c
; Sequence 3, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; FILE REFERENCE: Methods of Use Thereof
; CURRENT APPLICATION NUMBER: US/09/848,986
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/262321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-6 primer sense sequence
US-09-848-986-3

Query Match
Best Local Similarity 51.5%; Score 13.4; DB 10; Length 25;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACTTCA 24
Db 24 GTCCTTCGAGAGAGGAAGTCTCA 2

RESULT 28
US-10-098-263B-80455/c
; Sequence 80455, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 80455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-80455

Query Match
51.5%; Score 13.4; DB 15; Length 25;
```

```
Best Local Similarity 73.9%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTCGAGATCGGTACTTCTC 23
Db 23 CGTCTTCCAGATCGGGTCTCTC 1

RESULT 29
US-10-233-121A-3/c
; Sequence 3, Application US/10233121A
; Publication No. US20030125284A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, EVAL
; APPLICANT: LOIS, AUGUSTO
; APPLICANT: TAKABAYASHI, KENJI
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND
; FILE REFERENCE: UCAL-168DIV
; CURRENT APPLICATION NUMBER: US/10/233,121A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/848,986
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/262,321
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer oligonucleotide
US-10-233-121A-3

Query Match
Best Local Similarity 51.5%; Score 13.4; DB 15; Length 25;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACTTCA 24
Db 24 GTCCTTCGAGAGAGGAAGTCTCA 2

RESULT 30
US-10-602-234-3/c
; Sequence 3, Application US/10602234
; Publication No. US20040072346A1
; GENERAL INFORMATION:
; APPLICANT: M. Sawada
; TITLE OF INVENTION: ESTABLISHED CELL LINE OF MICROGLIA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Peter F. Corless
; STREET: Dike, Bronstein, Roberts & Cushman, LLP 130 Water St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-4280
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/602,234
; FILING DATE: 23-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/180,394
; FILING DATE: 1998-11-05
```



```
; APPLICATION NUMBER: PCT/JP98/00949
; FILING DATE: 1998-03-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Peter F. Corless
; REGISTRATION NUMBER: 33 860
; REFERENCE/DOCKET NUMBER: 1526-48781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-523-3400
; TELEFAX: (617)-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-602-234-3

Query Match          51.5%; Score 13.4; DB 16; Length 25;
Best Local Similarity 73.9%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2  GTCTTTCGAGATCGGTACCTCA 24
Db  24 GTCTTTCGAGAGAGAACTTCA 2

RESULT 31
US-9-875-228-31
; Sequence 31, Application US/09875228
; Patent No. US20020136707A1
; GENERAL INFORMATION:
; APPLICANT: Yu, D.
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
; FILE REFERENCE: 34802200900
; CURRENT APPLICATION NUMBER: US/09/875,228
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/127,834
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 60/076,545
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/054,523
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence is
; OTHER INFORMATION: produced synthetically.
US-9-875-228-31

Query Match          51.5%; Score 13.4; DB 9; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  12  GATCGGTACCTCAAT 26
Db  1  GATCGGTACCTCACT 15

RESULT 32
US-09-989-339-15
; Sequence 15, Application US/09989339
; Publication No. US2003008886A1
; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl
; APPLICANT: Famodu, Layo
; APPLICANT: Rafalski, Jan A.
; APPLICANT: Ramaker, Michael
; APPLICANT: Tarczynski, Mitchell C.
; APPLICANT: Thorpe, Catherine
; TITLE OF INVENTION: PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE
; FILE REFERENCE: BB-1067-B
; CURRENT APPLICATION NUMBER: US/09/989,339
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 08/703,829
; PRIOR FILING DATE: 1996-08-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-989-339-15

Query Match          51.5%; Score 13.4; DB 10; Length 31;
Best Local Similarity 93.3%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  12  GATCGGTACCTCAAT 26
Db  1  GATCGGTACCTCACT 15

RESULT 33
US-10-295-798-20
; Sequence 20, Application US/10295798
; Publication No. US20030162225A1
; GENERAL INFORMATION:
; APPLICANT: Isis Innovation Ltd
; APPLICANT: James, William Siward
; APPLICANT: Hope, James
; APPLICANT: Tahiri-Alaoui, Abdesamad
; TITLE OF INVENTION: Ligands Specific for an isoform of the prion protein
; FILE REFERENCE: KILBURN1130
; CURRENT APPLICATION NUMBER: US/10/295,798
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: PCT/GB01/02228
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: GB 0012054.3
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 20
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Aptamer
US-10-295-798-20

Query Match          51.5%; Score 13.4; DB 15; Length 48;
Best Local Similarity 52.2%; Pred. No. 1.4e+04;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy  4  CTTTCGAGATCGGTACCTCAAT 26
Db  6  CUAGCGCACAGCGUACCUU 28

RESULT 34
US-10-215-112-5216/c
; Sequence 5216, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5216
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-5216

Query Match      50.8%; Score 13.2; DB 14; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 TCGCAGATCGGTACCTCA 24
    ||||| ||||| |||||
DB 18 TCACAGACAGGTACCTCA 1

RESULT 35
US-10-098-263B-86304/c
; Sequence 86304, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86304
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-86304

Query Match      50.8%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 TCGCAGATCGGTACCTCA 24
    ||||| ||||| |||||
DB 22 TCGCAGATCGTTCTCTAA 5

RESULT 36
US-10-098-263B-121702/c
; Sequence 121702, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121702
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-121702
```

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Query Match      50.8%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 CTTTCGCAGATCGGTACC 21
    ||||| ||||| |||||
DB 23 CTTTCGTAGATGGTCCC 6

RESULT 37
US-10-098-263B-128873/c
; Sequence 128873, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 128873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-128873

Query Match      50.8%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 TCGCAGATCGGTACCTCA 24
    ||||| ||||| |||||
DB 18 TCACAGACAGGTACCTCA 1

RESULT 38
US-09-729-821-13
; Sequence 13, Application US/09729821
; Publication No. US20020069430A1
; GENERAL INFORMATION:
; APPLICANT: KISAKA, HIROAKI
; APPLICANT: KIDA, TAKAO
; TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC PLANTS HAVING IMPROVED AMINO ACID
; TITLE OF INVENTION: COMPOSITION
; FILE REFERENCE: 200496USO
; CURRENT APPLICATION NUMBER: US/09/729,821
; CURRENT FILING DATE: 2000-12-06
; PRIOR FILING DATE: JP 11-376719
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-729-821-13

Query Match      50.8%; Score 13.2; DB 9; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 GCAGATCGGTACCTCAAT 26
    ||||| ||||| |||||
DB 3 GCAGATGGCTTCCTCAAT 20

RESULT 39
```

US-09-729-821-19
; Sequence 19, Application US/09729821
; Publication No. US20020069430A1
; GENERAL INFORMATION:
; APPLICANT: KISAKA, HIROAKI
; APPLICANT: KIDA, TAKAO
; TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC PLANTS HAVING IMPROVED AMINO ACID
; TITLE OF INVENTION: COMPOSITION
; FILE REFERENCE: 200496USO
; CURRENT APPLICATION NUMBER: US/09/729,821
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11-376719
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-729-821-19

Query Match 50.8%; Score 13.2; DB 9; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GCAGATCGGTACCTCAAT 26
|||||
Db 3 GCAGATGGCTTCCTCAAT 20

RESULT 40
US-09-729-821-13
; Sequence 13, Application US/09729821
; Publication No. US20040093647A9
; GENERAL INFORMATION:
; APPLICANT: KISAKA, HIROAKI
; APPLICANT: KIDA, TAKAO
; TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC PLANTS HAVING IMPROVED AMINO ACID
; TITLE OF INVENTION: COMPOSITION
; FILE REFERENCE: 200496USO
; CURRENT APPLICATION NUMBER: US/09/729,821
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11-376719
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-729-821-13

Query Match 50.8%; Score 13.2; DB 11; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GCAGATCGGTACCTCAAT 26
|||||
Db 3 GCAGATGGCTTCCTCAAT 20

Search completed: November 24, 2004, 03:43:00
Job time : 131.018 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1246.54 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-8

Perfect score: 26

Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	55.4	35	8	A2959628
2	13.8	53.1	44	8	B2289495
3	13.8	53.1	49	9	TA58C07Q
4	13.8	53.1	50	7	CN921174
5	13.6	52.3	50	1	AU105805
6	13.6	52.3	50	1	AU107934
7	13.4	51.5	37	9	TA344B09Q
8	13.2	50.8	49	8	BH642496
9	13	50.0	39	9	TA60E09Q
10	12.8	49.2	27	8	A2838579
11	12.8	49.2	43	9	EX891607
12	12.8	49.2	44	8	A4868626
13	12.8	49.2	45	8	BH628960
14	12.8	49.2	49	8	BH846331
15	12.4	47.7	34	1	AA972865
16	12.4	47.7	39	9	CR360589
17	12.4	47.7	49	6	CA935542
18	12.4	47.7	50	1	AU105437
19	12.2	46.9	22	9	AJ590848
20	12.2	46.9	43	1	AV847149
21	12.2	46.9	45	9	AL766296
22	12	46.2	26	8	AZ955231
23	12	46.2	28	7	CN973502
24	12	46.2	37	9	TA383E12Q

42	8	BH796117	46.2	12	25	c
43	8	AZ778700	46.2	12	26	c
44	8	BZ664508	46.2	27	27	c
45	9	CL521995	46.2	28	28	c
46	9	CL521997	46.2	29	29	c
47	8	AZ462540	46.2	30	30	c
48	8	AJ594944	46.2	31	31	c
49	8	AZ805662	46.2	32	32	c
50	8	AZ803827	46.2	33	33	c
51	8	AZ797143	46.2	34	34	c
52	8	AZ942892	46.2	35	35	c
53	8	CL655958	46.2	36	36	c
54	8	AZ810604	46.2	37	37	c
55	8	AZ803114	46.2	38	38	c
56	8	AZ805718	46.2	39	39	c
57	8	AZ810670	46.2	40	40	c
58	8	AZ799177	46.2	41	41	c
59	8	EX660365	46.2	42	42	c
60	8	BH853770	46.2	43	43	c
61	8	AL756145	46.2	44	44	c
62	8	BJ076662	46.2	45	45	c
63	7	CF640952	46.2	46	46	c
64	8	BZ357881	46.2	47	47	c
65	8	AZ832586	46.2	48	48	c
66	8	AJ587854	46.2	49	49	c
67	8	AJ590199	46.2	50	50	c
68	8	CC797215	46.2	51	51	c
69	8	AZ832536	46.2	52	52	c
70	8	AU105218	46.2	53	53	c
71	8	CG711750	46.2	54	54	c
72	8	AL757862	46.2	55	55	c
73	8	AJ622556	46.2	56	56	c
74	8	BH908374	46.2	57	57	c
75	8	BZ663584	46.2	58	58	c
76	8	BZ663743	46.2	59	59	c
77	8	AI496013	46.2	60	60	c
78	8	AU102560	46.2	61	61	c
79	8	CG711504	46.2	62	62	c
80	8	CG711504	46.2	63	63	c
81	8	CG711726	46.2	64	64	c
82	8	AA863634	46.2	65	65	c
83	8	AZ493301	46.2	66	66	c
84	8	CG712020	46.2	67	67	c
85	8	AA920462	46.2	68	68	c
86	8	BH905344	46.2	69	69	c
87	8	AZ760019	46.2	70	70	c
88	8	TA244H01Q	46.2	71	71	c
89	8	CG711529	46.2	72	72	c
90	8	CG711601	46.2	73	73	c
91	8	CG711666	46.2	74	74	c
92	8	CG711701	46.2	75	75	c
93	8	CL528762	46.2	76	76	c
94	8	CG711830	46.2	77	77	c
95	8	CG711947	46.2	78	78	c
96	8	CG714964	46.2	79	79	c
97	8	CG707426	46.2	80	80	c
98	8	CG711504	46.2	81	81	c
99	8	CG711778	46.2	82	82	c
100	8	CG711843	46.2	83	83	c
101	8	AZ480323	46.2	84	84	c
102	8	AL765906	46.2	85	85	c
103	8	CL438939	46.2	86	86	c
104	8	CG711375	46.2	87	87	c
105	8	AU104333	46.2	88	88	c
106	8	AU104948	46.2	89	89	c
107	8	AU106028	46.2	90	90	c
108	8	AU107971	46.2	91	91	c
109	8	AQ025638	46.2	92	92	c
110	8	AQ025638	46.2	93	93	c
111	8	BX661901	46.2	94	94	c
112	8	CR230947	46.2	95	95	c
113	8	CG711462	46.2	96	96	c
114	8	CG712042	46.2	97	97	c

c 98	11.2	43.1	22	9	AJ591018	Arabidops	AJ591018	Arabidops	c 171	10.8	41.5	36	1	AU257681	AU257681
c 99	11.2	43.1	26	8	CC459557	SALK_1304	CC459557	SALK_1304	c 172	10.8	41.5	37	1	AI876199	uJ59b06.y
c 100	11.2	43.1	32	8	CC454447	CC454447	CC454447	CC454447	c 173	10.8	41.5	37	8	BZ354507	SALK_1252
c 101	11.2	43.1	34	1	AA706263	AGS2028-0	AA706263	AGS2028-0	c 174	10.8	41.5	37	8	BZ382343	SALK_1181
c 102	11.2	43.1	35	1	AV954369	AV954369	AV954369	AV954369	c 175	10.8	41.5	37	8	BZ382741	SALK_1187
c 103	11.2	43.1	35	8	BH863096	BH863096	BH863096	SALK_0931	c 176	10.8	41.5	38	8	BZ382108	SALK_1178
c 104	11.2	43.1	36	9	ALJ94446	Arabidops	ALJ94446	Arabidops	c 177	10.8	41.5	38	8	BZ382870	SALK_1190
c 105	11.2	43.1	37	2	AW245295	AW245295	AW245295	28S0036.3	c 178	10.8	41.5	38	9	CC795484	SALK_0809
c 106	11.2	43.1	38	6	CB884322	CB884322	CB884322	ES700153	c 179	10.8	41.5	39	2	BE512831	601171854
c 107	11.2	43.1	38	9	CG706098	CG706098	CG706098	01S0651-0	c 180	10.8	41.5	39	6	CF331123	NACL--07-
c 108	11.2	43.1	41	9	DME547050	DME547050	DME547050	Drosophil	c 181	10.8	41.5	39	9	AL942107	Arabidops
c 109	11.2	43.1	42	5	BQ589344	BQ589344	BQ589344	S014008-0	c 182	10.8	41.5	40	7	W78594	me85e07.r1
c 110	11.2	43.1	43	1	AA986127	AA986127	AA986127	uc82a05.x	c 183	10.8	41.5	40	8	BH608730	BH608730
c 111	11.2	43.1	45	1	AA449195	AA449195	AA449195	zx33910.r	c 184	10.8	41.5	40	8	BZ769399	SALK_1421
c 112	11.2	43.1	45	8	AL755968	AL755968	AL755968	Arabidops	c 185	10.8	41.5	41	4	BG284664	602408844
c 113	11.2	43.1	45	9	AL757297	AL757297	AL757297	Arabidops	c 186	10.8	41.5	41	4	BJ031143	BJ031143
c 114	11.2	43.1	49	9	AL757297	AL757297	AL757297	Arabidops	c 187	10.8	41.5	43	1	AA734820	YP38402.r
c 115	11.2	43.1	50	1	AA210000	AA210000	AA210000	mu39c03.r	c 188	10.8	41.5	43	1	AI364988	ct21g10.x
c 116	11.2	43.1	50	1	AU105834	AU105834	AU105834	AU105834	c 189	10.8	41.5	43	8	BZ591170	35901.82
c 117	11.2	43.1	50	1	AU107495	AU107495	AU107495	AU107495	c 190	10.8	41.5	43	2	BE267956	601125354
c 118	11.2	43.1	50	1	AU107495	AU107495	AU107495	AU107495	c 191	10.8	41.5	45	2	BE513871	601345809
c 119	11.2	43.1	50	1	AU107497	AU107497	AU107497	AU107497	c 192	10.8	41.5	45	2	BE560611	601345809
c 120	11.2	43.1	50	1	AU107502	AU107502	AU107502	AU107502	c 193	10.8	41.5	46	2	BE267872	601125422
c 121	11.2	43.1	50	8	BH789191	BH789191	BH789191	SALK_0009	c 194	10.8	41.5	47	2	BE270087	601185780
c 122	11.2	43.1	50	8	BH905738	BH905738	BH905738	SALK_1076	c 195	10.8	41.5	47	2	BE259594	601174272
c 123	11.2	43.1	26	8	CC060035	CC060035	CC060035	EX06009.3	c 196	10.8	41.5	47	2	BE513247	6013455302
c 124	11.2	43.1	30	8	AZ782713	AZ782713	AZ782713	2M0033M21	c 197	10.8	41.5	47	2	BE513247	6013455302
c 125	11.2	43.1	32	9	TA6C01Q	TA6C01Q	TA6C01Q	1M0553102	c 198	10.8	41.5	48	5	EX569233	EX569233
c 126	11.2	43.1	34	9	AO254734	AO254734	AO254734	EP(3)3554	c 199	10.8	41.5	48	8	AO25076	EP(3)0408
c 127	11.2	43.1	35	8	CR405222	CR405222	CR405222	Arabidops	c 200	10.8	41.5	49	2	BF055829	7174403.y
c 128	11.2	43.1	36	9	BQ595099	BQ595099	BQ595099	E012711-0	c 201	10.8	41.5	49	2	BF055829	7174403.y
c 129	11.2	43.1	37	6	CB724584	CB724584	CB724584	EST0401.R	c 202	10.8	41.5	49	4	BF055829	7174403.y
c 130	11.2	43.1	37	8	AZ6640839	AZ6640839	AZ6640839	1M0503105	c 203	10.8	41.5	49	6	CF099786	rd77Q06.y
c 131	11.2	43.1	39	8	CC458595	CC458595	CC458595	SALK_1201	c 204	10.8	41.5	49	8	T47207	YB53911.r1
c 132	11.2	43.1	39	8	BX656234	BX656234	BX656234	Arabidops	c 205	10.8	41.5	49	8	AZ619548	AZ619548
c 133	11.2	43.1	40	8	BH905777	BH905777	BH905777	SALK_1077	c 206	10.8	41.5	50	1	AU103380	AU103380
c 134	11.2	43.1	40	9	EX133759	EX133759	EX133759	Danio rer	c 207	10.8	41.5	50	1	AU104588	AU104588
c 135	11.2	43.1	40	9	EX133759	EX133759	EX133759	Danio rer	c 208	10.8	41.5	50	1	AU105397	AU105397
c 136	11.2	43.1	41	8	AZ798444	AZ798444	AZ798444	2M0055G15	c 209	10.8	41.5	50	1	AU105399	AU105399
c 137	11.2	43.1	41	8	AA502093	AA502093	AA502093	9g72107.s	c 210	10.8	41.5	50	1	AU105400	AU105400
c 138	11.2	43.1	43	1	AL756491	AL756491	AL756491	Arabidops	c 211	10.8	41.5	50	1	AU105402	AU105402
c 139	11.2	43.1	44	9	AL760705	AL760705	AL760705	Arabidops	c 212	10.8	41.5	50	1	BH903773	SALK_1033
c 140	11.2	43.1	44	9	AL760705	AL760705	AL760705	Arabidops	c 213	10.8	41.5	50	1	CG710737	CG710737
c 141	11.2	43.1	45	2	BE251857	BE251857	BE251857	601115885	c 214	10.8	41.5	50	9	CG722042	1119070B0
c 142	11.2	43.1	46	1	AV851679	AV851679	AV851679	ag89h06.r	c 215	10.8	41.5	50	9	CG722042	1119070B0
c 143	11.2	43.1	46	1	AV851679	AV851679	AV851679	ag89h06.r	c 216	10.8	41.5	50	9	AJ799595	AJ799595
c 144	11.2	43.1	46	8	BH798621	BH798621	BH798621	1008121E0	c 217	10.6	40.8	30	7	T61480	Yc06a06.r1
c 145	11.2	43.1	48	8	AZ308119	AZ308119	AZ308119	1M0010L13	c 218	10.6	40.8	30	9	AJ622413	Drosophil
c 146	11.2	43.1	49	8	AZ596631	AZ596631	AZ596631	1M0410F06	c 219	10.6	40.8	31	9	AL938308	AL938308
c 147	11.2	43.1	49	8	CC886568	CC886568	CC886568	SALK_1487	c 220	10.6	40.8	34	1	AL932495	AL932495
c 148	11.2	43.1	50	1	AU105215	AU105215	AU105215	AU105215	c 221	10.6	40.8	34	1	AL472306	AL472306
c 149	11.2	43.1	50	4	BI416961	BI416961	BI416961	hasp002XP	c 222	10.6	40.8	35	8	BH865745	BH865745
c 150	11.2	43.1	50	5	BQ479330	BQ479330	BQ479330	ku33a12.y	c 223	10.6	40.8	35	9	CL675637	CL675637
c 151	11.2	43.1	50	9	EX208307	EX208307	EX208307	Danio rer	c 224	10.6	40.8	37	2	BF794126	BF794126
c 152	10.8	41.5	24	1	AJ671616	AJ671616	AJ671616	AJ671616	c 225	10.6	40.8	37	8	BH792052	BH792052
c 153	10.8	41.5	25	7	BZ295389	BZ295389	BZ295389	SALK_0869	c 226	10.6	40.8	38	9	TA753738	TA753738
c 154	10.8	41.5	25	9	TA379F07Q	TA379F07Q	TA379F07Q	T. brucei	c 227	10.6	40.8	38	9	CR359706	CR359706
c 155	10.8	41.5	29	8	CC057376	CC057376	CC057376	SALK_1410	c 228	10.6	40.8	39	9	TA274G03Q	TA274G03Q
c 156	10.8	41.5	30	4	BN398771	BN398771	BN398771	SALK_0083	c 229	10.6	40.8	40	1	AA864982	AA864982
c 157	10.8	41.5	30	8	BH846479	BH846479	BH846479	SALK_0083	c 230	10.6	40.8	40	9	CL459283	CL459283
c 158	10.8	41.5	30	6	C01612	C01612	C01612	yb01f01.s1	c 231	10.6	40.8	41	9	AZ442277	IM0234P20
c 159	10.8	41.5	31	7	T48676	T48676	T48676	yb01f01.s1	c 232	10.6	40.8	41	9	TA26A10P	TA26A10P
c 160	10.8	41.5	31	8	AZ773758	AZ773758	AZ773758	2M0001N22	c 233	10.6	40.8	42	8	AZ344566	AZ344566
c 161	10.8	41.5	31	8	BH847453	BH847453	BH847453	SALK_0544	c 234	10.6	40.8	44	8	BH902418	BH902418
c 162	10.8	41.5	31	8	BH847728	BH847728	BH847728	SALK_0559	c 235	10.6	40.8	45	9	AX534920	AX534920
c 163	10.8	41.5	31	8	BH847760	BH847760	BH847760	SALK_0564	c 236	10.6	40.8	46	1	AA884752	AA884752
c 164	10.8	41.5	31	8	BH847765	BH847765	BH847765	SALK_0564	c 237	10.6	40.8	46	1	AA884752	AA884752
c 165	10.8	41.5	32	8	BH847765	BH847765	BH847765	SALK_0564	c 238	10.6	40.8	46	1	AA884752	AA884752
c 166	10.8	41.5	32	8	BH847765	BH847765	BH847765	SALK_0564	c 239	10.6	40.8	47	1	AA059894	AA059894
c 167	10.8	41.5	34	1	A1654467	A1654467	A1654467	tg91c04.x	c 240	10.6	40.8	47	1	AG204311	AG204311
c 168	10.8	41.5	34	1	BZ291138	BZ291138	BZ291138	SALK_1124	c 241	10.6	40.8	48	9	AX289740	AX289740
c 169	10.8	41.5	34	8	AZ839096	AZ839096	AZ839096	2M0135N03	c 242	10.6	40.8	48	9	AX289740	AX289740
c 170	10.8	41.5	35	8	AZ839096	AZ839096	AZ839096	2M0135N03	c 243	10.6	40.8	49	1	AV848976	AV848976

C 244	10.6	40.8	49	2	AW071297	AW071297 xa63f07.x	C 317	10.4	40.0	50	8	B287226	BZ87226	BZ87226	SALK_0205
C 245	10.6	40.8	50	1	AU103850	AU103850 AU103850	C 318	10.4	40.0	50	9	BX890678	BX890678	BX890678	ArabiDops
C 246	10.6	40.8	50	1	AU104951	AU104951 AU104951	C 319	10.2	39.2	19	8	AZ810607	AZ810607	AZ810607	2M0076D14
C 247	10.6	40.8	50	1	AU106027	AU106027 AU106027	C 320	10.2	39.2	19	8	AZ810643	AZ810643	AZ810643	2M0076L16
C 248	10.6	40.8	50	1	AU106644	AU106644 AU106644	C 321	10.2	39.2	20	8	AZ816645	AZ816645	AZ816645	1M0115N07
C 249	10.6	40.8	50	1	AU106645	AU106645 AU106645	C 322	10.2	39.2	20	8	AZ807939	AZ807939	AZ807939	2M0071F07
C 250	10.6	40.8	50	1	AU107510	AU107510 AU107510	C 323	10.2	39.2	20	8	AZ817227	AZ817227	AZ817227	2M0086P21
C 251	10.6	40.8	50	1	AU107510	AU107510 AU107510	C 324	10.2	39.2	20	8	AZ822119	AZ822119	AZ822119	2M0095M03
C 252	10.6	40.8	50	8	AQ073822	EP(3)3211	C 325	10.2	39.2	21	8	AZ303723	AZ303723	AZ303723	1M003001
C 253	10.6	40.8	50	9	AZ944956	2M020611-1	C 326	10.2	39.2	21	8	AZ471445	AZ471445	AZ471445	1M0286K01
C 254	10.4	40.0	21	8	AZ360212	1M0103K04	C 327	10.2	39.2	21	8	AZ828796	AZ828796	AZ828796	2M0106G04
C 255	10.4	40.0	28	6	CF321235	HD--12-G1	C 328	10.2	39.2	21	8	AZ828796	AZ828796	AZ828796	2M0106G04
C 256	10.4	40.0	30	8	BZ765015	SALK_1278	C 329	10.2	39.2	22	8	AZ799125	AZ799125	AZ799125	2M0056N17
C 257	10.4	40.0	31	8	BZ357533	SALK_1308	C 330	10.2	39.2	22	8	AZ807377	AZ807377	AZ807377	2M0070L11
C 258	10.4	40.0	31	8	BZ357535	SALK_1308	C 331	10.2	39.2	22	8	AZ808061	AZ808061	AZ808061	2M0071D23
C 259	10.4	40.0	32	9	CL519910	SAI7E10 F	C 332	10.2	39.2	22	8	AZ808062	AZ808062	AZ808062	2M0071D24
C 260	10.4	40.0	32	9	AG188480	Pan trogl	C 333	10.2	39.2	22	8	AZ813858	AZ813858	AZ813858	2M0081P21
C 261	10.4	40.0	33	7	D25860	HUMGS04237	C 334	10.2	39.2	22	8	AZ830066	AZ830066	AZ830066	2M0109M06
C 262	10.4	40.0	33	9	AG202038	Pan trogl	C 335	10.2	39.2	22	8	AZ832004	AZ832004	AZ832004	2M0112M04
C 263	10.4	40.0	34	1	AA967101	ua40c08.r	C 336	10.2	39.2	22	8	AZ832575	AZ832575	AZ832575	2M0113M01
C 264	10.4	40.0	34	1	AV845568	AV845568	C 337	10.2	39.2	22	8	AZ833754	AZ833754	AZ833754	2M0116L02
C 265	10.4	40.0	34	8	BH857135	BH857135 SALK_0766	C 338	10.2	39.2	22	8	AZ833507	AZ833507	AZ833507	2M0129C10
C 266	10.4	40.0	37	1	AI647510	uk40e11.x	C 339	10.2	39.2	23	8	AZ806754	AZ806754	AZ806754	2M0069G05
C 267	10.4	40.0	37	5	B0587909	E012339-0	C 340	10.2	39.2	23	8	AZ808048	AZ808048	AZ808048	2M0071D13
C 268	10.4	40.0	38	8	BH905215	SALK_1057	C 341	10.2	39.2	23	8	AZ808766	AZ808766	AZ808766	2M0072021
C 269	10.4	40.0	39	8	CC053623	SALK_0458	C 342	10.2	39.2	23	8	AZ810539	AZ810539	AZ810539	2M0076D12
C 270	10.4	40.0	40	1	AA631276	mq92c01.s	C 343	10.2	39.2	23	8	AZ822128	AZ822128	AZ822128	2M0095O02
C 271	10.4	40.0	40	8	AZ311244	1M0026N06	C 344	10.2	39.2	23	8	AZ822132	AZ822132	AZ822132	2M0095P01
C 272	10.4	40.0	40	9	AB082694	Drosophi1	C 345	10.2	39.2	24	8	AZ825913	AZ825913	AZ825913	2M0101B22
C 273	10.4	40.0	41	4	BJ034814	BJ034814	C 346	10.2	39.2	24	8	AZ946318	AZ946318	AZ946318	2M0208N02
C 274	10.4	40.0	41	9	AL754611	ArabiDops	C 347	10.2	39.2	24	8	AZ946318	AZ946318	AZ946318	2M0208N02
C 275	10.4	40.0	42	1	AA627436	mq47h01.s	C 348	10.2	39.2	25	8	AZ341661	AZ341661	AZ341661	2M0280K02
C 276	10.4	40.0	42	8	BH865278	SALK_0980	C 349	10.2	39.2	25	8	AZ807384	AZ807384	AZ807384	2M0070N09
C 277	10.4	40.0	43	6	CF308230	ABF--01-P	C 350	10.2	39.2	25	8	AZ817162	AZ817162	AZ817162	2M0086N14
C 278	10.4	40.0	43	8	CL183341	XE744 Bay	C 351	10.2	39.2	25	8	AZ832533	AZ832533	AZ832533	2M0113E02
C 279	10.4	40.0	44	9	AL756121	ArabiDops	C 352	10.2	39.2	25	8	AZ988387	AZ988387	AZ988387	2M0271P13
C 280	10.4	40.0	45	9	CL439197	CL439197 PST8831-N	C 353	10.2	39.2	25	8	AZ998374	AZ998374	AZ998374	2M0285117
C 281	10.4	40.0	46	7	R13482	YF77901.r1	C 354	10.2	39.2	26	8	AZ308315	AZ308315	AZ308315	1M0011L08
C 282	10.4	40.0	46	7	W99234	W99234 mf39c11.r1	C 355	10.2	39.2	26	8	AZ790537	AZ790537	AZ790537	2M0039B07
C 283	10.4	40.0	47	4	B1835227	B1835227 603089126	C 356	10.2	39.2	26	8	AZ809250	AZ809250	AZ809250	2M0073J08
C 284	10.4	40.0	48	8	BH757340	SALK_0560	C 357	10.2	39.2	26	8	AZ810543	AZ810543	AZ810543	2M0076F07
C 285	10.4	40.0	48	8	BH813146	BH813146 SALK_0637	C 358	10.2	39.2	26	8	AZ830220	AZ830220	AZ830220	2M0109N18
C 286	10.4	40.0	49	4	BM281964	ki23e08.y	C 359	10.2	39.2	26	8	AZ832614	AZ832614	AZ832614	2M0113K18
C 287	10.4	40.0	49	8	AZ438829	1M0229B10	C 360	10.2	39.2	26	8	AZ832633	AZ832633	AZ832633	2M0113Q14
C 288	10.4	40.0	49	8	BH626011	1007110F0	C 361	10.2	39.2	26	8	AZ866540	AZ866540	AZ866540	2M0177M03
C 289	10.4	40.0	49	9	CL528213	CL528213 EY10202-3	C 362	10.2	39.2	26	8	AZ957509	AZ957509	AZ957509	2M0224119
C 290	10.4	40.0	49	9	CL705938	EY08057-3	C 363	10.2	39.2	26	8	AZ809250	AZ809250	AZ809250	2M0073J08
C 291	10.4	40.0	50	1	AU102580	AU102580	C 364	10.2	39.2	26	8	AZ810543	AZ810543	AZ810543	2M0076F07
C 292	10.4	40.0	50	1	AU102861	AU102861	C 365	10.2	39.2	26	8	AZ830220	AZ830220	AZ830220	2M0109N18
C 293	10.4	40.0	50	1	AU104159	AU104159	C 366	10.2	39.2	26	8	AZ832614	AZ832614	AZ832614	2M0113K18
C 294	10.4	40.0	50	1	AU104160	AU104160	C 367	10.2	39.2	26	8	AZ832633	AZ832633	AZ832633	2M0113Q14
C 295	10.4	40.0	50	1	AU105806	AU105806	C 368	10.2	39.2	26	8	AZ866540	AZ866540	AZ866540	2M0177M03
C 296	10.4	40.0	50	1	AU105807	AU105807	C 369	10.2	39.2	26	8	AZ957509	AZ957509	AZ957509	2M0224119
C 297	10.4	40.0	50	1	AU105808	AU105808	C 370	10.2	39.2	26	8	AZ972389	AZ972389	AZ972389	2M0246B15
C 298	10.4	40.0	50	1	AU105809	AU105809	C 371	10.2	39.2	26	9	CL656519	CL656519	CL656519	PR101268
C 299	10.4	40.0	50	1	AU105810	AU105810	C 372	10.2	39.2	27	8	AZ313034	AZ313034	AZ313034	1M0029P09
C 300	10.4	40.0	50	1	AU105811	AU105811	C 373	10.2	39.2	27	8	AZ313131	AZ313131	AZ313131	1M0029B21
C 301	10.4	40.0	50	1	AU105812	AU105812	C 374	10.2	39.2	27	8	AZ791292	AZ791292	AZ791292	2M0041I07
C 302	10.4	40.0	50	1	AU105813	AU105813	C 375	10.2	39.2	27	8	AZ794515	AZ794515	AZ794515	2M0048O14
C 303	10.4	40.0	50	1	AU105814	AU105814	C 376	10.2	39.2	27	8	AZ795786	AZ795786	AZ795786	2M0051M10
C 304	10.4	40.0	50	1	AU105816	AU105816	C 377	10.2	39.2	27	8	AZ796535	AZ796535	AZ796535	2M0052M14
C 305	10.4	40.0	50	1	AU105817	AU105817	C 378	10.2	39.2	27	8	AZ799212	AZ799212	AZ799212	2M0056M17
C 306	10.4	40.0	50	1	AU105818	AU105818	C 379	10.2	39.2	27	8	AZ799549	AZ799549	AZ799549	2M0057P04
C 307	10.4	40.0	50	1	AU105819	AU105819	C 380	10.2	39.2	27	8	AZ799604	AZ799604	AZ799604	2M0057J07
C 308	10.4	40.0	50	1	AU105820	AU105820	C 381	10.2	39.2	27	8	AZ800386	AZ800386	AZ800386	2M0058C19
C 309	10.4	40.0	50	1	AU105821	AU105821	C 382	10.2	39.2	27	8	AZ801592	AZ801592	AZ801592	2M0060C08
C 310	10.4	40.0	50	1	AU105822	AU105822	C 383	10.2	39.2	27	8	AZ806789	AZ806789	AZ806789	2M0069N05
C 311	10.4	40.0	50	1	AU105824	AU105824	C 384	10.2	39.2	27	8	AZ808042	AZ808042	AZ808042	2M0071M17
C 312	10.4	40.0	50	1	AU105825	AU105825	C 385	10.2	39.2	27	8	AZ808073	AZ808073	AZ808073	2M0071H19
C 313	10.4	40.0	50	1	AU105826	AU105826	C 386	10.2	39.2	27	8	AZ810590	AZ810590	AZ810590	2M0076P07
C 314	10.4	40.0	50	1	AU107943	AU107943	C 387	10.2	39.2	27	8	AZ819504	AZ819504	AZ819504	2M0091K08
C 315	10.4	40.0	50	4	BM565712	BM565712	C 388	10.2	39.2	27	8	AZ820845	AZ820845	AZ820845	2M0093N17
C 316	10.4	40.0	50	6	CF292903	30DGS--01	C 389	10.2	39.2	27	8	AZ821277	AZ821277	AZ821277	2M0094A06

390	10.2	39.2	27	8	AZ826443	AZ826443	2M0102M09	463	10.2	39.2	29	8	AZ807973	AZ807973	2M0071M10
391	10.2	39.2	27	8	AZ832524	AZ832524	2M0113B03	464	10.2	39.2	29	8	AZ808472	AZ808472	2M0072H05
392	10.2	39.2	27	8	AZ833744	AZ833744	2M0116I05	465	10.2	39.2	29	8	AZ808587	AZ808587	2M0072M11
393	10.2	39.2	27	8	AZ833747	AZ833747	2M0133I11	466	10.2	39.2	29	8	AZ808606	AZ808606	2M0072P12
394	10.2	39.2	27	8	AZ833933	AZ833933	2M0135I22	467	10.2	39.2	29	8	AZ808768	AZ808768	2M0072O23
395	10.2	39.2	27	8	AZ847608	AZ847608	2M0148P13	468	10.2	39.2	29	8	AZ809230	AZ809230	2M0073F11
396	10.2	39.2	27	8	AZ868099	AZ868099	2M0179N07	469	10.2	39.2	29	8	AZ815939	AZ815939	2M0084O06
397	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	470	10.2	39.2	29	8	AZ822251	AZ822251	2M0095K17
398	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	471	10.2	39.2	29	8	AZ826392	AZ826392	2M0102O06
399	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	472	10.2	39.2	29	8	AZ828971	AZ828971	2M0106O15
400	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	473	10.2	39.2	29	8	AZ829352	AZ829352	2M0107A04
401	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	474	10.2	39.2	29	8	AZ829352	AZ829352	2M0107A04
402	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	475	10.2	39.2	29	8	AZ830289	AZ830289	2M0109O20
403	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	476	10.2	39.2	29	8	AZ836266	AZ836266	2M0131J05
404	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	477	10.2	39.2	29	8	AZ836960	AZ836960	2M0132K01
405	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	478	10.2	39.2	29	8	AZ837020	AZ837020	2M0132E10
406	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	479	10.2	39.2	29	8	AZ837893	AZ837893	2M0133D19
407	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	480	10.2	39.2	29	8	AZ837943	AZ837943	2M0133L24
408	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	481	10.2	39.2	29	8	AZ838373	AZ838373	2M0134J01
409	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	482	10.2	39.2	29	8	AZ838437	AZ838437	2M0134E11
410	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	483	10.2	39.2	29	8	AZ838658	AZ838658	2M0135B22
411	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	484	10.2	39.2	29	8	AZ839306	AZ839306	2M0135K19
412	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	485	10.2	39.2	29	8	AZ839342	AZ839342	2M0136L04
413	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	486	10.2	39.2	29	8	AZ839782	AZ839782	2M0136D13
414	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	487	10.2	39.2	29	8	AZ839920	AZ839920	2M0136D13
415	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	488	10.2	39.2	29	8	AZ840691	AZ840691	2M0138B19
416	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	489	10.2	39.2	29	8	AZ841372	AZ841372	2M0138B19
417	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	490	10.2	39.2	29	8	AZ841769	AZ841769	2M0144G17
418	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	491	10.2	39.2	29	8	AZ844546	AZ844546	2M0145E15
419	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	492	10.2	39.2	29	8	AZ846108	AZ846108	2M0146J09
420	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	493	10.2	39.2	29	8	AZ846128	AZ846128	2M0146M12
421	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	494	10.2	39.2	29	8	AZ847552	AZ847552	2M0148L08
422	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	495	10.2	39.2	29	8	AZ849587	AZ849587	2M0151N06
423	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	496	10.2	39.2	29	8	AZ852552	AZ852552	2M0155I19
424	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	497	10.2	39.2	29	8	AZ853928	AZ853928	2M0157O16
425	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	498	10.2	39.2	29	8	AZ856704	AZ856704	2M0161A14
426	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	499	10.2	39.2	29	8	AZ857502	AZ857502	2M0162N16
427	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	500	10.2	39.2	29	8	AZ864014	AZ864014	2M0173F19
428	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	501	10.2	39.2	29	8	AZ866656	AZ866656	2M0177P11
429	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	502	10.2	39.2	29	8	AZ867550	AZ867550	2M0178F20
430	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	503	10.2	39.2	29	8	AZ868052	AZ868052	2M0179F07
431	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	504	10.2	39.2	29	8	AZ873428	AZ873428	2M0187L10
432	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	505	10.2	39.2	29	8	AZ875048	AZ875048	2M0189G23
433	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	506	10.2	39.2	29	8	AZ876254	AZ876254	2M0191K12
434	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	507	10.2	39.2	29	8	AZ87923	AZ87923	2M0196J13
435	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	508	10.2	39.2	29	8	AZ8941569	AZ8941569	2M0201D19
436	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	509	10.2	39.2	29	8	AZ8942033	AZ8942033	2M0202G06
437	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	510	10.2	39.2	29	8	AZ894219	AZ894219	2M0205K09
438	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	511	10.2	39.2	29	8	AZ8944228	AZ8944228	2M0205M07
439	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	512	10.2	39.2	29	8	AZ8944852	AZ8944852	2M0206G06
440	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	513	10.2	39.2	29	8	AZ8947000	AZ8947000	2M0209J05
441	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	514	10.2	39.2	29	8	AZ8947090	AZ8947090	2M0209K08
442	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	515	10.2	39.2	29	8	AZ8948662	AZ8948662	2M0212N03
443	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	516	10.2	39.2	29	8	AZ8950397	AZ8950397	2M0214O22
444	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	517	10.2	39.2	29	8	AZ8952485	AZ8952485	2M0217P13
445	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	518	10.2	39.2	29	8	AZ8955096	AZ8955096	2M0221M01
446	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	519	10.2	39.2	29	8	AZ8955972	AZ8955972	2M0222H16
447	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	520	10.2	39.2	29	8	AZ8957452	AZ8957452	2M0224O16
448	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	521	10.2	39.2	29	8	AZ8957539	AZ8957539	2M0224N19
449	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	522	10.2	39.2	29	8	AZ8957539	AZ8957539	2M0225A15
450	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	523	10.2	39.2	29	8	AZ8958089	AZ8958089	2M0225E22
451	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	524	10.2	39.2	29	8	AZ8958190	AZ8958190	2M0230H12
452	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	525	10.2	39.2	29	8	AZ8961641	AZ8961641	2M0230H12
453	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	526	10.2	39.2	29	8	AZ8963957	AZ8963957	2M0233M23
454	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	527	10.2	39.2	29	8	AZ8966026	AZ8966026	2M0236B20
455	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	528	10.2	39.2	29	8	AZ8966609	AZ8966609	2M0237I12
456	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	529	10.2	39.2	29	8	AZ8967447	AZ8967447	2M0238G20
457	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	530	10.2	39.2	29	8	AZ8972393	AZ8972393	2M0246C13
458	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	531	10.2	39.2	29	8	AZ8972972	AZ8972972	2M0247H06
459	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	532	10.2	39.2	29	8	AZ8975143	AZ8975143	2M0250C07
460	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	533	10.2	39.2	29	8	AZ8975306	AZ8975306	2M0250O13
461	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	534	10.2	39.2	29	8	AZ8975947	AZ8975947	2M0251O08
462	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	535	10.2	39.2	29	8	AZ8976696	AZ8976696	2M0252E16

536	10.2	39.2	29	8	AZ978859	2M0255B22	AZ978859	2M0255B22	609	10.2	39.2	30	8	AZ857530	2M0162C23
537	10.2	39.2	29	8	AZ979444	2M0256F09	AZ979444	2M0256F09	610	10.2	39.2	30	8	AZ861962	2M0169E05
538	10.2	39.2	29	8	AZ979467	2M0256G09	AZ979467	2M0256G09	611	10.2	39.2	30	8	AZ862555	2M0170J17
539	10.2	39.2	29	8	AZ979505	2M0256P12	AZ979505	2M0256P12	612	10.2	39.2	30	8	AZ863351	2M0171M18
540	10.2	39.2	29	8	AZ980127	2M0257L02	AZ980127	2M0257L02	613	10.2	39.2	30	8	AZ865376	2M0175O22
541	10.2	39.2	29	8	AZ980803	2M0258A04	AZ980803	2M0258A04	614	10.2	39.2	30	8	AZ867225	2M0178B06
542	10.2	39.2	29	8	AZ982334	2M0263B08	AZ982334	2M0263B08	615	10.2	39.2	30	8	AZ868611	2M0180S24
543	10.2	39.2	29	8	AZ982439	2M0263D13	AZ982439	2M0263D13	616	10.2	39.2	30	8	AZ869107	2M0181P03
544	10.2	39.2	29	8	AZ982876	2M0267K20	AZ982876	2M0267K20	617	10.2	39.2	30	8	AZ869999	2M0182N17
545	10.2	39.2	29	8	AZ988276	2M0271K09	AZ988276	2M0271K09	618	10.2	39.2	30	8	AZ871865	2M0185A04
546	10.2	39.2	29	8	AZ989655	2M0273C02	AZ989655	2M0273C02	619	10.2	39.2	30	8	AZ873389	2M0187E10
547	10.2	39.2	29	8	AZ990319	2M0274C03	AZ990319	2M0274C03	620	10.2	39.2	30	8	AZ874186	2M0188A16
548	10.2	39.2	29	8	AZ990421	2M0274E11	AZ990421	2M0274E11	621	10.2	39.2	30	8	AZ936961	2M0195A06
549	10.2	39.2	29	8	AZ990528	2M0274I15	AZ990528	2M0274I15	622	10.2	39.2	30	8	AZ937764	2M0196M06
550	10.2	39.2	29	8	AZ990565	2M0274O18	AZ990565	2M0274O18	623	10.2	39.2	30	8	AZ938710	2M0197F22
551	10.2	39.2	29	8	AZ990639	2M0275O24	AZ990639	2M0275O24	624	10.2	39.2	30	8	AZ943674	2M0204L20
552	10.2	39.2	29	8	AZ991039	2M0275I02	AZ991039	2M0275I02	625	10.2	39.2	30	8	AZ945910	2M0207P22
553	10.2	39.2	29	8	AZ991170	2M0275A13	AZ991170	2M0275A13	626	10.2	39.2	30	8	AZ946358	2M0208E10
554	10.2	39.2	29	8	AZ991194	2M0275E17	AZ991194	2M0275E17	627	10.2	39.2	30	8	AZ947065	2M0209F12
555	10.2	39.2	29	8	AZ991204	2M0275G17	AZ991204	2M0275G17	628	10.2	39.2	30	8	AZ947527	2M0210G14
556	10.2	39.2	29	8	AZ991844	2M0276F18	AZ991844	2M0276F18	629	10.2	39.2	30	8	AZ948181	2M0211H07
557	10.2	39.2	29	8	AZ991324	2M0275M19	AZ991324	2M0275M19	630	10.2	39.2	30	8	AZ948361	2M0211F23
558	10.2	39.2	29	8	AZ991778	2M0276K11	AZ991778	2M0276K11	631	10.2	39.2	30	8	AZ948369	2M0211H19
559	10.2	39.2	29	8	AZ991800	2M0276G09	AZ991800	2M0276G09	632	10.2	39.2	30	8	AZ948819	2M0212F06
560	10.2	39.2	29	8	AZ991835	2M0276E15	AZ991835	2M0276E15	633	10.2	39.2	30	8	AZ949638	2M0213K01
561	10.2	39.2	29	8	AZ991844	2M0276F18	AZ991844	2M0276F18	634	10.2	39.2	30	8	AZ950186	2M0214I08
562	10.2	39.2	29	8	AZ991898	2M0276P14	AZ991898	2M0276P14	635	10.2	39.2	30	8	AZ950989	2M0215H14
563	10.2	39.2	29	8	AZ991927	2M0276F19	AZ991927	2M0276F19	636	10.2	39.2	30	8	AZ953191	2M0218L16
564	10.2	39.2	29	8	AZ991953	2M0276J23	AZ991953	2M0276J23	637	10.2	39.2	30	8	AZ953639	2M0219B01
565	10.2	39.2	29	8	AZ991972	2M0276N19	AZ991972	2M0276N19	638	10.2	39.2	30	8	AZ955241	2M0221F15
566	10.2	39.2	29	8	AZ991979	2M0276O21	AZ991979	2M0276O21	639	10.2	39.2	30	8	AZ955367	2M0221L23
567	10.2	39.2	29	8	AZ992645	2M0277E20	AZ992645	2M0277E20	640	10.2	39.2	30	8	AZ958813	2M0226F14
568	10.2	39.2	29	8	AZ992674	2M0277J19	AZ992674	2M0277J19	641	10.2	39.2	30	8	AZ964444	2M0234F07
569	10.2	39.2	29	8	AZ995222	2M0281A03	AZ995222	2M0281A03	642	10.2	39.2	30	8	AZ969397	2M0242H09
570	10.2	39.2	30	8	AZ319002	1M0038H19	AZ319002	1M0038H19	643	10.2	39.2	30	8	AZ970104	2M0243B08
571	10.2	39.2	30	8	AZ790771	2M0039K20	AZ790771	2M0039K20	644	10.2	39.2	30	8	AZ973179	2M0247L14
572	10.2	39.2	30	8	AZ803600	2M0064F03	AZ803600	2M0064F03	645	10.2	39.2	30	8	AZ974462	2M0249K05
573	10.2	39.2	30	8	AZ804386	2M0065O16	AZ804386	2M0065O16	646	10.2	39.2	30	8	AZ975128	2M0250O05
574	10.2	39.2	30	8	AZ805635	2M0067E10	AZ805635	2M0067E10	647	10.2	39.2	30	8	AZ975394	2M0250N20
575	10.2	39.2	30	8	AZ808562	2M0072I08	AZ808562	2M0072I08	648	10.2	39.2	30	8	AZ977930	2M0254F04
576	10.2	39.2	30	8	AZ808589	2M0072N07	AZ808589	2M0072N07	649	10.2	39.2	30	8	AZ978604	2M0255F06
577	10.2	39.2	30	8	AZ817222	2M0086M24	AZ817222	2M0086M24	650	10.2	39.2	30	8	AZ982577	2M0263L19
578	10.2	39.2	30	8	AZ829526	2M0107E17	AZ829526	2M0107E17	651	10.2	39.2	30	8	AZ985411	2M0267E18
579	10.2	39.2	30	8	AZ829704	2M0107F20	AZ829704	2M0107F20	652	10.2	39.2	30	8	AZ987758	2M0270L23
580	10.2	39.2	30	8	AZ832660	2M0113E19	AZ832660	2M0113E19	653	10.2	39.2	30	8	AZ990317	2M0274C01
581	10.2	39.2	30	8	AZ837070	2M0132N07	AZ837070	2M0132N07	654	10.2	39.2	30	8	AZ990618	2M0274K19
582	10.2	39.2	30	8	AZ837657	2M0133J01	AZ837657	2M0133J01	655	10.2	39.2	30	8	AZ990637	2M0274O20
583	10.2	39.2	30	8	AZ838321	2M0134A03	AZ838321	2M0134A03	656	10.2	39.2	30	8	AZ991051	2M0275K02
584	10.2	39.2	30	8	AZ838416	2M0134A11	AZ838416	2M0134A11	657	10.2	39.2	30	8	AZ991195	2M0275E18
585	10.2	39.2	30	8	AZ838494	2M0134O11	AZ838494	2M0134O11	658	10.2	39.2	30	8	AZ991235	2M0275M15
586	10.2	39.2	30	8	AZ839722	2M0136B04	AZ839722	2M0136B04	659	10.2	39.2	30	8	AZ991250	2M0275O18
587	10.2	39.2	30	8	AZ839735	2M0136D05	AZ839735	2M0136D05	660	10.2	39.2	30	8	AZ991316	2M0275K23
588	10.2	39.2	30	8	AZ839758	2M0136H04	AZ839758	2M0136H04	661	10.2	39.2	30	8	AZ991336	2M0275O23
589	10.2	39.2	30	8	AZ839786	2M0136M02	AZ839786	2M0136M02	662	10.2	39.2	30	8	AZ991788	2M0276M09
590	10.2	39.2	30	8	AZ839788	2M0136N04	AZ839788	2M0136N04	663	10.2	39.2	30	8	AZ992456	2M0277D09
591	10.2	39.2	30	8	AZ839900	2M0136P10	AZ839900	2M0136P10	664	10.2	39.2	30	8	AZ992609	2M0277O13
592	10.2	39.2	30	8	AZ840014	2M0136C24	AZ840014	2M0136C24	665	10.2	39.2	30	8	AZ992640	2M0277D20
593	10.2	39.2	30	8	AZ840026	2M0136B24	AZ840026	2M0136B24	666	10.2	39.2	30	8	AZ992708	2M0277O23
594	10.2	39.2	30	8	AZ843426	2M0142J15	AZ843426	2M0142J15	667	10.2	39.2	30	8	AZ993143	2M0278L04
595	10.2	39.2	30	8	AZ846173	2M0146E15	AZ846173	2M0146E15	668	10.2	39.2	30	8	AZ993180	2M0278D07
596	10.2	39.2	30	8	AZ846310	2M0146M24	AZ846310	2M0146M24	669	10.2	39.2	30	8	AZ993447	2M0280O24
597	10.2	39.2	30	8	AZ847602	2M0148D17	AZ847602	2M0148D17	670	10.2	39.2	30	8	AZ994847	2M0282L22
598	10.2	39.2	30	8	AZ847620	2M0148H13	AZ847620	2M0148H13	671	10.2	39.2	30	8	AZ996296	2M0282L22
599	10.2	39.2	30	8	AZ848426	2M0149I22	AZ848426	2M0149I22	672	10.2	39.2	30	9	CL610227	EH08868-5
600	10.2	39.2	30	8	AZ848931	2M0150H09	AZ848931	2M0150H09	673	10.2	39.2	31	8	AZ806127	2M0068C03
601	10.2	39.2	30	8	AZ851249	2M0153I23	AZ851249	2M0153I23	674	10.2	39.2	31	8	AZ806944	2M0069P16
602	10.2	39.2	30	8	AZ852447	2M0155K12	AZ852447	2M0155K12	675	10.2	39.2	31	8	AZ807391	2M0070F07
603	10.2	39.2	30	8	AZ852472	2M0155M19	AZ852472	2M0155M19	676	10.2	39.2	31	8	AZ807531	2M0070M17
604	10.2	39.2	30	8	AZ852582	2M0155A23	AZ852582	2M0155A23	677	10.2	39.2	31	8	AZ807948	2M0071H10
605	10.2	39.2	30	8	AZ852622	2M0155M23	AZ852622	2M0155M23	678	10.2	39.2	31	8	AZ808111	2M0071P23
606	10.2	39.2	30	8	AZ853915	2M0157M15	AZ853915	2M0157M15	679	10.2	39.2	31	8	AZ809197	2M0073P05
607	10.2	39.2	30	8	AZ854509	2M0158E10	AZ854509	2M0158E10	680	10.2	39.2	31	8	AZ820919	2M0093O20
608	10.2	39.2	30	8	AZ855251	2M0159A13	AZ855251	2M0159A13	681	10.2	39.2	31	8	AZ831604	2M0111L20

682	10.2	39.2	31	8	AZ832155	2M0112D24	AZ832155	2M0112D24	755	10.2	39.2	31	8	AZ991782	2M0276L09
683	10.2	39.2	31	8	AZ832809	2M0113O20	AZ832809	2M0113O20	756	10.2	39.2	31	8	AZ991782	2M0276H24
684	10.2	39.2	31	8	AZ836914	2M0132B06	AZ836914	2M0132B06	757	10.2	39.2	31	8	AZ991951	2M0276G21
685	10.2	39.2	31	8	AZ837069	2M0132M12	AZ837069	2M0132M12	758	10.2	39.2	31	8	AZ991957	2M0276K21
686	10.2	39.2	31	8	AZ837184	2M0132A22	AZ837184	2M0132A22	759	10.2	39.2	31	8	AZ993789	2M0279A06
687	10.2	39.2	31	8	AZ838326	2M0134B02	AZ838326	2M0134B02	760	10.2	39.2	31	8	AZ994488	2M0280A03
688	10.2	39.2	31	8	AZ838401	2M0134M01	AZ838401	2M0134M01	761	10.2	39.2	31	8	AZ995944	2M0280A02
689	10.2	39.2	31	8	AZ838570	2M0134A01	AZ838570	2M0134A01	762	10.2	39.2	31	8	AZ996181	2M0282I14
690	10.2	39.2	31	8	AZ838577	2M0134N16	AZ838577	2M0134N16	763	10.2	39.2	32	5	Q0584220	S013209W-
691	10.2	39.2	31	8	AZ838677	2M0134O14	AZ838677	2M0134O14	764	10.2	39.2	32	8	AZ996181	2M0282I14
692	10.2	39.2	31	8	AZ839335	2M0135W20	AZ839335	2M0135W20	765	10.2	39.2	32	8	Q0584220	S013209W-
693	10.2	39.2	31	8	AZ839737	2M0136E01	AZ839737	2M0136E01	766	10.2	39.2	32	8	AZ996181	2M0282I14
694	10.2	39.2	31	8	AZ839817	2M0136B09	AZ839817	2M0136B09	767	10.2	39.2	32	8	AZ996181	2M0282I14
695	10.2	39.2	31	8	AZ839874	2M0136L08	AZ839874	2M0136L08	768	10.2	39.2	32	8	AZ996181	2M0282I14
696	10.2	39.2	31	8	AZ839979	2M0136N13	AZ839979	2M0136N13	769	10.2	39.2	32	8	AZ996181	2M0282I14
697	10.2	39.2	31	8	AZ839999	2M0136A21	AZ839999	2M0136A21	770	10.2	39.2	32	8	AZ996181	2M0282I14
698	10.2	39.2	31	8	AZ840068	2M0136N19	AZ840068	2M0136N19	771	10.2	39.2	32	8	AZ996181	2M0282I14
699	10.2	39.2	31	8	AZ840618	2M0138D16	AZ840618	2M0138D16	772	10.2	39.2	32	8	AZ996181	2M0282I14
700	10.2	39.2	31	8	AZ840618	2M0138D16	AZ840618	2M0138D16	773	10.2	39.2	32	8	AZ996181	2M0282I14
701	10.2	39.2	31	8	AZ844613	2M0144L03	AZ844613	2M0144L03	774	10.2	39.2	32	8	AZ996181	2M0282I14
702	10.2	39.2	31	8	AZ846161	2M0146C15	AZ846161	2M0146C15	775	10.2	39.2	32	8	AZ996181	2M0282I14
703	10.2	39.2	31	8	AZ846193	2M0146I13	AZ846193	2M0146I13	776	10.2	39.2	32	8	AZ996181	2M0282I14
704	10.2	39.2	31	8	AZ847512	2M0148E08	AZ847512	2M0148E08	777	10.2	39.2	32	8	AZ996181	2M0282I14
705	10.2	39.2	31	8	AZ847662	2M0148O15	AZ847662	2M0148O15	778	10.2	39.2	32	8	AZ996181	2M0282I14
706	10.2	39.2	31	8	AZ848397	2M0149D19	AZ848397	2M0149D19	779	10.2	39.2	32	8	AZ996181	2M0282I14
707	10.2	39.2	31	8	AZ848397	2M0149D19	AZ848397	2M0149D19	780	10.2	39.2	32	8	AZ996181	2M0282I14
708	10.2	39.2	31	8	AZ849074	2M0151E01	AZ849074	2M0151E01	781	10.2	39.2	32	8	AZ996181	2M0282I14
709	10.2	39.2	31	8	AZ849534	2M0151E11	AZ849534	2M0151E11	782	10.2	39.2	32	8	AZ996181	2M0282I14
710	10.2	39.2	31	8	AZ849626	2M0151E11	AZ849626	2M0151E11	783	10.2	39.2	32	8	AZ996181	2M0282I14
711	10.2	39.2	31	8	AZ851886	2M0154P13	AZ851886	2M0154P13	784	10.2	39.2	32	8	AZ996181	2M0282I14
712	10.2	39.2	31	8	AZ852376	2M0155G09	AZ852376	2M0155G09	785	10.2	39.2	32	8	AZ996181	2M0282I14
713	10.2	39.2	31	8	AZ853312	2M0156L24	AZ853312	2M0156L24	786	10.2	39.2	32	8	AZ996181	2M0282I14
714	10.2	39.2	31	8	AZ853949	2M0157C20	AZ853949	2M0157C20	787	10.2	39.2	32	8	AZ996181	2M0282I14
715	10.2	39.2	31	8	AZ856742	2M0161G18	AZ856742	2M0161G18	788	10.2	39.2	32	8	AZ996181	2M0282I14
716	10.2	39.2	31	8	AZ862384	2M0170L02	AZ862384	2M0170L02	789	10.2	39.2	32	8	AZ996181	2M0282I14
717	10.2	39.2	31	8	AZ863759	2M0173G04	AZ863759	2M0173G04	790	10.2	39.2	32	8	AZ996181	2M0282I14
718	10.2	39.2	31	8	AZ866666	2M0177B16	AZ866666	2M0177B16	791	10.2	39.2	32	8	AZ996181	2M0282I14
719	10.2	39.2	31	8	AZ867945	2M0179C05	AZ867945	2M0179C05	792	10.2	39.2	32	8	AZ996181	2M0282I14
720	10.2	39.2	31	8	AZ868583	2M0180B24	AZ868583	2M0180B24	793	10.2	39.2	32	8	AZ996181	2M0282I14
721	10.2	39.2	31	8	AZ869784	2M0182I03	AZ869784	2M0182I03	794	10.2	39.2	32	8	AZ996181	2M0282I14
722	10.2	39.2	31	8	AZ877191	2M0192O17	AZ877191	2M0192O17	795	10.2	39.2	32	8	AZ996181	2M0282I14
723	10.2	39.2	31	8	AZ937090	2M0195H07	AZ937090	2M0195H07	796	10.2	39.2	32	8	AZ996181	2M0282I14
724	10.2	39.2	31	8	AZ946289	2M0208H05	AZ946289	2M0208H05	797	10.2	39.2	32	8	AZ996181	2M0282I14
725	10.2	39.2	31	8	AZ948419	2M0211P23	AZ948419	2M0211P23	798	10.2	39.2	32	8	AZ996181	2M0282I14
726	10.2	39.2	31	8	AZ949024	2M0212K15	AZ949024	2M0212K15	799	10.2	39.2	32	8	AZ996181	2M0282I14
727	10.2	39.2	31	8	AZ950178	2M0214G12	AZ950178	2M0214G12	800	10.2	39.2	32	8	AZ996181	2M0282I14
728	10.2	39.2	31	8	AZ950345	2M0214F20	AZ950345	2M0214F20	801	10.2	39.2	32	8	AZ996181	2M0282I14
729	10.2	39.2	31	8	AZ952436	2M0217G17	AZ952436	2M0217G17	802	10.2	39.2	32	8	AZ996181	2M0282I14
730	10.2	39.2	31	8	AZ956025	2M0222A23	AZ956025	2M0222A23	803	10.2	39.2	32	8	AZ996181	2M0282I14
731	10.2	39.2	31	8	AZ956788	2M0223L19	AZ956788	2M0223L19	804	10.2	39.2	32	8	AZ996181	2M0282I14
732	10.2	39.2	31	8	AZ956788	2M0225A17	AZ956788	2M0225A17	805	10.2	39.2	32	8	AZ996181	2M0282I14
733	10.2	39.2	31	8	AZ958091	2M0225A17	AZ958091	2M0225A17	806	10.2	39.2	32	8	AZ996181	2M0282I14
734	10.2	39.2	31	8	AZ961858	2M0230P19	AZ961858	2M0230P19	807	10.2	39.2	32	8	AZ996181	2M0282I14
735	10.2	39.2	31	8	AZ964331	2M0234B05	AZ964331	2M0234B05	808	10.2	39.2	32	8	AZ996181	2M0282I14
736	10.2	39.2	31	8	AZ964336	2M0234F16	AZ964336	2M0234F16	809	10.2	39.2	32	8	AZ996181	2M0282I14
737	10.2	39.2	31	8	AZ965330	2M0235D22	AZ965330	2M0235D22	810	10.2	39.2	32	8	AZ996181	2M0282I14
738	10.2	39.2	31	8	AZ967454	2M0238H23	AZ967454	2M0238H23	811	10.2	39.2	32	8	AZ996181	2M0282I14
739	10.2	39.2	31	8	AZ969428	2M0242M12	AZ969428	2M0242M12	812	10.2	39.2	32	8	AZ996181	2M0282I14
740	10.2	39.2	31	8	AZ970731	2M0244A03	AZ970731	2M0244A03	813	10.2	39.2	32	8	AZ996181	2M0282I14
741	10.2	39.2	31	8	AZ972460	2M0246N16	AZ972460	2M0246N16	814	10.2	39.2	32	8	AZ996181	2M0282I14
742	10.2	39.2	31	8	AZ973678	2M0248C06	AZ973678	2M0248C06	815	10.2	39.2	32	8	AZ996181	2M0282I14
743	10.2	39.2	31	8	AZ982525	2M0263C19	AZ982525	2M0263C19	816	10.2	39.2	32	8	AZ996181	2M0282I14
744	10.2	39.2	31	8	AZ983340	2M0264N09	AZ983340	2M0264N09	817	10.2	39.2	32	8	AZ996181	2M0282I14
745	10.2	39.2	31	8	AZ986024	2M0268O01	AZ986024	2M0268O01	818	10.2	39.2	32	8	AZ996181	2M0282I14
746	10.2	39.2	31	8	AZ9866024	2M0274C04	AZ9866024	2M0274C04	819	10.2	39.2	32	8	AZ996181	2M0282I14
747	10.2	39.2	31	8	AZ990320	2M0274M17	AZ990320	2M0274M17	820	10.2	39.2	32	8	AZ996181	2M0282I14
748	10.2	39.2	31	8	AZ990607	2M0274I20	AZ990607	2M0274I20	821	10.2	39.2	32	8	AZ996181	2M0282I14
749	10.2	39.2	31	8	AZ991234	2M0275E16	AZ991234	2M0275E16	822	10.2	39.2	32	8	AZ996181	2M0282I14
750	10.2	39.2	31	8	AZ991234	2M0275M14	AZ991234	2M0275M14	823	10.2	39.2	32	8	AZ996181	2M0282I14
751	10.2	39.2	31	8	AZ991242	2M0275N16	AZ991242	2M0275N16	824	10.2	39.2	32	8	AZ996181	2M0282I14
752	10.2	39.2	31	8	AZ991318	2M0275L19	AZ991318	2M0275L19	825	10.2	39.2	32	8	AZ996181	2M0282I14
753	10.2	39.2	31	8	AZ991345	2M0275M20	AZ991345	2M0275M20	826	10.2	39.2	32	8	AZ996181	2M0282I14
754	10.2	39.2	31	8	AZ991642	2M0276D01	AZ991642	2M0276D01	827	10.2	39.2	32	8	AZ996181	2M0282I14

828	10.2	39.2	33	8	A2826390	AZ826390	2M0102003	901	10.2	39.2	35	8	A2938626	AZ938626	2M0197H13
829	10.2	39.2	33	8	A2838402	AZ838402	2M0134002	902	10.2	39.2	35	8	A2946432	AZ946432	2M0208B18
830	10.2	39.2	33	8	A2838431	AZ838431	2M0134D10	903	10.2	39.2	35	8	A2947164	AZ947164	2M0209H14
831	10.2	39.2	33	8	A2839073	AZ839073	2M0135105	904	10.2	39.2	35	8	A2952355	AZ952355	2M0217I12
832	10.2	39.2	33	8	A2839159	AZ839159	2M0135110	905	10.2	39.2	35	8	A2953900	AZ953900	2M0219A21
833	10.2	39.2	33	8	A2845297	AZ845297	2M0145101	906	10.2	39.2	35	8	A2956772	AZ956772	2M0223I20
834	10.2	39.2	33	8	A2854110	AZ854110	2M0157R20	907	10.2	39.2	35	8	A2958131	AZ958131	2M0225I16
835	10.2	39.2	33	8	A2862423	AZ862423	2M0170C08	908	10.2	39.2	35	8	A2961764	AZ961764	2M0230N18
836	10.2	39.2	33	8	A2863745	AZ863745	2M0173E02	909	10.2	39.2	35	8	A2970172	AZ970172	2M0234A14
837	10.2	39.2	33	8	A2940735	AZ940735	2M0200A15	910	10.2	39.2	35	8	A2979538	AZ979538	2M0256F15
838	10.2	39.2	33	8	A2942924	AZ942924	2M0203N18	911	10.2	39.2	35	8	A2979538	AZ979538	2M0256F15
839	10.2	39.2	33	8	A2952522	AZ952522	2M0217F22	912	10.2	39.2	35	8	A2980857	AZ980857	2M0258L05
840	10.2	39.2	33	8	A2952958	AZ952958	2M0218B06	913	10.2	39.2	35	8	A2983984	AZ983984	2M0265O15
841	10.2	39.2	33	8	A2955142	AZ955142	2M0221E08	914	10.2	39.2	35	8	A2984070	AZ984070	2M0265K24
842	10.2	39.2	33	8	A2957332	AZ957332	2M0224J12	915	10.2	39.2	35	8	A2986047	AZ986047	2M0268C07
843	10.2	39.2	33	8	A2957440	AZ957440	2M0224M15	916	10.2	39.2	35	8	BZ596652	BZ596652	SALK 0929
844	10.2	39.2	33	8	A2958047	AZ958047	2M0225H11	917	10.2	39.2	36	8	A2971443	AZ971443	2M0041C23
845	10.2	39.2	33	8	A2958229	AZ958229	2M0225L24	918	10.2	39.2	36	8	A2810526	AZ810526	2M0076A09
846	10.2	39.2	33	8	A2960194	AZ960194	2M0228H12	919	10.2	39.2	36	8	A2837047	AZ837047	2M0132J07
847	10.2	39.2	33	8	A2967483	AZ967483	2M0238N19	920	10.2	39.2	36	8	A2839996	AZ839996	2M0136F18
848	10.2	39.2	33	8	A2967973	AZ967973	2M0240F10	921	10.2	39.2	36	8	A2874214	AZ874214	2M0188F15
849	10.2	39.2	33	8	A2968802	AZ968802	2M0241M16	922	10.2	39.2	36	8	A2947026	AZ947026	2M0209O04
850	10.2	39.2	33	8	A2970166	AZ970166	2M0243P07	923	10.2	39.2	36	8	A2949119	AZ949119	2M0212L23
851	10.2	39.2	33	8	A2983785	AZ983785	2M0265L06	924	10.2	39.2	36	8	A2950188	AZ950188	2M0214I10
852	10.2	39.2	33	8	A2986967	AZ986967	2M0269E22	925	10.2	39.2	36	8	A2958098	AZ958098	2M0225C13
853	10.2	39.2	33	8	A2990307	AZ990307	2M0274A03	926	10.2	39.2	36	8	A2974514	AZ974514	2M0249E10
854	10.2	39.2	33	8	A2990553	AZ990553	2M0274M18	927	10.2	39.2	36	8	A2974570	AZ974570	2M0249P08
855	10.2	39.2	33	8	A2991008	AZ991008	2M0275C04	928	10.2	39.2	36	8	A2983835	AZ983835	2M0265E10
856	10.2	39.2	33	8	A2993876	AZ993876	2M0279A07	929	10.2	39.2	36	8	A2984658	AZ984658	2M0266E16
857	10.2	39.2	33	8	A2994505	AZ994505	2M0280D02	930	10.2	39.2	36	8	A2991248	AZ991248	2M0275O16
858	10.2	39.2	33	8	A2996961	AZ996961	2M0283N14	931	10.2	39.2	36	8	A2994842	AZ994842	2M0280O19
859	10.2	39.2	33	8	BH758934	BH758934	P(5'why)1	932	10.2	39.2	36	9	AL757413	AL757413	Arabidops
860	10.2	39.2	33	1	CU797625	CU797625	SALK 1451	933	10.2	39.2	37	4	BG340929	BG340929	602462648
861	10.2	39.2	34	1	AU255089	AU255089	AU255089	934	10.2	39.2	37	8	A2810690	AZ810690	2M0076I21
862	10.2	39.2	34	8	A2784465	AZ784465	2M0027O12	935	10.2	39.2	37	8	A2835881	AZ835881	2M0130P17
863	10.2	39.2	34	8	A2800395	AZ800395	2M0058D23	936	10.2	39.2	37	8	A2838465	AZ838465	2M0134J09
864	10.2	39.2	34	8	A2820901	AZ820901	2M0093K24	937	10.2	39.2	37	8	A2839334	AZ839334	2M0135I23
865	10.2	39.2	34	8	A2832199	AZ832199	2M0112P22	938	10.2	39.2	37	8	A2839725	AZ839725	2M0136C01
866	10.2	39.2	34	8	A2836559	AZ836559	2M0131M19	939	10.2	39.2	37	8	A2840073	AZ840073	2M0136N24
867	10.2	39.2	34	8	A2838543	AZ838543	2M0134H14	940	10.2	39.2	37	8	A2846075	AZ846075	2M0146D12
868	10.2	39.2	34	8	A2838578	AZ838578	2M0134N17	941	10.2	39.2	37	8	A2846252	AZ846252	2M0146C22
869	10.2	39.2	34	8	A2839356	AZ839356	2M0135M21	942	10.2	39.2	37	8	A2877196	AZ877196	2M0192O22
870	10.2	39.2	34	8	A2839378	AZ839378	2M0136M18	943	10.2	39.2	37	8	A2958064	AZ958064	2M0225L08
871	10.2	39.2	34	8	A2840431	AZ840431	2M0138C02	944	10.2	39.2	37	8	A2960363	AZ960363	2M0228F22
872	10.2	39.2	34	8	A2845480	AZ845480	2M0145K15	945	10.2	39.2	37	8	A2966579	AZ966579	2M0237D12
873	10.2	39.2	34	8	A2846247	AZ846247	2M0146B23	946	10.2	39.2	37	8	A2966608	AZ966608	2M0237L11
874	10.2	39.2	34	8	A2846782	AZ846782	2M0147D09	947	10.2	39.2	37	8	A2978697	AZ978697	2M0255F12
875	10.2	39.2	34	8	A2847627	AZ847627	2M0148I14	948	10.2	39.2	37	8	A2989928	AZ989928	2M0273N24
876	10.2	39.2	34	8	A2852328	AZ852328	2M0155J17	949	10.2	39.2	37	8	A2991963	AZ991963	2M0276L21
877	10.2	39.2	34	8	A2853746	AZ853746	2M0157P04	950	10.2	39.2	37	8	A2995580	AZ995580	2M0281P19
878	10.2	39.2	34	8	A2855078	AZ855078	2M0159A03	951	10.2	39.2	37	8	BH789722	BH789722	SALK 0445
879	10.2	39.2	34	8	A2860323	AZ860323	2M0166G14	952	10.2	39.2	37	9	AL770434	AL770434	Arabidops
880	10.2	39.2	34	8	A2875088	AZ875088	2M0189N23	953	10.2	39.2	38	2	BE739510	BE739510	601556438
881	10.2	39.2	34	8	A2875578	AZ875578	2M0190H01	954	10.2	39.2	38	8	A2839728	AZ839728	2M0136C04
882	10.2	39.2	34	8	A2942009	AZ942009	2M0202C04	955	10.2	39.2	38	8	A2839977	AZ839977	2M0136M17
883	10.2	39.2	34	8	A2947569	AZ947569	2M0210N15	956	10.2	39.2	38	8	A2945774	AZ945774	2M0207I15
884	10.2	39.2	34	8	A2950280	AZ950280	2M0214K11	957	10.2	39.2	38	8	A2947169	AZ947169	2M0209J13
885	10.2	39.2	34	8	A2950330	AZ950330	2M0214L22	958	10.2	39.2	38	8	A2947546	AZ947546	2M0210J15
886	10.2	39.2	34	8	A2955329	AZ955329	2M0221F19	959	10.2	39.2	38	8	A2952470	AZ952470	2M0217M16
887	10.2	39.2	34	8	A2960338	AZ960338	2M0229L08	960	10.2	39.2	38	8	A2958109	AZ958109	2M0225E16
888	10.2	39.2	34	8	A2966536	AZ966536	2M0237L01	961	10.2	39.2	38	8	A2991799	AZ991799	2M0276O08
889	10.2	39.2	34	8	A2973866	AZ973866	2M0248D13	962	10.2	39.2	38	8	A2996969	AZ996969	2M0283O16
890	10.2	39.2	34	8	A2979561	AZ979561	2M0256J15	963	10.2	39.2	38	8	BH853122	BH853122	SALK 0760
891	10.2	39.2	34	8	A2984814	AZ984814	2M0266P19	964	10.2	39.2	38	8	BZ766550	BZ766550	SALK 1375
892	10.2	39.2	34	8	A2985987	AZ985987	2M0268H03	965	10.2	39.2	38	9	BX536344	BX536344	Arabidops
893	10.2	39.2	34	8	A2990626	AZ990626	2M0274M19	966	10.2	39.2	39	1	AU266424	AU266424	2M0266424
894	10.2	39.2	34	8	A2991298	AZ991298	2M0275F20	967	10.2	39.2	39	7	D74282	D74282	CELK079A5F
895	10.2	39.2	34	8	A2999092	AZ999092	2M0286K17	968	10.2	39.2	39	8	A2337982	AZ337982	1M0068E19
896	10.2	39.2	35	8	A2807270	AZ807270	2M0070D04	969	10.2	39.2	39	8	A2807468	AZ807468	2M0070A21
897	10.2	39.2	35	8	A2822134	AZ822134	2M0095P03	970	10.2	39.2	39	8	A2810534	AZ810534	2M0076C07
898	10.2	39.2	35	8	A2835004	AZ835004	2M0129D04	971	10.2	39.2	39	8	A2838400	AZ838400	2M0134N06
899	10.2	39.2	35	8	A2839805	AZ839805	2M0136P03	972	10.2	39.2	39	8	A2838622	AZ838622	2M0134F22
900	10.2	39.2	35	8	A2846212	AZ846212	2M0146L14	973	10.2	39.2	39	8	A2862284	AZ862284	2M0169J19

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974 10.2 39.2 39 8 AZ862314 2M0169P23
975 10.2 39.2 39 8 AZ942083 2M0202P04
976 10.2 39.2 39 8 AZ942716 2M0203A03
977 10.2 39.2 39 8 AZ947232 2M0209D20
978 10.2 39.2 39 8 AZ958896 2M0226D20
979 10.2 39.2 39 8 AZ970039 2M0243J03
980 10.2 39.2 39 8 AZ989699 2M0273G07
981 10.2 39.2 39 8 AZ990508 2M0274R15
982 10.2 39.2 39 8 AZ990997 2M0275A03
983 10.2 39.2 39 8 AZ990598 2M0067F20
984 10.2 39.2 40 8 AZ805795 2M0107O16
985 10.2 39.2 40 8 AZ834909 2M0117B21
986 10.2 39.2 40 8 AZ838469 2M0134K07
987 10.2 39.2 40 8 AZ838520 2M0134D15
988 10.2 39.2 40 8 AZ847468 2M0148M01
989 10.2 39.2 40 8 AZ855417 2M0159M20
990 10.2 39.2 40 8 AZ942732 2M0203B02
991 10.2 39.2 40 8 AZ951777 2M0216P17
992 10.2 39.2 40 8 AZ952424 2M0217E17
993 10.2 39.2 40 8 AZ953244 2M0218G22
994 10.2 39.2 40 8 AZ955197 2M0221N10
995 10.2 39.2 40 8 AZ971816 2M0245N23
996 10.2 39.2 40 8 AZ975993 2M0251G13
997 10.2 39.2 40 8 AZ990597 2M0274G19
998 10.2 39.2 40 9 BX660365 Arabidops
999 10.2 39.2 41 7 D19129 MUSGS01345
1000 10.2 39.2 41 8 AZ839173 2M0135L07
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ALIGNMENTS

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RESULT 1
AZ959628 35 bp DNA linear GSS 27-APR-2001
LOCUS 2M0272D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0272D23 F, genomic survey sequence.
ACCESSION AZ959628.1 GI:13830855
VERSION AZ959628
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 35)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weises, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduenne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: D column: 23
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
1. .35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0272D23"
/sex="Female"
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FEATURES

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source
Location/Qualifiers
1. .35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0272D23"
/sex="Female"
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/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pMD42rv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ORIGIN

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Query Match 55.4%; Score 14.4; DB 8; Length 35;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 TCTTTCCAGATCGGTACCTCAAT 26
DB 5 TCGTACGTAGTCGACATGAT 28
```

RESULT 2

```
BZ289495 44 bp DNA linear GSS 24-OCT-2002
LOCUS SALK_022894.23.05.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_022894.23.05.x, genomic
survey sequence.
```

ACCESSION

```
BZ289495
BZ289495.1 GI:24331195
```

VERSION

```
BZ289495
```

KEYWORDS

```
GSS.
```

SOURCE

```
Arabidopsis thaliana (thale cress)
```

ORGANISM

```
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
```

REFERENCE

```
1 (bases 1 to 44)
```

AUTHORS

```
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
```

TITLE

```
A Sequence-Indexed Library of Insertion Mutations in the
```

Arabidopsis Genome

Unpublished (2001)

CONTACT

```
Contact: Joseph R. Ecker
```

COMMENT

```
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
```

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At4g17530. Class: TDNA tagged.

FEATURES

Location/Qualifiers

1. .44

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_022894.23.05.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion"

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html.

ORIGIN
Query Match 53.1%; Score 13.8; DB 8; Length 44;
Best Local Similarity 72.0%; Pred. No. 5.2e+04;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CGTCTTCGACGATCGGTACTCTCA 25
Db 44 CTTGTTCCAGACGGATCCCA 20

RESULT 3
TA58C07Q 49 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 58c07, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL455710
VERSION AL455710.1 GI:11857988
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
REFERENCE 1 (bases 1 to 49)
AUTHORS Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
Melville S.E., Rajandream M.A. and Barrell B.G.

TITLE
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsaved@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1..49
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRU927"
/db_xref="taxon:5691"
/clone="58c07"

ORIGIN

Query Match 53.1%; Score 13.8; DB 9; Length 49;
Best Local Similarity 72.0%; Pred. No. 5.2e+04;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACGATCGGTACTCTCA 26
Db 25 GTGTATAGCCGATCGGTGGACAAT 49

RESULT 4
CN921174/c 50 bp mRNA linear EST 07-JUN-2004
LOCUS 000225AELA001423HT (AELA) Royal Gala young expanding leaf Malus x
DEFINITION domestica cDNA clone AELA001423, mRNA sequence.
ACCESSION CN921174
VERSION CN921174.1 GI:48393987

KEYWORDS

SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
JOURNAL rosid; eurosid 1; Rosales; Rosaceae; Maloideae; Malus.

1 (bases 1 to 50)
Beuning L., Bowen J., Crowhurst R., Gleave A., Janssen B.,
McCarthy S., Newcomb R., Ross G., Snowden K., Walton E. and Yauk Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4201
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES

source
1..50
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AELA001423"
/tissue_type="Leaf"
/dev_stage="Young, expanding"
/clone_lib="(AELA) Royal Gala young expanding leaf"
/note="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"

ORIGIN

Query Match 53.1%; Score 13.8; DB 7; Length 50;
Best Local Similarity 72.0%; Pred. No. 5.2e+04;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CGTCTTCGACGATCGGTACTCTCA 25
Db 25 CGTCTTCGACGATCGGTACTCTCA 1

RESULT 5

AU105805 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU105805 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION COL02839, mRNA sequence.

ACCESSION AU105805
VERSION AU105805.1 GI:13555326
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki Y., Taira H., Tsunoda T., Mizushima-Sugano J., Sese J.,
Hata H., Ota T., Isogai T., Tanaka T., Morishita S., Okubo K.,
Sakaki Y., Nakamura Y., Suyama A. and Sugano S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki Y., Yoshitomo-Nakagawa K., Maruyama K., Suyama A. and
Sugano S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"

```

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 37)
REFERENCE
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsaved@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
Location/Qualifiers
1..37
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="344b09"
ORIGIN
Query Match 51.5%; Score 13.4; DB 9; Length 37;
Best Local Similarity 93.3%; Pred. No. 8.1e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 TTTCGCAGATCGGTA 19
Db 19 TGTGCGCAGATCGGTA 5
RESULT 8
BH642496 49 bp DNA linear GSS 14-FEB-2002
LOCUS 1008040H04.2BL_y1 1008 - RescueMu Grid I Zea mays genomic, genomic
survey sequence.
DEFINITION
ACCESSION BH642496
VERSION BH642496.1 GI:18671293
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 49)
REFERENCE
AUTHORS
Walbot,V.
TITLE
Maize genomic sequences found using engineered RescueMu transposon
JOURNAL
Unpublished (2001)
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008040 row: 30
Class: transposon-tagged
Location/Qualifiers
1..49
/organism="Zea mays"
/mol_type="genomic DNA"
FEATURES
source
Location/Qualifiers
1..49
/mol_type="genomic DNA"

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ORIGIN

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Query Match      49.2%; Score 12.8; DB 8; Length 44;
Best Local Similarity 70.8%; Pred. No. 1.6e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAAT 26
Db 5 TCCTTCACTGTGTTTACCTCAAT 28

RESULT 13
BH8428960
LOCUS      BH628960      45 bp      DNA      linear      GSS 30-JAN-2002
DEFINITION 1007075B10.1EL_y1 1007 - RescueMu Grid H Zea mays genomic, genomic
survey sequence.
ACCESSION  BH628960
VERSION     BH628960
KEYWORDS    BH628960.1 GI:18442211
SOURCE      GSS.
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 45)
REFERENCE   Walbot,V.
AUTHORS     Zea mays
TITLE       Maize genomic sequences found using engineered RescueMu transposon
JOURNAL     Unpublished (2001)
COMMENT     Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1007075 column: 36
            Class: transposon-tagged.
FEATURES    source
            Location/Qualifiers
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                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="mixed background W23/A188/B73"
                /db_xref="taxon:4577"
                /tissue type="leaf"
                /dev stage="adult"
                /lab_host="DH10B"
                /clone_lib="1007 - RescueMu Grid H"
                /note="Organ: leaf; Vector: RescueMu (engineered from
                pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
                RescueMu is a 4.9 kb, modified maize Mu transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription web
                units. For more information on RescueMu, go to the
                site 'www.zmldb.iastate.edu' and follow the links for
                'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
                was extracted from leaf punches, double digested using
                BamHI and BglII, and ligated to form circular plasmids.
                DH10B cells were transformed and then screened on LB
                plates with ampicillin."

ORIGIN
Query Match      49.2%; Score 12.8; DB 8; Length 45;
Best Local Similarity 70.8%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAAT 26
Db 2 TCATCCTCAGATCCGACGCCAAT 25

RESULT 14
BH846331/c
LOCUS      BH846331      49 bp      DNA      linear      GSS 13-JUN-2002
DEFINITION SALK_007296.28.80.x Arabidopsis thaliana TDNA insertion lines
survey sequence.
ACCESSION  BH846331
VERSION     BH846331.1 GI:21417202
KEYWORDS    BH846331
SOURCE      GSS.
ORGANISM    Arabidopsis thaliana (thale cress)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 49)
REFERENCE   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            The Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
                1..49
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /ecotype="Col-0"
                /db_xref="taxon:3702"
                /clone="SALK_007296.28.80.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      49.2%; Score 12.8; DB 8; Length 49;
Best Local Similarity 70.8%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAAT 26
Db 37 TTTTTCGCAATCGTTAAGGCATT 14

RESULT 15
AA972865/c
LOCUS      AA972865      34 bp      mRNA      linear      EST 21-DEC-1998
DEFINITION OP20G03.s1 NCI CGAP Col2 Homo sapiens cDNA clone IMAGE:1576276 3',
similar to TF:Q12905 Q12905 NF45 PROTEIN. ; mRNA sequence.
ACCESSION  AA972865
VERSION     AA972865.1 GI:3148045
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 34)
REFERENCE   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-romail.nih.gov

```


[illegible]

Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0281 row: B column: 06
 Seq primer: CTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

FEATURES

source

1..26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0281B06"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 46.2%; Score 12; DB 8; Length 26;
 Best Local Similarity 75.0%; Pred. No. 4e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TTCCGACATCGGTACTCTCAA 25

Db 7 TACGTAGATCGGACATCAA 26

RESULT 23

CN973502/c

LOCUS 28 bp mRNA linear EST 08-JUN-2004

DEFINITION 21001_45-39 Fundulus heteroclitus Heart Fundulus heteroclitus cDNA,

mRNA sequence.

ACCESSION CN973502

VERSION CN973502.1 GI:48455093

KEYWORDS EST.

SOURCE Fundulus heteroclitus (killifish)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthopterygia; Acanthopterygii; Percomorpha; Atherinomorpha;

Cyprinodontiformes; Fundulidae; Fundulus.

1 (bases 1 to 28)

REFERENCE Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,

Rosach,J.L. and Whitehead,J.A.

Fundulus Functional Genomics: EST Database for Teleost Fish

Unpublished (2004)

Contact: Crawford, Douglas L.

Marine Genomics - Crawford Lab

Rosenstiel School of Marine and Atmospheric Science - University of

Miami

4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA

Tel: 305 361 4121

Email: dcfarford@rsmas.miami.edu

Database Web Interface

http://genomics.rsmas.miami.edu/funnybase/super_craw3/

Plate: 45 row: B column: 5.

Location/Qualifiers

1..28

/organism="Fundulus heteroclitus"

/mol_type="mRNA"

/db_xref="taxon:8078"

/tissue_type="Heart"

/clone_lib="Fundulus heteroclitus Heart"

/note="Organ: Heart"

ORIGIN

Query Match 46.2%; Score 12; DB 7; Length 28;
 Best Local Similarity 68.2%; Pred. No. 4.1e+05;
 Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGACATCGGTACTCTCA 24

Db 22 TTTTACACAGATCGATNTCNCA 1

RESULT 24

TA383E12Q

LOCUS 37 bp DNA linear GSS 13-DEC-2000

DEFINITION T. brucei sheared genomic DNA clone 383e12, reverse sequence,

genomic survey sequence.

ACCESSION AL497988.1 GI:11873710

VERSION GSS.

KEYWORDS

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 37)

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1..37

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="383e12"

ORIGIN

Query Match 46.2%; Score 12; DB 9; Length 37;
 Best Local Similarity 75.0%; Pred. No. 4.1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACTCTCAAT 26

||||| ||||| ||||| ||||| |||||

Db	12	TCGCTGATAGGTTCTTGAAT	31
RESULT 25			
LOCUS	BH796117/c		
DEFINITION	1008092H05.1EL x1 1008 - RescueMu Grid I Zea mays genomic, genomic survey sequence.		
ACCESSION	BH796117	42 bp	DNA
VERSION	BH796117.1		
KEYWORDS	GSS.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	Walbot,V.		
TITLE	Maize genomic sequences found using engineered RescueMu transposon		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 1008092 row: 33 Class: transposon-tagged.		
FEATURES	<p>Location/Qualifiers</p> <p>1..42</p> <p>/organism="Zea mays"</p> <p>/mol_type="genomic DNA"</p> <p>/cultivar="mixed background W23/A188/B73"</p> <p>/db_xref="taxon:4577"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="adult"</p> <p>/lab_host="DH10B"</p> <p>/clone_lib="1008 - RescueMu Grid I"</p> <p>/note="Organ: leaf; Vector: RescueMu (engineered from pluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the site www.zmdb.tastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."</p>		
ORIGIN	<p>Query Match 46.2%; Score 12; DB 8; Length 42;</p> <p>Best Local Similarity 75.0%; Pred. No. 4.2e+05;</p> <p>Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;</p>		
QY	2	GTCTTCGCAGATCGGTACC	21
DB	20	GTCCGTCGATGTCAGTACC	1
RESULT 26			
AZ778700/c			
LOCUS	AZ778700	43 bp	DNA
DEFINITION	2M0014P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0014P03 F, genomic survey sequence.		
ACCESSION	AZ778700		
VERSION	AZ778700.1		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 43)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0014 row: P column: 03 Seq primer: GGTGTAAACGACGCGCAGT Class: plasmid ends High quality sequence stop: 43.		
FEATURES	<p>Location/Qualifiers</p> <p>1..43</p> <p>/organism="Mus musculus"</p> <p>/mol_type="genomic DNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="UUGC2M0014P03"</p> <p>/sex="Male"</p> <p>/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"</p> <p>/clone_lib="Mouse 10kb plasmid UUGC1M library"</p> <p>/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."</p>		
ORIGIN	<p>Query Match 46.2%; Score 12; DB 8; Length 43;</p> <p>Best Local Similarity 75.0%; Pred. No. 4.2e+05;</p> <p>Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;</p>		
QY	3	TCCTTCGCAGATCGGTACT	22
DB	32	TCCTTCACAGTCCGTAGCT	13
RESULT 27			
BZ664508			
LOCUS	BZ664508	45 bp	DNA
DEFINITION	SALK_075791.25.80.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_075791.25.80.x, genomic survey sequence.		
ACCESSION	BZ664508		
VERSION	BZ664508.1		
KEYWORDS	GSS.		

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.

REFERENCE 1 (bases 1 to 45)
 AUTHORS Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 The Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atig76710.
 Class: TDNA tagged.

FEATURES
 source Location/Qualifiers
 1..45
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_075791.25.80.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 46.2%; Score 12; DB 8; Length 45;
 Best Local Similarity 75.0%; Pred. No. 4.2e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTTTCGCAGATCGGTACCTC 23
 |||||
 DB 5 CTTTCGCAGATAGATATATC 24
 |||||

RESULT 28
 CL521995 45 bp DNA linear GSS 02-APR-2004
 LOCUS SALK7C08 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
 DEFINITION Oryza sativa (japonica cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL521995.1 GI:46148795
 VERSION GSS.
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 45)
 Sallaud,C., Gay,C., Larmande,P., Bes,M., Piffanelli,P., Piegou,B., Droc,G., Regad,F., Bourgeois,E., Meynard,D., Perin,C., Ghesquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.
 High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics
 Plant J. (2004) In press
 Contact: Guiderdoni
 UMR PIA Biotrop program
 CIRAD
 TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
 Tel: 33467615629

REFERENCE 1 (bases 1 to 45)
 AUTHORS Sallaud,C., Gay,C., Larmande,P., Bes,M., Piffanelli,P., Piegou,B., Droc,G., Regad,F., Bourgeois,E., Meynard,D., Perin,C., Ghesquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.
 TITLE High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics
 JOURNAL Plant J. (2004) In press
 COMMENT Contact: Guiderdoni
 UMR PIA Biotrop program
 CIRAD
 TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
 Tel: 33467615629

Fax: 33467615605
 Email: emmanuel.guiderdoni@cirad.fr
 Class: TDNA tagged.

FEATURES
 source Location/Qualifiers
 1..45
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"
 /note="PCR was performed on DNA of primary transformants of Oryza sativa plants. The DNA fragment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from June 2004 at <http://genoplante-info.infobiogen.fr/oryzatagline/>. This sequence has been generated in the framework of the French plant genomics program Genoplante (<http://www.genoplante.org> and <http://genoplante-info.infobiogen.fr>)."

ORIGIN
 Query Match 46.2%; Score 12; DB 9; Length 45;
 Best Local Similarity 75.0%; Pred. No. 4.2e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TTTCGCAGATCGGTACTCA 24
 |||||
 DB 38 TTTCGCAGACGTGAACGA 19
 |||||

RESULT 29
 CL521997 45 bp DNA linear GSS 02-APR-2004
 LOCUS SALK7E08 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
 DEFINITION Oryza sativa (japonica cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL521997.1 GI:46148797
 VERSION GSS.
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 45)
 Sallaud,C., Gay,C., Larmande,P., Bes,M., Piffanelli,P., Piegou,B., Droc,G., Regad,F., Bourgeois,E., Meynard,D., Perin,C., Ghesquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.
 High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics
 Plant J. (2004) In press
 Contact: Guiderdoni
 UMR PIA Biotrop program
 CIRAD
 TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
 Tel: 33467615629
 Fax: 33467615605
 Email: emmanuel.guiderdoni@cirad.fr
 Class: TDNA tagged.

FEATURES
 source Location/Qualifiers
 1..45
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"
 /note="PCR was performed on DNA of primary transformants of Oryza sativa plants. The DNA fragment(s) resulting of


```

Best Local Similarity 75.0%; Pred. No. 4.2e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTTTCGCAGATCGGTACCTC 23
    |||||
Db 28 CTTTCACAGAACGTGCCTC 9

RESULT 32
AZ805662
LOCUS 27 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0067K09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0067K09 F, genomic survey sequence.
ACCESSION AZ805662
VERSION AZ805662.1 GI:12966473
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: K column: 09
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
source
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0067K09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 27;

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Best Local Similarity 86.7%; Pred. No. 5.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAAT 26
    |||||
Db 12 GATCGGTACATGAAT 26

RESULT 33
AZ803827
LOCUS 28 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0064J20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0064J20 F, genomic survey sequence.
ACCESSION AZ803827
VERSION AZ803827.1 GI:12956150
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0064 row: J column: 20
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0064J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 28;

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Best Local Similarity 86.7%; Pred. No. 5.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACTCAAT 26
   |||||
Db 12 GATCGGTACATGAAT 26

RESULT 34
AZ9797143
LOCUS 2M053N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC2M0053N07 F, genomic survey sequence.
ACCESSION AZ9797143
VERSION AZ9797143.1 GI:12945917
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: N column: 07
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1..30
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0053N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203G18"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 30;

Best Local Similarity 86.7%; Pred. No. 5.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACTCAAT 26
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Db 12 GATCGGTACATGAAT 26

RESULT 35
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LOCUS 2M0203G18F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clone UUGC2M0203G18 F, genomic survey sequence.
ACCESSION AZ942892
VERSION AZ942892.1 GI:13806539
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 32)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: G column: 18
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203G18"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 32;

```

```

Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAAT 26
Db 13 GATCGGTACATGAAT 27

RESULT 36
CL655958/c
LOCUS
DEFINITION
PR10125b.C09 - PR10125b.B21 (32) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
CL655958
VERSION
CL655958.1 GI:50135823
KEYWORDS
GSS.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
Contact: Sommer RJ
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: rafif.sommer@cuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1..32
Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 45.4%; Score 11.8; DB 9; Length 32;
Best Local Similarity 69.6%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 CTTTCGCAGATCGGTACCTCAAT 26
Db 29 CTCCTCAGGTCGCTATTTCAGT 7

RESULT 37
AZ810604
LOCUS
DEFINITION
AZ810604 34 bp DNA linear GSS 20-FEB-2001
2M0076C16F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC2M0076C16 F, genomic survey sequence.
ACCESSION
AZ810604
VERSION
AZ810604.1 GI:12978019
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
REFERENCE
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Best Local Similarity 86.7%; Score 11.8; DB 8; Length 34;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAAT 26
Db 12 GATCGGTACATGAAT 26

RESULT 38
AZ803114
LOCUS
DEFINITION
AZ803114 35 bp DNA linear GSS 16-FEB-2001
2M0063N14F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC2M0063N14 F, genomic survey sequence.
ACCESSION
AZ803114
VERSION
AZ803114.1 GI:12955437
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
REFERENCE
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```

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Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 16
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0076C16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 34;
Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAAT 26
Db 12 GATCGGTACATGAAT 26

RESULT 38
AZ803114
LOCUS
DEFINITION
AZ803114 35 bp DNA linear GSS 16-FEB-2001
2M0063N14F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC2M0063N14 F, genomic survey sequence.
ACCESSION
AZ803114
VERSION
AZ803114.1 GI:12955437
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
REFERENCE
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```


Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: G column: 15
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers

TITLE
JOURNAL
COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: N column: 14
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers

TITLE
JOURNAL
COMMENT

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0067G15"
/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GII4732114[GB|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 45.4%; Score 11.8; DB 8; Length 35;
Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACCTCAAT 26
|||||
Db 11 GATCGGTACATGAAT 25

RESULT 40

AZ810670
LOCUS
DEFINITION
2M0076C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076C22 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ810670
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

AZ805718
LOCUS
DEFINITION
2M0067G15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0067G15 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ805718
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

ORIGIN

Query Match 45.4%; Score 11.8; DB 8; Length 35;
Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACCTCAAT 26
|||||
Db 9 GATCGGTACATGAAT 23

RESULT 39

AZ805718
LOCUS
DEFINITION
2M0067G15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0067G15 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ805718
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunnegene@utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0076 row: C column: 22
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 36.

FEATURES
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 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0076C22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 45.4%; Score 11.8; DB 8; Length 36;
 Best Local Similarity 86.7%; Pred. No. 5.2e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAAT 26
 |||||
 Db 12 GATCGGTACATGAAT 26

Search completed: November 23, 2004, 22:24:50
 Job time : 1268.54 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
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2	28	100.0	28	6	AX523950	AX523950 Sequence
3	28	100.0	28	6	AX524848	AX524848 Sequence
4	17	60.7	47	6	AX289945	AX289945 Sequence
C 5	15.4	55.0	36	6	AX710947	AX710947 Sequence
C 6	15.4	55.0	37	6	CQ779042	CQ779042 Sequence
C 7	15	53.6	15	6	BD244764	BD244764 Isolation
C 8	15	53.6	15	6	AX255271	AX255271 Sequence
C 9	15	53.6	19	6	AX645654	AX645654 Sequence
C 10	15	53.6	19	6	AX645658	AX645658 Sequence
C 11	14.6	52.1	21	6	AX097318	AX097318 Sequence
C 12	14.6	52.1	23	6	E31555	E31555 Cecropin gene
C 13	14.6	52.1	38	6	AR172071	AR172071 Sequence
C 14	14.6	52.1	38	6	AR173362	AR173362 Sequence
C 15	14.6	52.1	50	6	AR437662	AR437662 Sequence
C 16	14.6	52.1	50	6	AX026712	AX026712 Sequence
C 17	14.6	52.1	32	6	AR200549	AR200549 Sequence
C 18	14.4	51.4	38	6	AR082475	AR082475 Sequence
C 19	14.4	51.4	38	6	AR083603	AR083603 Sequence

93	13.2	47.1	45	6	AR237994 Sequence	AR237994 Sequence	166	12.6	45.0	20	6	BD080533	BD080533 Large-sca
c 94	13.2	47.1	47	6	E37138 Method for	E37138 Method for	c 167	12.6	45.0	24	6	AX116463 Sequence	AX116463 Sequence
c 95	13	46.4	21	6	BD144876 A method	BD144876 A method	168	12.6	45.0	25	6	BD169709 Human gli	BD169709 Human gli
c 96	13	46.4	23	6	BD097354 Method fo	BD097354 Method fo	169	12.6	45.0	26	6	AX117876 Sequence	AX117876 Sequence
c 97	13	46.4	25	6	AX500848 Sequence	AX500848 Sequence	c 170	12.6	45.0	30	6	AR220730 Sequence	AR220730 Sequence
c 98	13	46.4	25	6	AX500849 Sequence	AX500849 Sequence	c 171	12.6	45.0	30	6	BD091353 Method of	BD091353 Method of
c 99	13	46.4	25	6	AX500850 Sequence	AX500850 Sequence	c 172	12.6	45.0	30	6	BD137054 Method of	BD137054 Method of
c 100	13	46.4	25	6	AX500851 Sequence	AX500851 Sequence	c 173	12.6	45.0	38	6	A26131 Artificial	A26131 Artificial
c 101	13	46.4	25	6	AX500852 Sequence	AX500852 Sequence	174	12.6	45.0	38	6	A29558 K.lactis ge	A29558 K.lactis ge
c 102	13	46.4	26	6	BD078207 Modulator	BD078207 Modulator	175	12.6	45.0	38	6	AR045708 Sequence	AR045708 Sequence
c 103	13	46.4	27	6	AX253011 Sequence	AX253011 Sequence	176	12.6	45.0	38	6	AR047595 Sequence	AR047595 Sequence
c 104	13	46.4	30	6	I27669 Sequence 24	I27669 Sequence 24	177	12.6	45.0	38	6	133669 Sequence 12	133669 Sequence 12
c 105	13	46.4	32	6	A08190 Oligonucleo	A08190 Oligonucleo	178	12.6	45.0	38	6	143817 Sequence 4	143817 Sequence 4
c 106	13	46.4	36	6	AR206961 Sequence	AR206961 Sequence	179	12.6	45.0	38	6	152760 Sequence 50	152760 Sequence 50
c 107	13	46.4	36	6	AR206963 Sequence	AR206963 Sequence	180	12.6	45.0	38	6	154647 Sequence 23	154647 Sequence 23
c 108	13	46.4	36	6	BD107722 Tissue pl	BD107722 Tissue pl	c 181	12.6	45.0	38	6	AX111341 Sequence	AX111341 Sequence
c 109	13	46.4	36	6	BD107724 Tissue pl	BD107724 Tissue pl	c 182	12.6	45.0	39	9	AS1623 Sequence 33	AS1623 Sequence 33
c 110	13	46.4	40	6	BD180768 Array of	BD180768 Array of	c 183	12.6	45.0	39	9	250830 H.sapiens m	250830 H.sapiens m
c 111	13	46.4	43	6	AR034922 Sequence	AR034922 Sequence	c 184	12.6	45.0	41	6	BD249724 Productio	BD249724 Productio
c 112	13	46.4	47	6	AX590990 Sequence	AX590990 Sequence	c 185	12.6	45.0	41	6	AR316683 Sequence	AR316683 Sequence
c 113	13	46.4	47	6	AX591143 Sequence	AX591143 Sequence	c 186	12.6	45.0	41	6	AX134748 Sequence	AX134748 Sequence
c 114	13	46.4	47	6	AX717566 Sequence	AX717566 Sequence	c 187	12.6	45.0	42	6	BD249722 Productio	BD249722 Productio
c 115	12.8	45.7	20	6	AX294614 Sequence	AX294614 Sequence	c 188	12.6	45.0	42	6	AR306649 Sequence	AR306649 Sequence
c 116	12.8	45.7	21	6	BD217310 Detection	BD217310 Detection	c 189	12.6	45.0	42	6	AR316681 Sequence	AR316681 Sequence
c 117	12.8	45.7	21	6	AX009459 Sequence	AX009459 Sequence	c 190	12.6	45.0	42	6	AR340084 Sequence	AR340084 Sequence
c 118	12.8	45.7	24	6	AX173390 Sequence	AX173390 Sequence	c 191	12.6	45.0	42	6	AR412153 Sequence	AR412153 Sequence
c 119	12.8	45.7	24	6	AX289981 Sequence	AX289981 Sequence	c 192	12.6	45.0	42	6	AX134745 Sequence	AX134745 Sequence
c 120	12.8	45.7	27	6	AX356260 Sequence	AX356260 Sequence	c 193	12.6	45.0	42	6	AX301873 Sequence	AX301873 Sequence
c 121	12.8	45.7	30	6	AX598040 Sequence	AX598040 Sequence	c 194	12.6	45.0	42	6	AX301890 Sequence	AX301890 Sequence
c 122	12.8	45.7	38	6	AR082481 Sequence	AR082481 Sequence	c 195	12.6	45.0	45	6	AR262362 Sequence	AR262362 Sequence
c 123	12.8	45.7	38	6	AR083609 Sequence	AR083609 Sequence	c 196	12.6	45.0	45	6	BD102842 Beta-Lipo	BD102842 Beta-Lipo
c 124	12.8	45.7	38	6	AR111801 Sequence	AR111801 Sequence	c 197	12.6	45.0	47	6	AR289438 Sequence	AR289438 Sequence
c 125	12.8	45.7	38	6	AR124713 Sequence	AR124713 Sequence	c 198	12.6	45.0	50	14	AX289693 Sequence	AX289693 Sequence
c 126	12.8	45.7	38	6	AR171830 Sequence	AR171830 Sequence	c 199	12.4	44.3	24	6	AX290199 Sequence	AX290199 Sequence
c 127	12.8	45.7	38	6	BD267976 Inhibitor	BD267976 Inhibitor	c 200	12.4	44.3	24	6	AX110367 Sequence	AX110367 Sequence
c 128	12.8	45.7	38	6	BD267979 Inhibitor	BD267979 Inhibitor	c 201	12.4	44.3	26	6	AX2452 Sequence 1	AX2452 Sequence 1
c 129	12.8	45.7	38	6	BD270879 Inhibitor	BD270879 Inhibitor	c 202	12.4	44.3	30	6	AX057066 Sequence	AX057066 Sequence
c 130	12.8	45.7	38	6	BD272030 Inhibitor	BD272030 Inhibitor	c 203	12.4	44.3	31	6	AR142919 Sequence	AR142919 Sequence
c 131	12.8	45.7	38	6	BD272049 Inhibitor	BD272049 Inhibitor	c 204	12.4	44.3	31	6	AR142935 Sequence	AR142935 Sequence
c 132	12.8	45.7	38	6	BD274587 Inhibitor	BD274587 Inhibitor	c 205	12.4	44.3	32	6	AR065300 Sequence	AR065300 Sequence
c 133	12.8	45.7	38	6	BD274606 Inhibitor	BD274606 Inhibitor	c 206	12.4	44.3	32	6	AR065301 Sequence	AR065301 Sequence
c 134	12.8	45.7	38	6	AR181822 Sequence	AR181822 Sequence	c 207	12.4	44.3	33	6	AX427960 Sequence	AX427960 Sequence
c 135	12.8	45.7	38	6	AR195288 Sequence	AR195288 Sequence	c 208	12.4	44.3	36	6	I45574 Sequence 2	I45574 Sequence 2
c 136	12.8	45.7	38	6	AR195291 Sequence	AR195291 Sequence	c 209	12.4	44.3	36	6	AR481892 Sequence	AR481892 Sequence
c 137	12.8	45.7	38	6	AR200004 Sequence	AR200004 Sequence	c 210	12.4	44.3	36	6	AX111714 Sequence	AX111714 Sequence
c 138	12.8	45.7	38	6	AR201357 Sequence	AR201357 Sequence	c 211	12.4	44.3	36	6	AX167463 Sequence	AX167463 Sequence
c 139	12.8	45.7	38	6	AR201376 Sequence	AR201376 Sequence	c 212	12.4	44.3	36	6	BD250410 Methods f	BD250410 Methods f
c 140	12.8	45.7	38	6	AR201379 Sequence	AR201379 Sequence	c 213	12.4	44.3	37	6	BD269056 Method fo	BD269056 Method fo
c 141	12.8	45.7	38	6	AR216100 Sequence	AR216100 Sequence	c 214	12.4	44.3	37	6	AR349544 Sequence	AR349544 Sequence
c 142	12.8	45.7	38	6	AR216103 Sequence	AR216103 Sequence	c 215	12.4	44.3	37	6	AX097677 Sequence	AX097677 Sequence
c 143	12.8	45.7	38	6	AR224809 Sequence	AR224809 Sequence	c 216	12.4	44.3	37	6	AX166879 Sequence	AX166879 Sequence
c 144	12.8	45.7	38	6	AR224812 Sequence	AR224812 Sequence	c 217	12.4	44.3	37	6	AX167006 Sequence	AX167006 Sequence
c 145	12.8	45.7	38	6	AR317268 Sequence	AR317268 Sequence	c 218	12.4	44.3	38	6	AX167362 Sequence	AX167362 Sequence
c 146	12.8	45.7	38	6	AR317271 Sequence	AR317271 Sequence	c 219	12.4	44.3	38	6	AX197432 Sequence	AX197432 Sequence
c 147	12.8	45.7	38	6	AR337543 Sequence	AR337543 Sequence	c 220	12.4	44.3	39	6	AR031539 Sequence	AR031539 Sequence
c 148	12.8	45.7	38	6	AR337546 Sequence	AR337546 Sequence	c 221	12.4	44.3	42	6	AX052952 Sequence	AX052952 Sequence
c 149	12.8	45.7	38	6	AR366767 Sequence	AR366767 Sequence	c 222	12.4	44.3	42	6	AX614307 Sequence	AX614307 Sequence
c 150	12.8	45.7	38	6	AR368682 Sequence	AR368682 Sequence	c 223	12.4	44.3	45	6	AX0614307 Sequence	AX0614307 Sequence
c 151	12.8	45.7	38	6	AR383176 Sequence	AR383176 Sequence	c 224	12.4	44.3	47	6	AR290572 Sequence	AR290572 Sequence
c 152	12.8	45.7	38	6	AR383179 Sequence	AR383179 Sequence	c 225	12.4	44.3	50	6	CQ008319 Sequence	CQ008319 Sequence
c 153	12.8	45.7	38	6	AR409180 Sequence	AR409180 Sequence	c 226	12.4	44.3	50	6	AR218534 Sequence	AR218534 Sequence
c 154	12.8	45.7	38	6	AX029448 Sequence	AX029448 Sequence	c 227	12.4	44.3	50	6	AR218535 Sequence	AR218535 Sequence
c 155	12.8	45.7	38	6	BD075055 Method fo	BD075055 Method fo	c 228	12.4	44.3	50	6	AR218538 Sequence	AR218538 Sequence
c 156	12.8	45.7	38	6	BD075058 Method fo	BD075058 Method fo	c 229	12.4	44.3	50	6	AR218539 Sequence	AR218539 Sequence
c 157	12.8	45.7	43	6	A26231 MHC HGE pri	A26231 MHC HGE pri	c 230	12.4	44.3	50	6	AR391615 Sequence	AR391615 Sequence
c 158	12.8	45.7	43	6	A26233 MHC HGE pri	A26233 MHC HGE pri	c 231	12.4	44.3	50	6	AR433565 Sequence	AR433565 Sequence
c 159	12.8	45.7	43	6	AR208357 Sequence	AR208357 Sequence	c 232	12.4	44.3	50	6	AR433567 Sequence	AR433567 Sequence
c 160	12.8	45.7	43	6	AR208359 Sequence	AR208359 Sequence	c 233	12.4	44.3	50	6	AX433571 Sequence	AX433571 Sequence
c 161	12.8	45.7	45	6	AR030774 Sequence	AR030774 Sequence	c 234	12.4	44.3	50	6	AX411551 Sequence	AX411551 Sequence
c 162	12.8	45.7	45	6	AR101778 Sequence	AR101778 Sequence	c 235	12.4	44.3	50	6	AX411552 Sequence	AX411552 Sequence
c 163	12.8	45.7	45	6	AR228249 Sequence	AR228249 Sequence	c 236	12.4	44.3	50	6	AX411557 Sequence	AX411557 Sequence
c 164	12.6	45.0	20	6	A98454 Sequence 1	A98454 Sequence 1	c 237	12.4	44.3	50	6	AX411558 Sequence	AX411558 Sequence
c 165	12.6	45.0	20	6	AR071285 Sequence	AR071285 Sequence	c 238	12.4	44.3	50	6	AX411559 Sequence	AX411559 Sequence

C 239	12.4	44.3	50	6	AX411560 Sequence	AX411560 Sequence	312	12	42.9	20	6	BD272645	BD272645 Antisense
C 240	12.4	44.3	50	6	AX411565 Sequence	AX411565 Sequence	313	12	42.9	20	6	E12680	E12680 Anti-HTLV-1
C 241	12.4	44.3	50	6	AX657040 Sequence	AX657040 Sequence	314	12	42.9	20	6	AR367884	AR367884 Sequence
C 242	12.4	44.3	50	6	AX657041 Sequence	AX657041 Sequence	315	12	42.9	22	6	A80978	A80978 Sequence 30
C 243	12.4	44.3	50	6	AX657044 Sequence	AX657044 Sequence	316	12	42.9	22	6	A95357	A95357 Sequence 30
C 244	12.4	44.3	50	6	AX657045 Sequence	AX657045 Sequence	C 317	12	42.9	24	6	AX289027	AX289027 Sequence
C 245	12.4	44.3	50	6	AX773923 Sequence	AX773923 Sequence	C 318	12	42.9	25	6	AX500847	AX500847 Sequence
C 246	12.2	43.6	18	6	I26867	I26867 Sequence 90	C 319	12	42.9	25	6	AX500853	AX500853 Sequence
C 247	12.2	43.6	18	6	I31608	I31608 Sequence 90	C 320	12	42.9	25	6	AX609295	AX609295 Sequence
C 248	12.2	43.6	19	6	I30698	I30698 Sequence 13	C 321	12	42.9	26	6	A36732	A36732 Sequence 3
C 249	12.2	43.6	19	6	I30699	I30699 Sequence 13	C 322	12	42.9	27	6	CQ797777	CQ797777 Sequence
C 250	12.2	43.6	19	6	I46157	I46157 Sequence 13	C 323	12	42.9	27	6	I44736	I44736 Sequence 3
C 251	12.2	43.6	19	6	I46158	I46158 Sequence 13	324	12	42.9	29	6	BD227388	BD227388 Secreted
C 252	12.2	43.6	19	6	AR214558	AR214558 Sequence	325	12	42.9	29	6	AX923503	AX923503 Sequence
C 253	12.2	43.6	20	6	AR230871	AR230871 Sequence	326	12	42.9	30	6	E58660	E58660 Novel metal
C 254	12.2	43.6	21	6	AX224666	AX224666 Sequence	327	12	42.9	32	6	A41180	A41180 Sequence 14
C 255	12.2	43.6	22	6	AX591616	AX591616 Sequence	328	12	42.9	32	6	AR117410	AR117410 Sequence
C 256	12.2	43.6	22	6	BD088168	BD088168 A method	C 329	12	42.9	32	6	I69226	I69226 Sequence 49
C 257	12.2	43.6	22	12	AB068979	AB068979 Synthetic	C 330	12	42.9	32	6	AR253824	AR253824 Sequence
C 258	12.2	43.6	23	6	E40789	E40789 Antihuman F	331	12	42.9	32	6	AR309049	AR309049 Sequence
C 259	12.2	43.6	23	6	AR253010	AR253010 Sequence	C 332	12	42.9	32	6	AX696879	AX696879 Sequence
C 260	12.2	43.6	24	6	BD131526	BD131526 Heat shock	C 333	12	42.9	32	9	HUMCD1B6	M22173 Human corti
C 261	12.2	43.6	25	6	AR235165	AR235165 Sequence	334	12	42.9	33	6	AR098132	AR098132 Sequence
C 262	12.2	43.6	26	6	AR121161	AR121161 Sequence	335	12	42.9	33	6	AR428448	AR428448 Sequence
C 263	12.2	43.6	26	6	AX823459	AX823459 Sequence	336	12	42.9	33	6	AR428454	AR428454 Sequence
C 264	12.2	43.6	26	6	AX823462	AX823462 Sequence	337	12	42.9	33	6	BD080488	BD080488 Methods f
C 265	12.2	43.6	28	6	AR090254	AR090254 Sequence	C 338	12	42.9	34	6	AR211327	AR211327 Sequence
C 266	12.2	43.6	28	6	AR197289	AR197289 Sequence	C 339	12	42.9	35	6	A98633	A98633 Sequence 1
C 267	12.2	43.6	28	6	AR259443	AR259443 Sequence	C 340	12	42.9	35	6	AR121376	AR121376 Sequence
C 268	12.2	43.6	28	6	AX573803	AX573803 Sequence	C 341	12	42.9	35	6	AR124108	AR124108 Sequence
C 269	12.2	43.6	30	6	A52377	A52377 Sequence 5	C 342	12	42.9	35	6	BD268671	BD268671 Isolation
C 270	12.2	43.6	30	6	AR171267	AR171267 Sequence	343	12	42.9	35	6	E12667	E12667 Anti-HTLV-1
C 271	12.2	43.6	30	6	AX548447	AX548447 Sequence	C 344	12	42.9	35	6	E36131	E36131 Chimeric se
C 272	12.2	43.6	30	10	MWHEF113A	X66551 M.musculus	C 345	12	42.9	35	6	AR269039	AR269039 Sequence
C 273	12.2	43.6	31	6	A59676	A59676 Sequence 7	C 346	12	42.9	35	6	AR437549	AR437549 Sequence
C 274	12.2	43.6	33	6	AR004878	AR004878 Sequence	C 347	12	42.9	35	6	AX022590	AX022590 Sequence
C 275	12.2	43.6	33	6	AR020560	AR020560 Sequence	C 348	12	42.9	35	6	BD073319	BD073319 Recombina
C 276	12.2	43.6	33	6	BD076373	BD076373 Recombina	C 349	12	42.9	35	6	BD080322	BD080322 Zymogen p
C 277	12.2	43.6	35	6	AR161464	AR161464 Sequence	C 350	12	42.9	36	6	A04622	A04622 Nucleotide
C 278	12.2	43.6	35	6	CQ774874	CQ774874 Sequence	C 351	12	42.9	36	6	A04623	A04623 Nucleotide
C 279	12.2	43.6	35	6	CQ774876	CQ774876 Sequence	C 352	12	42.9	36	6	A14074	A14074 Nucleotide
C 280	12.2	43.6	36	6	BD102124	BD102124 Method of	C 353	12	42.9	36	6	A14075	A14075 Nucleotide
C 281	12.2	43.6	36	6	BD021225	BD102125 Method of	354	12	42.9	36	6	AR116802	AR116802 Sequence
C 282	12.2	43.6	38	6	AR407787	AR407787 Sequence	355	12	42.9	36	6	BD181183	BD181183 Human che
C 283	12.2	43.6	38	6	AR411243	AR411243 Sequence	356	12	42.9	36	6	AR256434	AR256434 Sequence
C 284	12.2	43.6	38	6	AX190638	AX190638 Sequence	C 357	12	42.9	36	6	AR436691	AR436691 Sequence
C 285	12.2	43.6	38	6	AX370310	AX370310 Sequence	C 358	12	42.9	37	6	I69227	I69227 Sequence 49
C 286	12.2	43.6	39	6	AX516385	AX516385 Sequence	359	12	42.9	37	6	AR253825	AR253825 Sequence
C 287	12.2	43.6	40	6	AX060288	AX060288 Sequence	C 360	12	42.9	37	6	AR436900	AR436900 Sequence
C 288	12.2	43.6	41	6	AR061553	AR061553 Sequence	361	12	42.9	37	6	AX696880	AX696880 Sequence
C 289	12.2	43.6	41	6	AR108452	AR108452 Sequence	C 362	12	42.9	38	6	AR156817	AR156817 Sequence
C 290	12.2	43.6	41	6	I16409	I16409 Sequence 23	C 363	12	42.9	38	6	AR220212	AR220212 Sequence
C 291	12.2	43.6	41	6	I66895	I66895 Sequence 23	364	12	42.9	38	6	AR329755	AR329755 Sequence
C 292	12.2	43.6	41	6	I84989	I84989 Sequence 23	C 365	12	42.9	38	6	AR366635	AR366635 Sequence
C 293	12.2	43.6	41	6	AR263413	AR263413 Sequence	C 366	12	42.9	38	6	AX358372	AX358372 Sequence
C 294	12.2	43.6	41	6	AX516722	AX516722 Sequence	C 367	12	42.9	41	6	AX097532	AX097532 Sequence
C 295	12.2	43.6	41	6	AX518886	AX518886 Sequence	C 368	12	42.9	41	6	AX520201	AX520201 Sequence
C 296	12.2	43.6	42	6	AX497900	AX497900 Sequence	C 369	12	42.9	42	6	AX840438	AX840438 Sequence
C 297	12.2	43.6	43	6	AR061564	AR061564 Sequence	C 370	12	42.9	45	6	I17261	I17261 Sequence 27
C 298	12.2	43.6	43	6	AR108463	AR108463 Sequence	371	12	42.9	45	6	I17262	I17262 Sequence 28
C 299	12.2	43.6	43	6	I16420	I16420 Sequence 24	C 372	12	42.9	45	6	I55020	I55020 Sequence 44
C 300	12.2	43.6	43	6	I66906	I66906 Sequence 24	373	12	42.9	45	6	AR481915	AR481915 Sequence
C 301	12.2	43.6	43	6	I85000	I85000 Sequence 24	374	12	42.9	45	6	AR481916	AR481916 Sequence
C 302	12.2	43.6	43	6	AR263424	AR263424 Sequence	375	12	42.9	47	6	I17263	I17263 Sequence 29
C 303	12.2	43.6	44	6	AR4734	AR4734 Sequence 12	C 376	12	42.9	47	6	AR288962	AR288962 Sequence
C 304	12.2	43.6	44	6	BD107486	BD107486 Method of	C 377	12	42.9	47	6	AR291516	AR291516 Sequence
C 305	12.2	43.6	45	6	AR263588	AR263588 Sequence	378	12	42.9	47	6	AR481917	AR481917 Sequence
C 306	12.2	43.6	45	6	BD168552	BD168552 Cells pro	379	12	42.9	48	6	I17260	I17260 Sequence 26
C 307	12.2	43.6	48	6	BD191587	BD191587 Single-ch	C 380	12	42.9	48	6	AR444664	AR444664 Sequence
C 308	12.2	43.6	48	6	AR262537	AR262537 Sequence	381	12	42.9	48	6	AR481914	AR481914 Sequence
C 309	12.2	43.6	50	6	CQ813892	CQ813892 Sequence	382	12	42.9	48	6	AX076591	AX076591 Sequence
C 310	12.2	43.6	50	6	E40770	E40770 Antihuman F	C 383	12	42.9	48	6	AX426699	AX426699 Sequence
C 311	12	42.9	20	6	AR121024	AR121024 Sequence	C 384	12	42.9	49	6	BD175537	BD175537 Secretary

C 385	12	42.9	49	6	AR410793	Sequence	458	11.8	42.1	37	6	AR181189	Sequence
C 386	12	42.9	49	6	AR410917	Sequence	459	11.8	42.1	37	6	AR220213	Sequence
C 387	12	42.9	49	6	AR439157	Sequence	460	11.8	42.1	37	6	AR366636	Sequence
C 388	12	42.9	49	6	AR439281	Sequence	461	11.8	42.1	37	6	AR358373	Sequence
C 389	12	42.9	49	6	AR473177	Sequence	462	11.8	42.1	37	6	AR769572	Sequence
C 390	12	42.9	49	6	AR473301	Sequence	C 463	11.8	42.1	38	6	AR082478	Sequence
C 391	12	42.9	49	6	AR473301	Sequence	C 464	11.8	42.1	38	6	AR083606	Sequence
C 392	12	42.9	49	6	AR697789	Sequence	C 465	11.8	42.1	38	6	AR111798	Sequence
C 393	12	42.9	49	6	BD075686	Secretory	C 466	11.8	42.1	38	6	AR124710	Sequence
C 394	12	42.9	49	6	BD172546	Secreted	C 467	11.8	42.1	38	6	AR171827	Sequence
C 395	12	42.9	49	6	BD172865	Secreted	C 468	11.8	42.1	38	6	BD267973	Inhibitor
C 396	12	42.9	49	6	BD173184	Secreted	C 469	11.8	42.1	38	6	BD270876	Inhibitor
C 397	12	42.9	49	6	BD173503	Secreted	C 470	11.8	42.1	38	6	BD272027	Inhibitor
C 398	12	42.9	50	6	CQ005575	Sequence	C 471	11.8	42.1	38	6	BD272046	Inhibitor
C 399	12	42.9	50	6	I09225	Sequence 26	C 472	11.8	42.1	38	6	BD274584	Inhibitor
C 400	11.8	42.1	18	6	AR073370	Sequence	C 473	11.8	42.1	38	6	BD274603	Inhibitor
C 401	11.8	42.1	18	6	BD250694	Identific	C 474	11.8	42.1	38	6	AR181819	Sequence
C 402	11.8	42.1	19	6	AR242594	Sequence	C 475	11.8	42.1	38	6	AR195285	Sequence
C 403	11.8	42.1	19	6	AR242603	Sequence	C 476	11.8	42.1	38	6	AR200001	Sequence
C 404	11.8	42.1	19	6	AX080228	Sequence	C 477	11.8	42.1	38	6	AR201354	Sequence
C 405	11.8	42.1	19	6	AX080237	Sequence	C 478	11.8	42.1	38	6	AR216097	Sequence
C 406	11.8	42.1	20	6	AR084397	Sequence	C 479	11.8	42.1	38	6	AR224806	Sequence
C 407	11.8	42.1	20	6	AR156820	Sequence	C 480	11.8	42.1	38	6	AR317255	Sequence
C 408	11.8	42.1	20	6	AR220187	Sequence	C 481	11.8	42.1	38	6	AR337540	Sequence
C 409	11.8	42.1	20	6	AR366638	Sequence	C 482	11.8	42.1	38	6	AR366764	Sequence
C 410	11.8	42.1	20	6	AX167253	Sequence	C 483	11.8	42.1	38	6	AR368679	Sequence
C 411	11.8	42.1	20	6	AX358347	Sequence	C 484	11.8	42.1	38	6	AR383173	Sequence
C 412	11.8	42.1	20	6	BD227358	Secreted	C 485	11.8	42.1	38	6	AR409177	Sequence
C 413	11.8	42.1	21	6	AX712188	Sequence	C 486	11.8	42.1	38	6	AX029445	Sequence
C 414	11.8	42.1	21	6	AX952294	Sequence 2	C 487	11.8	42.1	38	6	AX029445	Method fo
C 415	11.8	42.1	21	6	AX3656	Sequence	C 488	11.8	42.1	39	6	BD083663	Disulfide
C 416	11.8	42.1	22	6	AR003708	Sequence	C 489	11.8	42.1	40	6	BD185649	Methods f
C 417	11.8	42.1	22	6	AX504898	Sequence	C 490	11.8	42.1	40	6	BD185795	Methods f
C 418	11.8	42.1	23	6	AX504909	Sequence	C 491	11.8	42.1	40	6	BD187660	Methods f
C 419	11.8	42.1	23	6	AX504911	Sequence	C 492	11.8	42.1	40	6	BD187660	Methods f
C 420	11.8	42.1	23	6	AX959156	Sequence	C 493	11.8	42.1	40	6	BD189712	Methods f
C 421	11.8	42.1	23	6	AX959167	Sequence	C 494	11.8	42.1	40	6	AR342178	Sequence
C 422	11.8	42.1	24	6	I73496	Sequence 9	C 495	11.8	42.1	40	6	AX932208	Sequence
C 423	11.8	42.1	24	6	AX291696	Sequence	C 496	11.8	42.1	40	6	AR082473	Sequence
C 424	11.8	42.1	24	6	AX504899	Sequence	C 497	11.8	42.1	41	6	AR083601	Sequence
C 425	11.8	42.1	24	6	AX504911	Sequence	C 498	11.8	42.1	41	6	AR096931	Sequence
C 426	11.8	42.1	24	6	AX959157	Sequence	C 499	11.8	42.1	41	6	AR111793	Sequence
C 427	11.8	42.1	24	6	AX959169	Sequence	C 500	11.8	42.1	41	6	AR124705	Sequence
C 428	11.8	42.1	25	6	CQ628886	Sequence	C 501	11.8	42.1	41	6	AR124705	Sequence
C 429	11.8	42.1	25	6	CQ628887	Sequence	C 502	11.8	42.1	41	6	BD267968	Inhibitor
C 430	11.8	42.1	25	6	CQ628888	Sequence	C 503	11.8	42.1	41	6	BD270871	Inhibitor
C 431	11.8	42.1	25	6	AR469949	Sequence	C 504	11.8	42.1	41	6	BD272022	Inhibitor
C 432	11.8	42.1	25	6	AR469950	Sequence	C 505	11.8	42.1	41	6	BD272041	Inhibitor
C 433	11.8	42.1	25	6	AR469951	Sequence	C 506	11.8	42.1	41	6	BD274579	Inhibitor
C 434	11.8	42.1	25	6	AX179680	Sequence	C 507	11.8	42.1	41	6	BD274598	Inhibitor
C 435	11.8	42.1	25	6	AX504900	Sequence	C 508	11.8	42.1	41	6	AR181814	Sequence
C 436	11.8	42.1	25	6	AX504913	Sequence	C 509	11.8	42.1	41	6	AR195280	Sequence
C 437	11.8	42.1	25	6	AX744587	Sequence	C 510	11.8	42.1	41	6	AR199996	Sequence
C 438	11.8	42.1	25	6	AX744588	Sequence	C 511	11.8	42.1	41	6	AR201349	Sequence
C 439	11.8	42.1	25	6	AX744589	Sequence	C 512	11.8	42.1	41	6	AR201368	Sequence
C 440	11.8	42.1	25	6	AX782929	Sequence	C 513	11.8	42.1	41	6	AR216092	Sequence
C 441	11.8	42.1	25	6	AX782930	Sequence	C 514	11.8	42.1	41	6	AR224801	Sequence
C 442	11.8	42.1	25	6	AX782931	Sequence	C 515	11.8	42.1	41	6	AR317260	Sequence
C 443	11.8	42.1	25	6	AX959158	Sequence	C 516	11.8	42.1	41	6	AR337535	Sequence
C 444	11.8	42.1	25	6	AX959171	Sequence	C 517	11.8	42.1	41	6	AR366759	Sequence
C 445	11.8	42.1	25	6	AX959172	Sequence	C 518	11.8	42.1	41	6	AR368674	Sequence
C 446	11.8	42.1	25	6	AX959172	Sequence	C 519	11.8	42.1	41	6	AR383168	Sequence
C 447	11.8	42.1	25	6	BD161089	RNA molec	C 520	11.8	42.1	41	6	AR409172	Sequence
C 448	11.8	42.1	26	6	AX351788	Sequence	C 521	11.8	42.1	41	6	AX004513	Sequence
C 449	11.8	42.1	26	6	AX351788	Sequence	C 522	11.8	42.1	41	6	AX029440	Sequence
C 450	11.8	42.1	30	6	AX792831	Sequence	C 523	11.8	42.1	41	6	AX515248	Sequence
C 451	11.8	42.1	31	6	AX249623	Sequence	C 524	11.8	42.1	41	6	AX517745	Sequence
C 452	11.8	42.1	34	6	AX467532	Sequence	C 525	11.8	42.1	41	6	AX518216	Sequence
C 453	11.8	42.1	36	6	BD174700	Ribozyme	C 526	11.8	42.1	41	6	BD075047	Method fo
C 454	11.8	42.1	37	6	AR003401	Sequence	C 527	11.8	42.1	41	6	BD136126	Vaccines
C 455	11.8	42.1	37	6	AR156818	Sequence	C 528	11.8	42.1	41	6	L39570 Homo sapien	
C 456	11.8	42.1	37	6	I21190	Sequence 36	C 529	11.8	42.1	41	9	HUMTCRWJ32	
C 457	11.8	42.1	37	6	I74457	Sequence 36	C 530	11.8	42.1	43	6	AX601642	Sequence

531	11.8	42.1	44	6	AR442669	Sequence	604	11.6	41.4	28	6	AX193528	Sequence
532	11.8	42.1	44	6	AX513493	Sequence	c 605	11.6	41.4	28	6	AX358202	Sequence
533	11.8	42.1	45	9	HUMIGHABH	L06994 Homo sapien	606	11.6	41.4	30	6	AX135796	Sequence
c 534	11.8	42.1	47	6	AR161514	Sequence	c 607	11.6	41.4	30	6	AX791082	Sequence
c 535	11.8	42.1	47	6	AR161530	Sequence	c 608	11.6	41.4	30	6	AX791177	Sequence
c 536	11.8	42.1	47	6	AR284752	Sequence	c 609	11.6	41.4	30	6	BD107206	Base sequ
c 537	11.8	42.1	47	6	AR289051	Sequence	c 610	11.6	41.4	33	6	AX033184	Sequence
538	11.8	42.1	48	9	S82552	rearranged	c 611	11.6	41.4	34	11	C75763	
539	11.8	42.1	50	6	CQ002681	Sequence	c 612	11.6	41.4	35	6	BD264035	
540	11.8	42.1	50	6	CQ005437	Sequence	613	11.6	41.4	35	6	I92423	Sequence 75
c 541	11.8	42.1	50	6	CQ006595	Sequence	614	11.6	41.4	35	6	AX751490	Sequence
c 542	11.8	42.1	50	6	AR218536	Sequence	615	11.6	41.4	36	6	AR041542	Sequence
c 543	11.8	42.1	50	6	AR218537	Sequence	616	11.6	41.4	36	6	AR045320	Sequence
c 544	11.8	42.1	50	6	AR218540	Sequence	617	11.6	41.4	36	6	AR132686	Sequence
c 545	11.8	42.1	50	6	AR433566	Sequence	618	11.6	41.4	36	6	AR132687	Sequence
c 546	11.8	42.1	50	6	AR433568	Sequence	619	11.6	41.4	36	6	AR133762	Sequence
c 547	11.8	42.1	50	6	AR433570	Sequence	620	11.6	41.4	36	6	BD251317	Pancreas
c 548	11.8	42.1	50	6	AX411553	Sequence	621	11.6	41.4	36	6	I52372	Sequence 11
c 549	11.8	42.1	50	6	AX411554	Sequence	622	11.6	41.4	36	6	I77550	Sequence 25
c 550	11.8	42.1	50	6	AX411555	Sequence	623	11.6	41.4	36	6	I77974	Sequence 68
551	11.8	42.1	50	6	AX411556	Sequence	624	11.6	41.4	36	6	I78008	Sequence 71
c 552	11.8	42.1	50	6	AX657042	Sequence	625	11.6	41.4	36	6	AR200546	Sequence
c 553	11.8	42.1	50	6	AX657043	Sequence	626	11.6	41.4	36	6	AX421424	Sequence
c 554	11.8	42.1	50	6	AX657046	Sequence	627	11.6	41.4	36	6	AX573483	Sequence
555	11.8	42.1	50	8	NFA538887	Nicotiana	628	11.6	41.4	36	6	AX637000	Sequence
c 556	11.6	41.4	18	6	AX254790	Sequence	629	11.6	41.4	36	6	AX638269	Sequence
c 557	11.6	41.4	18	6	AX254792	Sequence	630	11.6	41.4	36	6	AX638511	Sequence
558	11.6	41.4	19	6	AR166701	Sequence	631	11.6	41.4	36	6	AX638545	Sequence
c 559	11.6	41.4	19	6	BD084003	Diagnosi	632	11.6	41.4	37	6	BD266828	Human bra
c 560	11.6	41.4	20	6	AR310857	Sequence	633	11.6	41.4	37	6	BD266830	Human bra
c 561	11.6	41.4	20	6	AX512395	Sequence	c 634	11.6	41.4	37	6	AX278121	Sequence
c 562	11.6	41.4	21	6	AR225951	Sequence	635	11.6	41.4	38	6	AR045746	Sequence
c 563	11.6	41.4	21	6	AX096736	Sequence	636	11.6	41.4	38	6	AR046785	Sequence
564	11.6	41.4	21	6	AX145813	Sequence	637	11.6	41.4	38	6	AR047653	Sequence
565	11.6	41.4	21	6	BD094209	Genes for	638	11.6	41.4	38	6	AR047787	Sequence
c 566	11.6	41.4	22	6	AR303962	Sequence	639	11.6	41.4	38	6	I52798	Sequence 53
c 567	11.6	41.4	22	6	AX551577	Sequence	640	11.6	41.4	38	6	I53837	Sequence 15
c 568	11.6	41.4	23	6	AR148148	Sequence	641	11.6	41.4	38	6	I54705	Sequence 24
569	11.6	41.4	23	6	BD179348	Insulin-1	642	11.6	41.4	38	6	I54839	Sequence 25
c 570	11.6	41.4	23	6	BD243865	STE20-rel	643	11.6	41.4	38	6	AX222424	Sequence
c 571	11.6	41.4	23	6	E30554	Neurogenesi	644	11.6	41.4	38	6	AX776711	Sequence
c 572	11.6	41.4	23	6	AR217407	Sequence	c 645	11.6	41.4	38	6	BD143241	Fucose-ep
c 573	11.6	41.4	23	6	AR256813	Sequence	c 646	11.6	41.4	39	6	CQ778839	Sequence
574	11.6	41.4	23	6	AR268842	Sequence	c 647	11.6	41.4	39	6	CQ778871	Sequence
c 575	11.6	41.4	23	6	AR369300	Sequence	c 648	11.6	41.4	39	6	AX081636	Sequence
c 576	11.6	41.4	23	6	AR435618	Sequence	c 649	11.6	41.4	39	6	AX374817	Sequence
c 577	11.6	41.4	23	6	AR453219	Sequence	650	11.6	41.4	40	6	A05823	Oligonucleo
c 578	11.6	41.4	23	6	BD000639	Formation	c 651	11.6	41.4	40	6	AR302069	Sequence
c 579	11.6	41.4	23	6	BD105356	Novel ins	c 652	11.6	41.4	40	6	AR338170	Sequence
580	11.6	41.4	24	6	AR066370	Sequence	c 653	11.6	41.4	40	6	AR343087	Sequence
c 581	11.6	41.4	24	6	AR130356	Sequence	c 654	11.6	41.4	40	6	BD137947	Antigen 1
c 582	11.6	41.4	24	6	E11684	PCR primer.	c 655	11.6	41.4	40	9	S80819	gamma delta
c 583	11.6	41.4	24	6	E13116	Oligonucleo	656	11.6	41.4	41	6	A40462	Sequence 8
c 584	11.6	41.4	25	6	CQ619815	Sequence	c 657	11.6	41.4	41	6	BD249710	Productio
c 585	11.6	41.4	25	6	CQ619816	Sequence	c 658	11.6	41.4	41	6	AR316670	Sequence
c 586	11.6	41.4	25	6	CQ619817	Sequence	c 659	11.6	41.4	41	6	AX134733	Sequence
c 587	11.6	41.4	25	6	CQ619818	Sequence	660	11.6	41.4	41	6	AX278092	Sequence
c 588	11.6	41.4	25	6	CQ619819	Sequence	c 661	11.6	41.4	41	6	AX301861	Sequence
c 589	11.6	41.4	25	6	CQ619820	Sequence	662	11.6	41.4	41	6	AX516543	Sequence
c 590	11.6	41.4	25	6	CQ619821	Sequence	663	11.6	41.4	42	6	AR195558	Sequence
c 591	11.6	41.4	25	6	CQ619822	Sequence	c 664	11.6	41.4	43	6	AX268517	Sequence
c 592	11.6	41.4	25	6	AR460878	Sequence	665	11.6	41.4	45	6	A18444	primer B se
c 593	11.6	41.4	25	6	AR460879	Sequence	c 666	11.6	41.4	45	6	A40463	Sequence 9
c 594	11.6	41.4	25	6	AR460880	Sequence	c 667	11.6	41.4	47	6	AR284532	Sequence
c 595	11.6	41.4	25	6	AR460881	Sequence	668	11.6	41.4	47	6	AR284697	Sequence
c 596	11.6	41.4	25	6	AR460882	Sequence	669	11.6	41.4	47	6	AR291148	Sequence
c 597	11.6	41.4	25	6	AR460883	Sequence	c 670	11.6	41.4	47	6	AR292047	Sequence
c 598	11.6	41.4	25	6	AR460884	Sequence	c 671	11.6	41.4	47	6	AX252287	Sequence
c 599	11.6	41.4	25	6	AR460885	Sequence	c 672	11.6	41.4	48	6	A49833	Sequence 6
c 600	11.6	41.4	27	6	CQ771800	Sequence	c 673	11.6	41.4	48	6	CQ767217	Sequence
601	11.6	41.4	28	6	CQ797707	Sequence	c 674	11.6	41.4	48	6	AX222314	Sequence
602	11.6	41.4	28	6	AR428335	Sequence	c 675	11.6	41.4	48	6	AX426278	Sequence
c 603	11.6	41.4	28	6	AR491480	Sequence	c 676	11.6	41.4	48	6	AX426656	Sequence

677	11.6	41.4	48	11	AX465937	AX465937 Arabidopsis	c 750	11.4	40.7	38	6	AX134698	AX134698 Sequence
678	11.6	41.4	49	6	A05822	A05822 Oligonucleo	c 751	11.4	40.7	39	6	A93648	A93648 Sequence 2
679	11.6	41.4	50	3	DVGLDXYR	DVGLDXYR D.virilis Y	c 752	11.4	40.7	39	6	AR225171	AR225171 Sequence
680	11.6	41.4	50	6	CQ003082	CQ003082 Infectious	753	11.4	40.7	39	6	AX591009	AX591009 Sequence
681	11.6	41.4	50	6	E49327	E49327 Infectious	754	11.4	40.7	39	6	AX591162	AX591162 Sequence
682	11.6	41.4	50	6	I22461	I22461 Sequence 10	755	11.4	40.7	39	6	AX717585	AX717585 Sequence
683	11.6	41.4	50	6	I45537	I45537 Sequence 10	c 756	11.4	40.7	40	6	BD179484	BD179484 Gene expr
684	11.6	41.4	50	6	I45537	I45537 Sequence 10	c 757	11.4	40.7	40	6	BD188823	BD188823 Gene expr
685	11.6	41.4	50	6	AR269185	AR269185 Sequence	758	11.4	40.7	40	9	AF505564	AF505564 Homo sapi
686	11.6	41.4	50	6	AR427256	AR427256 Sequence	759	11.4	40.7	41	6	AR454201	AR454201 Sequence
687	11.6	41.4	50	6	AX987950	AX987950 Sequence	760	11.4	40.7	42	6	AR317221	AR317221 Sequence
688	11.6	41.4	50	6	BD015910	BD015910 Infectiou	c 761	11.4	40.7	44	6	BD224796	BD224796 Novel pla
689	11.6	41.4	50	6	BD016278	BD016278 Infectiou	c 762	11.4	40.7	44	6	AX601752	AX601752 Sequence
690	11.6	41.4	50	6	BD122809	BD122809 EST and e	c 763	11.4	40.7	44	6	AX601753	AX601753 Sequence
691	11.4	40.7	20	6	AR315809	AR315809 Sequence	c 764	11.4	40.7	44	6	AX601754	AX601754 Sequence
692	11.4	40.7	20	6	AX069245	AX069245 Sequence	c 765	11.4	40.7	44	6	AX601755	AX601755 Sequence
693	11.4	40.7	20	6	AX295403	AX295403 Sequence	c 766	11.4	40.7	44	6	AX601756	AX601756 Sequence
694	11.4	40.7	22	6	E13354	E13354 Primer. 4/1	c 767	11.4	40.7	44	6	AX601757	AX601757 Sequence
695	11.4	40.7	22	6	I17617	I17617 Sequence 9	c 768	11.4	40.7	44	6	AX601758	AX601758 Sequence
696	11.4	40.7	22	6	I17623	I17623 Sequence 15	c 769	11.4	40.7	44	6	AX601762	AX601762 Sequence
697	11.4	40.7	22	6	I38399	I38399 Sequence 9	c 770	11.4	40.7	44	6	AX601763	AX601763 Sequence
698	11.4	40.7	22	6	I38405	I38405 Sequence 15	c 771	11.4	40.7	44	6	AX601764	AX601764 Sequence
699	11.4	40.7	23	6	AX776584	AX776584 Sequence	c 772	11.4	40.7	44	6	AX601765	AX601765 Sequence
700	11.4	40.7	24	6	AR364493	AR364493 Sequence	c 773	11.4	40.7	44	6	AX601766	AX601766 Sequence
701	11.4	40.7	24	6	AR204662	AR204662 Sequence	c 774	11.4	40.7	44	6	AX601767	AX601767 Sequence
702	11.4	40.7	24	6	AX290770	AX290770 Sequence	c 775	11.4	40.7	45	6	A59387	A59387 Sequence 37
703	11.4	40.7	25	6	AX444442	AX444442 Sequence	c 776	11.4	40.7	45	6	AR036051	AR036051 Sequence
704	11.4	40.7	25	6	AR049774	AR049774 Sequence	c 777	11.4	40.7	45	6	AR179651	AR179651 Sequence
705	11.4	40.7	25	6	AR149668	AR149668 Sequence	c 778	11.4	40.7	45	6	I00829	I00829 Sequence 3
706	11.4	40.7	25	6	E09751	E09751 Primer used	c 779	11.4	40.7	45	6	I00829	I00829 Sequence 3
707	11.4	40.7	25	6	E09955	E09955 Primer for	c 780	11.4	40.7	46	6	AX343260	AX343260 Sequence
708	11.4	40.7	25	6	E34112	E34112 Protein par	c 781	11.4	40.7	46	6	AX351640	AX351640 Sequence
709	11.4	40.7	25	6	AR404797	AR404797 Sequence	c 782	11.4	40.7	47	6	MUSLINB1	MUSLINB1 Mouse (BALB
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ALIGNMENTS

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LOCUS A method for determination of a nucleic acid using a control.
DEFINITION
BD181370.1 GI:30792288
VERSION JP 2002335981-A/9.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 28)
Jaeger,S.
AUTHORS A method for determination of a nucleic acid using a control
TITLE Patent: JP 2002335981-A 9 26-NOV-2002;
JOURNAL F. HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 2002335981-A/9
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/566,G01N33/58,
PC C12N15/00
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FH Key Location/Qualifiers
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DEFINITION
ACCESSION AX523950
VERSION AX523950.1 GI:25168881
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
Jaeger,S.
AUTHORS A method for determination of a nucleic acid using a control
TITLE Patent: EP 1236804-A 9 04-SEP-2002;
JOURNAL Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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AX524848 28 bp DNA linear PAT 21-NOV-2002
LOCUS Sequence 9 from Patent EP1236805.
DEFINITION
ACCESSION AX524848
VERSION AX524848.1 GI:25169942
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
Jaeger,S.
AUTHORS A method for the determination of a nucleic acid using a control
TITLE Patent: EP 1236805-A 9 04-SEP-2002;
JOURNAL Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES Location/Qualifiers
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ACCESSION    AR289945
VERSION      AR289945.1 GI:31677229
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 47)
AUTHORS      Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE        Biallelic markers for use in constructing a high density
JOURNAL      disequilibrium map of the human genome
FEATURES     Patent: US 6537751-A 1680 25-MAR-2003;
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ACCESSION    AX710947
VERSION      AX710947.1 GI:29787328
KEYWORDS     Human herpesvirus 5
SOURCE       Human herpesvirus 5
ORGANISM     Human herpesvirus 5
REFERENCE    1 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
              Betaherpesvirinae; Cytomegalovirus.
AUTHORS      Draper,K.G., Mcswiggen,J.A., Holecck,J.J., Dudycz,L.W.,
              Macejak,D.G. and Mamone,J.A.
TITLE        Method and reagent for inhibiting HBV viral replication
JOURNAL      Patent: EP 1288296-A 247 05-MAR-2003;
              RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES     Location/Qualifiers
              1..36
              /organism="Human herpesvirus 5"
              /mol_type="unassigned RNA"
              /db_xref="taxon:10359"
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Query Match      55.0%; Score 15.4; DB 6; Length 36;
Best Local Similarity 70.4%; Pred. No. 1.4e+04;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy      2 GTTCGTGGGATAGTCCGTCATGGTGT 28
Db      28 GTACTGGGGAAAGACCTTCATGGWGAT 2

RESULT 6
LOCUS       CQ779042/c                    37 bp    DNA
DEFINITION   Sequence 30 from Patent WO2004015117.
ACCESSION    CQ779042
VERSION      CQ779042.1 GI:45381689
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.

REFERENCE    1 te,Riele,H.P.
              Targeted gene modification by single-stranded dna oligonucleotides
              Patent: WO 2004015117-A 30 19-FEB-2004;
              Het Nederlands Kanker Instituut (NL)
              Location/Qualifiers
              1..37
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              /db_xref="taxon:32630"
              /note="ss DNA oligonucleotide"
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Query Match      53.6%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 TCGTGGGATAGTCCG 18
Db      15 TCGTGGGATAGTCCG 1

RESULT 7
LOCUS       BD244764/c                    15 bp    DNA
DEFINITION   Isolation method of primer extension products by modular
              oligonucleotide.
ACCESSION    BD244764
VERSION      BD244764.1 GI:33054534
KEYWORDS     JP 2002525076-A/43.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Lundberg,J. and Uhlen,M.
TITLE        Isolation method of primer extension products by modular
JOURNAL      Patent: JP 2002525076-A 43 13-AUG-2002;
              DYNAL AS
COMMENT      OS Artificial Sequence
              PN JP 2002525076-A/43
              PD 13-AUG-2002
              PF 15-SEP-1999 JP 2000570369
              PR 15-SEP-1998 US 09/153242,16-SEP-1998 GB 9820185.8 PI
              PC C12N15/09,C12Q1/68,C12N15/00
              CC Description of Artificial Sequence: Synthetic oligonucleotide
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FEATURES     Location/Qualifiers
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              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
ORIGIN
Query Match      53.6%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 TCGTGGGATAGTCCG 18
Db      15 TCGTGGGATAGTCCG 1

RESULT 8
LOCUS       AR255271/c                    15 bp    DNA
DEFINITION   Sequence 37 from patent US 6482592.
ACCESSION    AR255271
VERSION      AR255271.1 GI:27304320
KEYWORDS     Sequence 37 from patent US 6482592.
SOURCE       AR255271
ORGANISM     AR255271.1 GI:27304320

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KEYWORDS	Unknown.	
	SOURCE Unknown.	
	ORGANISM Unclassified.	
REFERENCE	1 (bases 1 to 15)	
	Lundeberg,J. and Uhlen,M.	
	Methods and kits for isolating primer extension products using modular oligonucleotides	
JOURNAL	Patent: US 6482592-A 37 19-NOV-2002;	
	TITLE Location/Qualifiers	
	1. .15	
FEATURES	source	
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	Best Local Similarity 100.0%; Pred. No. 2.1e+04;	
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QY	4 TCGTGGGATGTCG 18	
	15 TCGTGGGATGTCG 1	
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RESULT 9	AX645654/c	
	LOCUS AX645654 19 bp DNA linear PAT 03-MAR-2003	
	DEFINITION Sequence 8 from Patent EP1270738.	
ACCESSION	AX645654	
	VERSION AX645654.1 GI:28798009	
	KEYWORDS	
SOURCE	synthetic construct	
	synthetic construct	
	artificial sequences.	
REFERENCE	1	
	Niemeyer,C.M., Wacker,R. and Adler,M.	
	Method for detecting substances in liquids	
TITLE	Patent: EP 1270738-A 8 02-JAN-2003;	
	JOURNAL Chimera Biotec GmbH (DE)	
FEATURES	Location/Qualifiers	
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misc_feature	/mol_type="unassigned DNA"	
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	/note="biotinyliert"	
Query Match	53.6%; Score 15; DB 6; Length 19;	
	Best Local Similarity 100.0%; Pred. No. 2.2e+04;	
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGTTCGTGGGATAGT 15	
	15 CGTTCGTGGGATAGT 1	
Db		
RESULT 10	AX645658	
	LOCUS AX645658 19 bp DNA linear PAT 03-MAR-2003	
	DEFINITION Sequence 12 from Patent EP1270738.	
ACCESSION	AX645658	
	VERSION AX645658.1 GI:28798013	
	KEYWORDS	
SOURCE	synthetic construct	
	synthetic construct	
	artificial sequences.	
REFERENCE	1	
	Niemeyer,C.M., Wacker,R. and Adler,M.	
	Method for detecting substances in liquids	
TITLE	Patent: EP 1270738-A 12 02-JAN-2003;	
	JOURNAL Chimera Biotec GmbH (DE)	
FEATURES	Location/Qualifiers	
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ORIGIN	1	
	/note="biotinyliert"	
Query Match	53.6%; Score 15; DB 6; Length 19;	
	Best Local Similarity 100.0%; Pred. No. 2.2e+04;	
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGTTCGTGGGATAGT 15	
	15 CGTTCGTGGGATAGT 1	
Db		
RESULT 11	AX097318/c	
	LOCUS AX097318 21 bp DNA linear PAT 30-MAR-2001	
	DEFINITION Sequence 2496 from Patent WO0118250.	
ACCESSION	AX097318	
	VERSION AX097318.1 GI:13513795	
	KEYWORDS	
SOURCE	Homo sapiens (human)	
	Homo sapiens	
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
	Lander,E.S., Gargill,M., Ireland,J.S., Bolck,S., Daley,G.Q. and McCarthy,J.J.	
	Single nucleotide polymorphisms in genes	
TITLE	Patent: WO 0118250-A 2496 15-MAR-2001;	
	JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)	
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	52.1%; Score 14.6; DB 6; Length 21;	
	Query Match 81.0%; Pred. No. 3.5e+04;	
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QY	2 GTTCGTGGGATAGTCCGTGTCAT 22	
	21 GTTCGTGGGATAGTCCGTGTCAT 1	
Db		
RESULT 12	E31555/c	
	LOCUS E31555 Cecropin gene.	
	DEFINITION E31555 GI:13017395	
ACCESSION	E31555.1 GI:13017395	
	VERSION JP 1999313680-A/6.	
	KEYWORDS	
SOURCE	unidentified	
	unidentified	
	unclassified.	
REFERENCE	1 (bases 1 to 23)	
	Yoshio,M., Kazumi,S., Tomohisa,K., Yasushi,H. and Keiko,N.	
	Cecropin gene	
TITLE	Patent: JP 1999313680-A 6 16-NOV-1999;	
	JOURNAL IWATE PREF	
COMMENT	OS Unidentified	
	PN JP 1999313680-A/6	
	PD 16-NOV-1999	
PF	30-APR-1998 JP 1998121309	
	PI	
	YOSHIO MIURA, KAZUMI SUZUKI, TOMOHISA KURODA, YASUSHI HIKIJI, PI KEIKO NASU	

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PC C12N15/09,A01H5/00,C07K14/415,C12N5/10//A01N63/00,C12N15/00,
PC C12N5/00
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Best Local Similarity 81.0%; Pred. No. 3.5e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22
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Db 22 GATAGTGGGATTGTGCGTCAT 2

RESULT 13
AR172071/c
LOCUS AR172071 38 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 25 from patent US 6297425.
ACCESSION AR172071
VERSION AR172071.1 GI:17911021
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6297425-A 25 02-OCT-2001;
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Query Match 52.1%; Score 14.6; DB 6; Length 38;
Best Local Similarity 81.0%; Pred. No. 3.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22
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Db 22 GATAGTGGGATTGTGCGTCAT 2

RESULT 14
AR173362/c
LOCUS AR173362 38 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 25 from patent US 6303846.
ACCESSION AR173362
VERSION AR173362.1 GI:17912853
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6303846-A 25 16-OCT-2001;
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Best Local Similarity 81.0%; Pred. No. 3.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

PC C12N15/09,A01H5/00,C07K14/415,C12N5/10//A01N63/00,C12N15/00,
PC C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
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FT source Location/Qualifiers
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Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22
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Db 22 GATAGTGGGATTGTGCGTCAT 2

RESULT 15
AR437662/c
LOCUS AR437662 50 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6660524.
ACCESSION AR437662
VERSION AR437662.1 GI:40202820
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Turck,J.A. and Archer,J.A.C.
TITLE Control of gene expression in eukaryotes
JOURNAL Patent: US 6660524-A 14 09-DEC-2003;
FEATURES
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Best Local Similarity 81.0%; Pred. No. 3.7e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22
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Db 22 GATAGTGGGATTGTGCGTCAT 2

RESULT 16
AX026712/c
LOCUS AX026712 50 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 14 from Patent WO039300.
ACCESSION AX026712
VERSION AX026712.1 GI:10187879
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Archer,J.A. and Tuerck,J.A.
TITLE Control of gene expression in eukaryotes
JOURNAL Patent: WO 0039300-A 14 06-JUL-2000;
CAMBRIDGE ADVANCED TECH (GB)
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Query Match 52.1%; Score 14.6; DB 6; Length 50;
Best Local Similarity 81.0%; Pred. No. 3.7e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22
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Db 37 GATAGTGGGATTGTGCGTCAT 17

RESULT 17
AR200549/c
LOCUS AR200549 32 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 78 from patent US 6358505.
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LOCUS AR171824 38 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 18 from patent US 6297239.
ACCESSION AR171824
VERSION AR171824.1 GI:17910774
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Desolms,S.Jane., Hutchinson,J.H., Shaw,A.W., Graham,S.L. and Ciccarone,T.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6297239-A 18 02-OCT-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
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ORIGIN

Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 23
LOCUS BD267970 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD267970
VERSION BD267970.1 GI:33077738
KEYWORDS JP 2002519376-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Bell,I.M., Dinsmore,C.J., Stokker,G.E., Anthony,N.J., Beshore,D.C., Ciccarone,T.M. and Desolms,J.S.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002519376-A 11 02-JUL-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002519376-A/11
PD 02-JUL-2002
PF 29-JUN-1999 JP 2000557828
PR 02-JUL-1998 US 60/091513
PI IAN M BELL,CHRISTOPHER J DINSMORE,GERALD E STOKKER,NEVILLE J PI ANTHONY,
PI DOUGLAS C BRESHORE,TERRENCE M CICCARONE,JANE S DESOLMS PC
C07D498/08,A61K31/337,A61K31/4188,A61P9/00,A61P9/10,A61P13/12, PC
A61P27/02,
PC A61P31/10,A61P31/12,A61P31/14,A61P35/00,A61P43/00,A61P43/00,
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ORIGIN

Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

Db 28 ATATTCGTCATGGTG 13

RESULT 24
LOCUS BD270873 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD270873
VERSION BD270873.1 GI:33080641
KEYWORDS JP 2002528504-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002528504-A 11 03-SEP-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002528504-A/11
PD 03-SEP-2002
PF 26-OCT-1999 JP 2000579229
PR 29-OCT-1999 US 60/106177,05-JAN-1999 GB 9900148.9 PI
JEFFREY M BERGMAN
PC C07D498/18,A61P1/16,A61P9/10,A61P13/12,A61P25/00,A61P27/02, PC
A61P31/12,
PC A61P35/00,A61P43/00//A61K31/4985
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ORIGIN

Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 25
LOCUS BD272024 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD272024
VERSION BD272024.1 GI:33081792
KEYWORDS JP 2002538120-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Jr.W.C.L., Sisko,J.T., Smith,A.M., Tucker,T.J., Dinsmore,C.J. and Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002538120-A 11 12-NOV-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002538120-A/11
PD 12-NOV-2002
PF 01-MAR-2000 JP 2000602080
PR 03-MAR-1999 US 60/122771,31-MAR-1999 US 60/127257 PI
WILLIAM C LUMMA JR,JOHN T SISCO,ANTHONY M SMITH,THOMAS J PI
TUCKER,
PI CHRISTOPHER J DINSMORE,JEFFREY M BERGMAN
PC C07D233/64,A61K31/496,A61P9/10,A61P13/12,A61P27/02,A61P31/12, PC
A61P35/00,

PC A61P43/00
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ORIGIN
Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 ATAGTCCGTCATGGTG 26
DB 28 ATATCCGTCATGGTG 13

RESULT 26
BD272043/c
LOCUS BD272043 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferases.
ACCESSION BD272043
VERSION BD272043.1 GI:33081811
KEYWORDS JP 2002538121-A/11.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stump,C.A. and Williams,T.M.
TITLE Inhibitors of prenyl-protein transferases
JOURNAL Patent: JP 2002538121-A 11 12-NOV-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002538121-A/11
PD 12-NOV-2002
PF 01-MAR-2000 JP 2000602082
PR 03-MAR-1999 US 60/122971,31-MAR-1999 US 60/127252 PI
CRAIG A STUMP,THERESA M WILLIAMS
PC C07D233/64, A61K31/4164, A61K31/4709, A61K31/4725, A61K31/496, PC
A61P9/10, A61P31/12, A61P35/00, A61P43/00, C07D401/12, C07D403/12,
PC A61P13/12, A61P31/12, A61P35/00, A61P43/00, C07D401/12, C07D403/12,
PC C07D405/12
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Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 ATAGTCCGTCATGGTG 26
DB 28 ATATCCGTCATGGTG 13

RESULT 27
BD274581/c
LOCUS BD274581 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferases.
ACCESSION BD274581
VERSION BD274581.1 GI:33084349
KEYWORDS JP 2002542155-A/11.

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artificial sequences.
1 (bases 1 to 38)
Jr,W.C.L., Smith,A.M. and Sisko,J.T.
Inhibitors of prenyl-protein transferase
Patent: JP 2002542155-A 11 10-DEC-2002;
MERCK AND CO INC
OS Artificial Sequence
PN JP 2002542155-A/11
PD 10-DEC-2002
PF 01-MAR-2000 JP 2000602019
PR 03-MAR-1999 US 60/122970,31-MAR-1999 US 60/127259 PI
WILLIAM C LUMMA JR,ANTHONY M SMITH,JOHN T SISCO PC
C07D233/64, A61K31/454, A61P1/16, A61P9/10, A61P13/12, PC
A61P27/02, A61P31/12, A61P35/00, A61P35/02, A61P43/00, C07D401/06//
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PC C12N9/99
CC completely synthetic sequence
FH Key location/Qualifiers
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ORIGIN
Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 ATAGTCCGTCATGGTG 26
DB 28 ATATCCGTCATGGTG 13

RESULT 28
BD274600/c
LOCUS BD274600 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD274600
VERSION BD274600.1 GI:33084368
KEYWORDS JP 2002540072-A/11.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hartman,G.D., Jr,W.C.L., Sisko,J.T., Smith,A.M., Tucker,T.J. and
Stokker,G.E.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002540072-A 11 26-NOV-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002540072-A/11
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602079
PR 03-MAR-1999 US 60/122768,31-MAR-1999 US 60/127253 PI
GEORGE D HARTMAN,WILLIAM C LUMMA JR,JOHN T SISCO,ANTHONY M PI
SMITH,
PC C07D233/64, A61K31/496, A61P1/16, A61P9/00, A61P13/10, A61P13/12, PC
A61P27/02, A61P31/10, A61P31/12, A61P35/00, A61P35/02, A61P43/00, C07D401/12,
PC C07D405/12
CC completely synthetic sequence
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DEFINITION Sequence 13 from patent US 6355343.
ACCESSION AR181816
VERSION AR181816.1 GI:20224030
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Lumma,W.C., Jr., Smith,A.M. and Sisko,J.T.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6355343-A 13 01-JAN-2002;
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DEFINITION Sequence 14 from patent US 6350755.
ACCESSION AR195282
VERSION AR195282.1 GI:20244719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS deSolms,S.Jane. and Shaw,A.W.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6350755-A 14 26-FEB-2002;
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ACCESSION AR199998
VERSION AR199998.1 GI:20250072
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Lumma,W.C., Sisko,J.T., Smith,A.M., Tucker,T.J., Dinsmore,C.J. and Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6355643-A 13 12-MAR-2002;
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ACCESSION AR201351
VERSION AR201351.1 GI:20252239
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hartman,G.D., Lumma,W.C. Jr., Sisko,J.T., Smith,A.M., Tucker,T.J. and Stokker,G.E.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6358956-A 13 19-MAR-2002;
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DEFINITION Sequence 14 from patent US 6358985.
ACCESSION AR201370
VERSION AR201370.1 GI:20252258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Anthony,N.J., Bell,I.M., Beshore,D.C., Ciccarone,T.M., de Solms,S.Jane, Dinsmore,C.J. and Stokker,G.E.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6358985-A 14 19-MAR-2002;
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DEFINITION          Sequence 14 from patent US 6410534.
ACCESSION            AR216094
VERSION              AR216094.1 GI:23314382
KEYWORDS
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 38)
AUTHORS              Dinmore,C.J., Bell,I.M., Beshore,D.C. and Williams,T.M.
TITLE                Inhibitors of prenyl-protein transferase
JOURNAL              Patent: US 6410534-A 14 25-JUN-2002;
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DEFINITION          Sequence 13 from patent US 6441017.
ACCESSION            AR224803
VERSION              AR224803.1 GI:23333713
KEYWORDS
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 38)
AUTHORS              Bell,I.M., Beshore,D.C., Gallicchio,S.N. and Zartman,C.B.
TITLE                Inhibitors of prenyl-protein transferase
JOURNAL              Patent: US 6441017-A 13 27-AUG-2002;
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ACCESSION            AR317262
VERSION              AR317262.1 GI:33698226
KEYWORDS
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 38)
AUTHORS              Dinmore,C.J., Bergman,J.M., Graham,S.L., Nguyen,D.N.,
                    Stokker,G.E., Williams,T.M. and Zartman,C.B.
TITLE                Inhibitors of prenyl-protein transferase
JOURNAL              Patent: US 6562823-A 14 13-MAY-2003;
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DEFINITION          Sequence 14 from patent US 6566385.
ACCESSION            AR337537
VERSION              AR337537.1 GI:33723589
KEYWORDS
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 38)
AUTHORS              deSolms,S.J., Stokker,G.E. and Shaw,A.W.
TITLE                Inhibitors of prenyl-protein transferase
JOURNAL              Patent: US 6566385-A 14 20-MAY-2003;
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DEFINITION          Sequence 13 from patent US 6329376.
ACCESSION            AR366761
VERSION              AR366761.1 GI:34599663
KEYWORDS
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 38)
AUTHORS              Bergman,J.M.
TITLE                Inhibitors of prenyl-protein transferase
JOURNAL              Patent: US 6329376-A 13 11-DEC-2001;
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LOCUS      AR368676      38 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION      Sequence 13 from patent US 6376496.
ACCESSION      AR368676
VERSION      AR368676.1 GI:34602827
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 38)
AUTHORS      Hartman,G.D., Lumma,W.C. Jr., Sisko,J.T., Smith,A.M., Tucker,T.J.
and Bergman,J.M.
TITLE      Inhibitors of prenyl-protein transferase
JOURNAL      Patent: US 6376496-A 13 23-APR-2002;
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DEFINITION      Sequence 14 from patent US 6610722.
ACCESSION      AR383170
VERSION      AR383170.1 GI:40092623
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 38)
AUTHORS      Stump,C.A. and Williams,T.M.
TITLE      Inhibitors of prenyl-protein transferase
JOURNAL      Patent: US 6610722-A 14 26-AUG-2003;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 219 10.8 41.5 43 9 CC799108 Arabidops
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C 221 10.8 41.5 44 9 AL766974 Arabidops
C 222 10.8 41.5 44 9 AL766974 Arabidops
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C 225 10.8 41.5 46 8 A2948819 Arabidops
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C 236 10.8 41.5 50 1 AUI03368 Arabidops
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C 243 10.8 41.5 50 1 AUI07257 Arabidops

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AL497628 T. brucei
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AUI03376 AUI03376
AUI03376 AUI03376
AUI03763 AUI03763
AUI04255 AUI04255
AUI06985 AUI06985
AUI07257 AUI07257

244	10.8	41.5	50	1	AU107258	AU107258	317	10.6	40.8	50	1	AU105176	AU105176
245	10.8	41.5	50	1	AU107260	AU107260	C 318	10.6	40.8	50	1	AU105235	AU105235
246	10.8	41.5	50	1	AU107261	AU107261	319	10.6	40.8	50	1	AU107879	AU107879
247	10.8	41.5	50	1	AU107537	AU107537	320	10.6	40.8	50	8	BH905285	SALK 1058
248	10.8	41.5	50	7	CK225906	701613105	C 321	10.6	40.8	50	8	CH019705	3591_1_16
249	10.8	41.5	50	9	CG808002	1118088F1	C 322	10.4	40.0	19	6	CF293217	30DGS--02
250	10.6	40.8	21	8	AZ581771	1M0370F10	323	10.4	40.0	19	8	AZ450851	1M0249F13
251	10.6	40.8	23	8	AZ609364	1M0434004	324	10.4	40.0	21	4	BM400238	5009-0-7-
252	10.6	40.8	23	8	AZ871545	2M0184A04	325	10.4	40.0	22	9	TA239G01Q	
253	10.6	40.8	26	8	AZ602086	1M0420K07	C 326	10.4	40.0	24	8	AZ812591	2M0079D21
254	10.6	40.8	27	8	BH904657	SALK 1048	C 327	10.4	40.0	25	1	AU257461	AU257461
255	10.6	40.8	28	8	BH789687	SALK 0444	C 328	10.4	40.0	28	8	AZ621815	1M0455A08
256	10.6	40.8	29	8	AZ609543	1M0434C15	C 329	10.4	40.0	28	8	AZ665590	1M0547D08
257	10.6	40.8	31	9	BX656964	Arabidops	C 330	10.4	40.0	28	8	BH813863	SALK 0653
258	10.6	40.8	31	9	AG204587	Pan trogl	C 331	10.4	40.0	30	8	AZ623794	1M0461C19
259	10.6	40.8	32	15	AJ648311	AJ648311	332	10.4	40.0	31	1	AA980782	u45e10_r
260	10.6	40.8	32	8	BZ424912	100021301	333	10.4	40.0	32	9	AJ590509	Arabidops
261	10.6	40.8	34	1	A1200149	qf97b10_x	C 334	10.4	40.0	34	8	BH789679	SALK 0444
262	10.6	40.8	34	8	BH854533	KG02257-3	335	10.4	40.0	35	2	BE618566	601462356
263	10.6	40.8	34	8	BZ290881	SALK 0930	336	10.4	40.0	35	9	AL947040	Arabidops
264	10.6	40.8	35	8	BH865486	SALK 0986	C 337	10.4	40.0	35	9	TA100H06Q	
265	10.6	40.8	37	8	BZ358957	SALK 1335	C 338	10.4	40.0	36	8	BH911899	SALK 0727
266	10.6	40.8	37	9	CG722986	1119074C0	C 339	10.4	40.0	36	8	BH911900	SALK 0728
267	10.6	40.8	38	1	AA054107	zf50f06_r	C 340	10.4	40.0	36	9	CR396262	Arabidops
268	10.6	40.8	38	8	AZ785016	2M0028D05	341	10.4	40.0	37	8	AZ817489	2M0087C04
269	10.6	40.8	39	8	AZ603310	1M0422N12	C 342	10.4	40.0	37	8	BH023763	BG02168-5
270	10.6	40.8	43	1	AA926372	Om26a12_s	C 343	10.4	40.0	37	9	CL653059	
271	10.6	40.8	43	1	A1047023	uh57e09_r	344	10.4	40.0	38	8	AZ643994	1M0507E14
272	10.6	40.8	43	1	AV962349	AV962349	C 345	10.4	40.0	38	8	AZ974736	2M0249A03
273	10.6	40.8	43	1	AV962413	AV962413	C 346	10.4	40.0	40	1	AL657570	fc15c02_y
274	10.6	40.8	43	8	AZ623767	1M0461K16	C 347	10.4	40.0	40	9	AZ578532	AST-TD13S
275	10.6	40.8	43	8	AZ982083	2M0262D17	C 348	10.4	40.0	40	9	BX663464	Arabidops
276	10.6	40.8	43	9	CG797401	SALK 1448	349	10.4	40.0	40	9	CL639694	P028E11 G
277	10.6	40.8	45	4	BQ527007	602556245	350	10.4	40.0	41	8	BH080690	1008082A0
278	10.6	40.8	45	7	H67715	YK72C07_81	C 351	10.4	40.0	42	6	CA966788	CcLX06a23
279	10.6	40.8	45	8	AZ952610	2M0217E06	C 352	10.4	40.0	43	1	AL669008	AL669008
280	10.6	40.8	45	8	CC182796	XS533 Bay	C 353	10.4	40.0	43	7	W20560	mc20C04_x1
281	10.6	40.8	45	8	CC325928	RRG096 Ba	354	10.4	40.0	43	8	AZ949460	2M0212P24
282	10.6	40.8	45	9	TA379D04Q		C 355	10.4	40.0	43	9	TA114C01P	
283	10.6	40.8	45	9	CL256726	XS0211 Sa	356	10.4	40.0	44	5	BX548721	BX548721
284	10.6	40.8	45	9	CL669729	PRI0160a	C 357	10.4	40.0	44	9	AL771069	Arabidops
285	10.6	40.8	45	9	AG215618	Drosophi1	358	10.4	40.0	44	9	CG892045	01S0561-0
286	10.6	40.8	45	9	AG216773	Drosophi1	C 359	10.4	40.0	44	8	BH628960	1007075B1
287	10.6	40.8	46	9	CL525775	AG0018 Sa	C 360	10.4	40.0	45	8	BZ385312	SALK 1370
288	10.6	40.8	47	1	AJ657740	AJ657740	361	10.4	40.0	45	8	CC183529	XE347 Bay
289	10.6	40.8	47	9	BX533076	Arabidops	362	10.4	40.0	45	8	DME547098	
290	10.6	40.8	47	9	AG192238	Pan trogl	C 363	10.4	40.0	45	9	AA828568	od74b11_s
291	10.6	40.8	48	8	AZ427432	1M0209F20	C 364	10.4	40.0	46	1	AA828568	od74b11_s
292	10.6	40.8	48	8	BH790348	SALK 0568	365	10.4	40.0	46	1	AI935210	wpi7b09_x
293	10.6	40.8	48	8	BH910594	BH910594	C 366	10.4	40.0	46	8	BH865495	SALK 0986
294	10.6	40.8	48	8	BZ288754	SALK 0221	367	10.4	40.0	46	8	CC178563	NPX460 Ba
295	10.6	40.8	48	9	TA372F02Q		C 368	10.4	40.0	46	9	TA281A04Q	
296	10.6	40.8	48	9	AG217828	Drosophi1	C 369	10.4	40.0	47	8	BH901057	KG08638-5
297	10.6	40.8	49	1	AA427743	zw25h01_s	C 370	10.4	40.0	48	6	CO1973	HUMG000398
298	10.6	40.8	49	8	AZ500008	1M0338E09	371	10.4	40.0	48	7	R44463	YG28f03_81
299	10.6	40.8	49	9	CG427099	01S0723-0	C 372	10.4	40.0	48	8	AZ412179	1M0185H06
300	10.6	40.8	49	9	CL233809	01S0638-0	C 373	10.4	40.0	48	8	CC044288	3591_1_16
301	10.6	40.8	49	9	CL674014	PRI0111a	C 374	10.4	40.0	48	9	AG218724	Drosophi1
302	10.6	40.8	50	1	AU103015		C 375	10.4	40.0	49	1	AA588107	nk10e04_s
303	10.6	40.8	50	1	AU103753	AU103753	C 376	10.4	40.0	49	3	BX036579	Single re
304	10.6	40.8	50	1	AU104339	AU104339	377	10.4	40.0	49	4	BI753840	603027321
305	10.6	40.8	50	1	AU104344	AU104344	C 378	10.4	40.0	49	6	C20876	HUMG000494
306	10.6	40.8	50	1	AU104345	AU104345	379	10.4	40.0	49	8	BH800310	1008124B0
307	10.6	40.8	50	1	AU104354	AU104354	C 380	10.4	40.0	49	8	BH912865	3526_1_37
308	10.6	40.8	50	1	AU104359	AU104359	381	10.4	40.0	49	8	CC020451	3591_1_1
309	10.6	40.8	50	1	AU104360	AU104360	382	10.4	40.0	50	1	AU102827	AU102827
310	10.6	40.8	50	1	AU104361	AU104361	C 383	10.4	40.0	50	1	AU104332	AU104332
311	10.6	40.8	50	1	AU104362	AU104362	384	10.4	40.0	50	1	AU105349	AU105349
312	10.6	40.8	50	1	AU105169	AU105169	385	10.4	40.0	50	1	AU106596	AU106596
313	10.6	40.8	50	1	AU105170	AU105170	386	10.4	40.0	50	1	AU107637	AU107637
314	10.6	40.8	50	1	AU105171	AU105171	387	10.4	40.0	50	4	BI416796	hasp002xf
315	10.6	40.8	50	1	AU105174	AU105174	C 388	10.4	40.0	50	8	BH215111	1006025D0
316	10.6	40.8	50	1	AU105175	AU105175	C 389	10.4	40.0	50	9	CR027504	Forward s

C 390	10.4	40.0	50	9	CR059583	Forward s	CR059583	Forward s	C 463	10.2	39.2	49	1	AA497509	vh29ei2.r
C 391	10.4	40.0	50	9	TA34605Q		AL496230	T. brucei	C 464	10.2	39.2	49	4	BG222669	nah36d07.
C 392	10.2	39.2	15	4	BM398834	5009-0-5-	BM398834	5009-0-5-	C 465	10.2	39.2	49	4	BG222966	nah40b02.
C 393	10.2	39.2	19	8	AZ481008	1M0302M15	AZ481008	1M0302M15	C 466	10.2	39.2	49	4	BG223065	nah42g11.
C 394	10.2	39.2	22	6	CD535018	54P20 Ara	CD535018	54P20 Ara	C 467	10.2	39.2	49	4	BG223113	nah43f03.
C 395	10.2	39.2	25	8	AZ818242	2M0088G12	AZ818242	2M0088G12	C 468	10.2	39.2	49	4	BG223102	nah43b01.
C 396	10.2	39.2	26	8	AZ626635	1M0467L14	AZ626635	1M0467L14	C 469	10.2	39.2	49	4	BG223103	nah43h01.
C 397	10.2	39.2	27	8	AZ989950	2M0273D03	AZ989950	2M0273D03	C 470	10.2	39.2	49	4	BG223646	nah44a12.
C 398	10.2	39.2	27	9	CG723757	1119077H0	CG723757	1119077H0	C 471	10.2	39.2	49	4	BG271392	nah50a04.
C 399	10.2	39.2	27	9	CL681352	PR101300	CL681352	PR101300	C 472	10.2	39.2	49	4	BG271415	nah50d11.
C 400	10.2	39.2	28	9	AZ615744	1M0445B15	AZ615744	1M0445B15	C 473	10.2	39.2	49	4	BG271439	nah50h06.
C 401	10.2	39.2	28	9	TA297B09Q		AL489564	T. brucei	C 474	10.2	39.2	49	4	BG271529	nah58f01.
C 402	10.2	39.2	28	9	CG714953	1119039C0	CG714953	1119039C0	C 475	10.2	39.2	49	4	BG271560	nah59a07.
C 403	10.2	39.2	30	8	BZ352917	SALK_1194	BZ352917	SALK_1194	C 476	10.2	39.2	49	4	BG271601	nah59f07.
C 404	10.2	39.2	31	9	DR4308T	Danio rer	AL985946	Danio rer	C 477	10.2	39.2	49	4	BG271654	nah51e08.
C 405	10.2	39.2	31	9	CG719530	1119058A0	CG719530	1119058A0	C 478	10.2	39.2	49	4	BG271663	nah51g06.
C 406	10.2	39.2	33	4	BJ039102	BJ039102	BJ039102	BJ039102	C 479	10.2	39.2	49	4	BG271686	nah52b05.
C 407	10.2	39.2	33	8	AZ660655	1M0538D20	AZ660655	1M0538D20	C 480	10.2	39.2	49	4	BG271865	nah52d02.
C 408	10.2	39.2	33	9	DR23D20T	Danio rer	AL978858	Danio rer	C 481	10.2	39.2	49	4	BG272235	nah31g07.
C 409	10.2	39.2	34	4	BJ064751	BJ064751	BJ064751	BJ064751	C 482	10.2	39.2	49	4	BG272662	nah35b08.
C 410	10.2	39.2	34	4	BJ066450	BJ066450	BJ066450	BJ066450	C 483	10.2	39.2	49	4	BG370431	nah33e05.
C 411	10.2	39.2	34	9	TA227B06Q		AL479989	T. brucei	C 484	10.2	39.2	49	7	H55111	CHR220050 C
C 412	10.2	39.2	34	9	CLA38623	FST7894-N	CLA38623	FST7894-N	C 485	10.2	39.2	49	7	R08243	yf18f06.r1
C 413	10.2	39.2	35	8	BH852495	SALK_0747	BH852495	SALK_0747	C 486	10.2	39.2	50	1	AA948106	ons1a04.s
C 414	10.2	39.2	36	9	DR43A15T	Danio rer	AL973794	Danio rer	C 487	10.2	39.2	50	1	AJ650056	AJ650056
C 415	10.2	39.2	37	1	AI118163	ue38f01.x	AI118163	ue38f01.x	C 488	10.2	39.2	50	1	AU102316	AU102316
C 416	10.2	39.2	37	4	BM400556	5009-0-75	BM400556	5009-0-75	C 489	10.2	39.2	50	1	AU102529	AU102529
C 417	10.2	39.2	37	7	H53607	yq87h08.s1	H53607	yq87h08.s1	C 490	10.2	39.2	50	1	AU102733	AU102733
C 418	10.2	39.2	37	8	BH901965		BH901965		C 491	10.2	39.2	50	1	AU103795	AU103795
C 419	10.2	39.2	37	9	CG712023	1119023G0	CG712023	1119023G0	C 492	10.2	39.2	50	1	AU104346	AU104346
C 420	10.2	39.2	38	2	BF144195	601786804	BF144195	601786804	C 493	10.2	39.2	50	1	AU104959	AU104959
C 421	10.2	39.2	38	9	TA128E05P		AL464359	T. brucei	C 494	10.2	39.2	50	1	AU105238	AU105238
C 422	10.2	39.2	39	1	AV970688	AV970688	AV970688	AV970688	C 495	10.2	39.2	50	1	AU105314	AU105314
C 423	10.2	39.2	39	8	AZ391588	1M0153K18	AZ391588	1M0153K18	C 496	10.2	39.2	50	1	AU105549	AU105549
C 424	10.2	39.2	39	8	AZ836176	2M0130I22	AZ836176	2M0130I22	C 497	10.2	39.2	50	1	AU106767	AU106767
C 425	10.2	39.2	39	8	CC060550	EX04745-5	CC060550	EX04745-5	C 498	10.2	39.2	50	1	AU107095	AU107095
C 426	10.2	39.2	40	8	AZ862112	2M0169F03	AZ862112	2M0169F03	C 499	10.2	39.2	50	1	AU107467	AU107467
C 427	10.2	39.2	41	2	BF572131	602076910	BF572131	602076910	C 500	10.2	39.2	50	1	AU107468	AU107468
C 428	10.2	39.2	41	8	AZ345445	1M0080H07	AZ345445	1M0080H07	C 501	10.2	39.2	50	1	AU107552	AU107552
C 429	10.2	39.2	41	8	AZ788255	2M0035A16	AZ788255	2M0035A16	C 502	10.2	39.2	50	1	AU107634	AU107634
C 430	10.2	39.2	41	9	AZ936284	Arabidops	AZ936284	Arabidops	C 503	10.2	39.2	50	1	AU107952	AU107952
C 431	10.2	39.2	41	9	BX943466	Arabidops	BX943466	Arabidops	C 504	10.2	39.2	50	1	AA503797	ne51c06.s
C 432	10.2	39.2	42	6	CD029192	egns017XP	CD029192	egns017XP	C 505	10.2	39.2	50	2	AW248365	2820706.5
C 433	10.2	39.2	42	8	AQ026241	l(3)L1233	AQ026241	l(3)L1233	C 506	10.2	39.2	50	4	BG222716	nah37e07.
C 434	10.2	39.2	42	9	AL765117	Arabidops	AL765117	Arabidops	C 507	10.2	39.2	50	4	BG223051	nah42b11.
C 435	10.2	39.2	42	9	BL157082	Danio rer	BL157082	Danio rer	C 508	10.2	39.2	50	4	BG271426	nah42b01.
C 436	10.2	39.2	43	1	AA126556		AA126556		C 509	10.2	39.2	50	4	BG271427	nah50f05.
C 437	10.2	39.2	43	7	H14006	EST00032 Ch	H14006	EST00032 Ch	C 510	10.2	39.2	50	4	BG271427	nah50f05.
C 438	10.2	39.2	43	8	AZ588007	1M0396P08	AZ588007	1M0396P08	C 511	10.2	39.2	50	4	BG271665	nah51g08.
C 439	10.2	39.2	44	8	AZ376080	1M0129I13	AZ376080	1M0129I13	C 512	10.2	39.2	50	4	BG271710	nah52e08.
C 440	10.2	39.2	44	8	AZ830256	2M0109H20	AZ830256	2M0109H20	C 513	10.2	39.2	50	4	BG271931	nah60e02.
C 441	10.2	39.2	44	8	AZ834721		AZ834721		C 514	10.2	39.2	50	4	BG272024	nah61g09.
C 442	10.2	39.2	44	9	BX221218		BX221218		C 515	10.2	39.2	50	4	BG272395	nah29f02.
C 443	10.2	39.2	44	9	BX893266		BX893266		C 516	10.2	39.2	50	4	BG272610	nah28e03.
C 444	10.2	39.2	44	9	CG718685		CG718685		C 517	10.2	39.2	50	4	BG272631	nah28f06.
C 445	10.2	39.2	45	8	AZ473700		AZ473700		C 518	10.2	39.2	50	4	BG272640	nah28g09.
C 446	10.2	39.2	45	8	BH14770	SALK_0669	BH14770	SALK_0669	C 519	10.2	39.2	50	4	BG272691	nah35g01.
C 447	10.2	39.2	45	9	BX287479	Arabidops	BX287479	Arabidops	C 520	10.2	39.2	50	4	BG272917	nah56a06.
C 448	10.2	39.2	46	1	AA987637	or-93d11.s	AA987637	or-93d11.s	C 521	10.2	39.2	50	4	BG273145	nah34h09.
C 449	10.2	39.2	46	8	AZ784657		AZ784657		C 522	10.2	39.2	50	4	BG370313	nah30c10.
C 450	10.2	39.2	46	9	CG784706		CG784706		C 523	10.2	39.2	50	4	BG370398	nah33a04.
C 451	10.2	39.2	47	8	AZ481406		AZ481406		C 524	10.2	39.2	50	4	BI416779	hasp002xd
C 452	10.2	39.2	47	8	AZ665018	1M0545B15	AZ665018	1M0545B15	C 525	10.2	39.2	50	4	BM514736	ky07f07.y
C 453	10.2	39.2	47	8	AZ776409		AZ776409		C 526	10.2	39.2	50	4	H41744	yo06b09.s1
C 454	10.2	39.2	47	8	BH623585		BH623585		C 527	10.2	39.2	50	8	AZ326669	1M0049I08
C 455	10.2	39.2	47	8	BZ580301		BZ580301		C 528	10.2	39.2	50	9	AG189033	Pan trogl
C 456	10.2	39.2	48	8	BH623937		BH623937		C 529	10.2	39.2	50	9	AG194535	Pan trogl
C 457	10.2	39.2	48	8	BH624836		BH624836		C 530	10.2	39.2	50	9	CL436082	FST2274-N
C 458	10.2	39.2	48	8	CC050390	01S0536-0	CC050390	01S0536-0	C 531	10.2	39.2	50	9	AG194535	Pan trogl
C 459	10.2	39.2	49	1	AA792088		AA792088		C 532	10.2	39.2	50	9	AZ763325	1M0558B14
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C 462	10.2	39.2	49	1	AI958154	fc91d08.Y	AI958154	fc91d08.Y	C 535	10.2	39.2	50	9	AZ581228	1M0589P19

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C 539	10	38.5	30	4	BM396904	BM396904	5009-0-26	C 612	10	38.5	47	8	AZ765062	AZ765062	2M0561K15
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C 541	10	38.5	31	1	AA868559	AA868559	ak4902.s	C 614	10	38.5	47	8	BZ354183	BZ354183	SALK_1233
C 542	10	38.5	31	1	AA917290	AA917290	SWOVL3CAN	C 615	10	38.5	47	9	BX182559	BX182559	Danlo rer
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C 553	10	38.5	35	4	BM395896	BM395896	5009-0-13	C 626	10	38.5	50	1	AU103076	AU103076	AU103076
C 554	10	38.5	35	9	CL213092	CL213092	F032F01 G	C 627	10	38.5	50	1	AU103192	AU103192	AU103192
C 555	10	38.5	36	1	AU283358	AU283358	AU283358	C 628	10	38.5	50	1	AU103739	AU103739	AU103739
C 556	10	38.5	36	1	AV832509	AV832509	AV832509	C 629	10	38.5	50	1	AU103745	AU103745	AU103745
C 557	10	38.5	36	4	BI869626	BI869626	603393580	C 630	10	38.5	50	1	AU104027	AU104027	AU104027
C 558	10	38.5	36	7	R84783	R84783	Yt66C02.r1	C 631	10	38.5	50	1	AU104437	AU104437	AU104437
C 559	10	38.5	36	8	AZ439912	AZ439912	1M0230E15	C 632	10	38.5	50	1	AU106331	AU106331	AU106331
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C 562	10	38.5	37	5	EX627309	EX627309	EX627309	C 635	10	38.5	50	1	AU106680	AU106680	AU106680
C 563	10	38.5	37	8	AZ583188	AZ583188	1M0376P20	C 636	10	38.5	50	1	AU106744	AU106744	AU106744
C 564	10	38.5	38	4	BG704291	BG704291	602687674	C 637	10	38.5	50	1	AU106745	AU106745	AU106745
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C 567	10	38.5	39	1	AV834166	AV834166	AV834166	C 640	10	38.5	50	1	AU107846	AU107846	AU107846
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C 576	10	38.5	41	8	BH011375	BH011375	BG01248-5	C 649	9.8	37.7	18	9	CL696108	CL696108	PR1018a.G
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C 580	10	38.5	42	9	TA114F08P	TA114F08P		C 653	9.8	37.7	23	4	BM397858	BM397858	5009-0-38
C 581	10	38.5	42	9	TA130C07P	TA130C07P		C 654	9.8	37.7	25	1	AA918137	AA918137	on45g02.s
C 582	10	38.5	43	4	BG250039	BG250039	602362124	C 655	9.8	37.7	25	8	AZ815351	AZ815351	2M0083I02
C 583	10	38.5	43	4	BG259962	BG259962	602371733	C 656	9.8	37.7	25	9	TA6E12Q	TA6E12Q	T. brucei
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C 585	10	38.5	44	2	BE252118	BE252118	601113681	C 658	9.8	37.7	28	9	TA30F12Q	TA30F12Q	T. brucei
C 586	10	38.5	44	2	BE257268	BE257268	601108061	C 659	9.8	37.7	30	9	BX533497	BX533497	Arabidops
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C 602	10	38.5	46	1	AA129426	AA129426	zn78d03.s	C 675	9.8	37.7	35	8	BH846699	BH846699	SALK_0098
C 603	10	38.5	46	1	AI861936	AI861936	td18a12.x	C 676	9.8	37.7	36	8	AZ514452	AZ514452	1M0361N13
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C 831	9.6	36.9	33	9	TA204F11P	TA204F11P	T. brucei	C 904	9.6	36.9	44	9	CR297276	CR297276	Medicago
C 832	9.6	36.9	34	1	AA717376	AA717376	vp42h10. r	C 905	9.6	36.9	44	9	DR71117S	DR71117S	Danio rer
C 833	9.6	36.9	34	1	AA908764	AA908764	ol06a05. s	906	9.6	36.9	44	9	CG802823	CG802823	1118035A0
C 834	9.6	36.9	34	1	AA964889	AA964889	fc81d06. y	907	9.6	36.9	44	9	CL529668	CL529668	HIV30C01.
C 835	9.6	36.9	34	9	AL759526	AL759526	Arabidops	C 908	9.6	36.9	44	9	AG199967	AG199967	Pan trogl
C 836	9.6	36.9	35	8	AQ025554	AQ025554	EP(X)1632	C 909	9.6	36.9	45	1	AA676293	AA676293	ad37d03. s
C 837	9.6	36.9	35	9	BX290526	BX290526	Arabidops	C 910	9.6	36.9	45	4	BJ001124	BJ001124	BJ001124
C 838	9.6	36.9	35	9	BX532900	BX532900	Arabidops	C 911	9.6	36.9	45	8	BZ353038	BZ353038	SALK 1196
C 839	9.6	36.9	36	1	AV833092	AV833092	Arabidops	C 912	9.6	36.9	45	8	AJ600711	AJ600711	Arabidops
C 840	9.6	36.9	36	8	AZ781371	AZ781371	2M0021K14	C 913	9.6	36.9	45	9	EX893660	EX893660	Arabidops
C 841	9.6	36.9	36	8	BH854787	BH854787	SALK 0885	914	9.6	36.9	45	9	EX944839	EX944839	Arabidops
C 842	9.6	36.9	36	8	BZ381819	BZ381819	SALK 1173	915	9.6	36.9	45	9	TA247807Q	TA247807Q	T. brucei
C 843	9.6	36.9	36	9	AL760306	AL760306	Arabidops	916	9.6	36.9	45	9	TA372A04P	TA372A04P	T. brucei
C 844	9.6	36.9	36	9	CL681770	CL681770	PR10132a	917	9.6	36.9	45	9	CL212732	CL212732	G049E09 G
C 845	9.6	36.9	37	1	AI188871	AI188871	qd27b11. x	C 918	9.6	36.9	46	1	AA014473	AA014473	mi64h05. r
C 846	9.6	36.9	37	7	N40578	N40578	YW76C11. r1	919	9.6	36.9	46	1	AA903958	AA903958	OB16b03. s
C 847	9.6	36.9	37	8	AQ025345	AQ025345	EP(X)0491	C 920	9.6	36.9	46	1	AV959402	AV959402	AV959402
C 848	9.6	36.9	37	8	AZ949825	AZ949825	2M0213A08	C 921	9.6	36.9	46	1	AA389458	AA389458	np25e02. r
C 849	9.6	36.9	37	9	CG716645	CG716645	1119045H1	922	9.6	36.9	46	1	AA576353	AA576353	mh10g03. s
C 850	9.6	36.9	38	8	AZ616703	AZ616703	1M0446E11	923	9.6	36.9	46	4	BJ077575	BJ077575	BJ077575
C 851	9.6	36.9	38	8	BH902425	BH902425	SALK 0918	C 924	9.6	36.9	46	7	W69845	W69845	zd48b04. r1
C 852	9.6	36.9	38	8	AL760976	AL760976	Arabidops	C 925	9.6	36.9	46	8	BH894454	BH894454	3526_1_29
C 853	9.6	36.9	39	4	BI094710	BI094710	EST-CD34N	C 926	9.6	36.9	46	9	AJ598609	AJ598609	Arabidops
C 854	9.6	36.9	39	8	AZ841702	AZ841702	2M0139B20	927	9.6	36.9	46	9	AX124014	AX124014	Danio rer
C 855	9.6	36.9	39	9	AA547534	AA547534	Drosophil	928	9.6	36.9	46	9	AX126315	AX126315	Danio rer
C 856	9.6	36.9	40	1	AA916980	AA916980	ol54g07. s	929	9.6	36.9	47	6	CJ0881	CJ0881	HUMGS000495
C 857	9.6	36.9	40	1	AA137304	AA137304	mq80b07. r	930	9.6	36.9	47	8	BH865116	BH865116	SALK_0974
C 858	9.6	36.9	40	8	BZ761528	BZ761528	SALK 0008	931	9.6	36.9	47	8	BH893272	BH893272	3526_1_24
C 859	9.6	36.9	40	9	BX290497	BX290497	Arabidops	932	9.6	36.9	47	8	BH897386	BH897386	3526_1_7
C 860	9.6	36.9	40	9	TA14B10Q	TA14B10Q	T. brucei	C 933	9.6	36.9	47	8	CC459563	CC459563	SALK_1305
C 861	9.6	36.9	40	9	CT794669	CT794669	SALK 0537	C 934	9.6	36.9	47	8	TA248H10Q	TA248H10Q	T. brucei
C 862	9.6	36.9	40	9	AG192612	AG192612	Pan trogl	935	9.6	36.9	47	9	CG799430	CG799430	1118002D1
C 863	9.6	36.9	40	9	AG202802	AG202802	Pan trogl	C 936	9.6	36.9	47	9	CL522104	CL522104	SALBD10 F
C 864	9.6	36.9	41	1	AU259274	AU259274	AU259274	C 937	9.6	36.9	48	1	AV957074	AV957074	AV957074
C 865	9.6	36.9	41	4	BI602229	BI602229	603244161	C 938	9.6	36.9	48	1	AA423295	AA423295	zw07a04. r
C 866	9.6	36.9	41	4	BJ040593	BJ040593	BJ040593	C 939	9.6	36.9	48	4	BI764981	BI764981	603051127
C 867	9.6	36.9	41	6	CF281514	CF281514	14ETL--08	940	9.6	36.9	48	8	AZ443664	AZ443664	1M0238A03
C 868	9.6	36.9	41	6	CF330811	CF330811	NACL--06-	941	9.6	36.9	48	8	AZ505194	AZ505194	1M0345F16
C 869	9.6	36.9	41	7	CO788347	CO788347	NT004A A0	C 942	9.6	36.9	48	8	BH636387	BH636387	1008011A0
C 870	9.6	36.9	41	9	AX622426	AX622426	Drosophil	C 943	9.6	36.9	48	8	BH907825	BH907825	SALK_0442
C 871	9.6	36.9	41	9	BX661505	BX661505	Arabidops	C 944	9.6	36.9	48	8	BH910647	BH910647	SALK_0608
C 872	9.6	36.9	41	9	CC882364	CC882364	01S0576-0	945	9.6	36.9	48	9	AJ597909	AJ597909	Arabidops
C 873	9.6	36.9	41	9	CG730875	CG730875	1119130E0	C 946	9.6	36.9	48	9	AL752055	AL752055	Arabidops
C 874	9.6	36.9	42	8	AZ575712	AZ575712	AST-T31A0	C 947	9.6	36.9	48	9	TA194C12Q	TA194C12Q	T. brucei
C 875	9.6	36.9	42	8	BH759470	BH759470	KG04490-3	948	9.6	36.9	48	9	CG778060	CG778060	112302580
C 876	9.6	36.9	42	9	AE545593	AE545593	Drosophil	C 949	9.6	36.9	48	9	AG203889	AG203889	Pan trogl
C 877	9.6	36.9	42	9	CL423539	CL423539	01S0557-0	C 950	9.6	36.9	49	1	AA124006	AA124006	mq10a06. r
C 878	9.6	36.9	43	1	AA994992	AA994992	ou09b09. s	C 951	9.6	36.9	49	1	AV856631	AV856631	AV856631
C 879	9.6	36.9	43	1	AI301796	AI301796	qn08e06. x	C 952	9.6	36.9	49	1	AA429584	AA429584	zw77h05. r
C 880	9.6	36.9	43	1	AJ237217	AJ237217	AJ237217	C 953	9.6	36.9	49	4	BM397439	BM397439	5009-0-32
C 881	9.6	36.9	43	1	AJ239964	AJ239964	AJ239964	C 954	9.6	36.9	49	6	CA341266	CA341266	PK13c02. x
C 882	9.6	36.9	43	1	AA196741	AA196741	zq09d02. s	955	9.6	36.9	49	6	CF280034	CF280034	14ETL--06
C 883	9.6	36.9	43	2	AW247576	AW247576	2819553. s	C 956	9.6	36.9	49	7	WF7994	WF7994	mg07b01. r1
C 884	9.6	36.9	43	8	AZ592659	AZ592659	1M0403B17	C 957	9.6	36.9	49	8	AZ830102	AZ830102	2M0109E11
C 885	9.6	36.9	43	8	BZ355522	BZ355522	SALK 1268	958	9.6	36.9	49	8	AQ254822	AQ254822	EP(2)1132
C 886	9.6	36.9	43	8	BZ665236	BZ665236	SALK_1109	C 959	9.6	36.9	49	9	TA148C09P	TA148C09P	AL471860
C 887	9.6	36.9	43	8	BZ769930	BZ769930	SALK_1428	C 960	9.6	36.9	49	9	TA235H07Q	TA235H07Q	T. brucei
C 888	9.6	36.9	43	9	AJ587489	AJ587489	Arabidops	961	9.6	36.9	49	9	CG779221	CG779221	1123032D0
C 889	9.6	36.9	43	9	BX228681	BX228681	Danio rer	962	9.6	36.9	49	9	CL640727	CL640727	M012C08 G
C 890	9.6	36.9	43	9	AX949252	AX949252	Arabidops	C 963	9.6	36.9	50	1	AU102253	AU102253	AU102253
C 891	9.6	36.9	43	9	CG893482	CG893482	03S3041-0	964	9.6	36.9	50	1	AU102452	AU102452	AU102452
C 892	9.6	36.9	44	1	AU013131	AU013131	AU013131	965	9.6	36.9	50	1	AU102554	AU102554	AU102554
C 893	9.6	36.9	44	1	AU013167	AU013167	AU013167	966	9.6	36.9	50	1	AU102742	AU102742	AU102742
C 894	9.6	36.9	44	1	AU013168	AU013168	AU013168	C 967	9.6	36.9	50	1	AU103407	AU103407	AU103407
C 895	9.6	36.9	44	1	AU259010	AU259010	AU259010	C 968	9.6	36.9	50	1	AU103746	AU103746	AU103746
C 896	9.6	36.9	44	4	BM400772	BM400772	5009-0-79	C 969	9.6	36.9	50	1	AU103761	AU103761	AU103761
C 897	9.6	36.9	44	5	BX569683	BX569683	BX569683	C 970	9.6	36.9	50	1	AU103834	AU103834	AU103834
C 898	9.6	36.9	44	6	CA970051	CA970051	CCLX06325	C 971	9.6	36.9	50	1	AU104186	AU104186	AU104186
C 899	9.6	36.9	44	6	CF332083	CF332083	NACL--08-	C 972	9.6	36.9	50	1	AU104487	AU104487	AU104487
C 900	9.6	36.9	44	8	AZ393428	AZ393428	1M0156B06	C 973	9.6	36.9	50	1	AU104850	AU104850	AU104850

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c 974 9.6 36.9 50 1 AUI04851
c 975 9.6 36.9 50 1 AUI05003
c 976 9.6 36.9 50 1 AUI05005
c 977 9.6 36.9 50 1 AUI05081
c 978 9.6 36.9 50 1 AUI05111
c 979 9.6 36.9 50 1 AUI05114
c 980 9.6 36.9 50 1 AUI05126
c 981 9.6 36.9 50 1 AUI05142
c 982 9.6 36.9 50 1 AUI05148
c 983 9.6 36.9 50 1 AUI05153
c 984 9.6 36.9 50 1 AUI05157
c 985 9.6 36.9 50 1 AUI05159
c 986 9.6 36.9 50 1 AUI05160
c 987 9.6 36.9 50 1 AUI05161
c 988 9.6 36.9 50 1 AUI05163
c 989 9.6 36.9 50 1 AUI05200
c 990 9.6 36.9 50 1 AUI05203
c 991 9.6 36.9 50 1 AUI05376
c 992 9.6 36.9 50 1 AUI05851
c 993 9.6 36.9 50 1 AUI05854
c 994 9.6 36.9 50 1 AUI05952
c 995 9.6 36.9 50 1 AUI06748
c 996 9.6 36.9 50 1 AUI07659
c 997 9.6 36.9 50 1 AUI07661
c 998 9.6 36.9 50 1 AUI07663
c 999 9.6 36.9 50 1 AUI07664
1000 9.6 36.9 50 1 AUI07717
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ALIGNMENTS

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RESULT 1
A1492591/c 31 bp mRNA linear EST 11-MAR-1999
t129h07.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2131933 3'
similar to SW:ETV6_HUMAN P41212 ETS-RELATED PROTEIN TEL ; mRNA
sequence.
A1492591 A1492591.1 GI:4393594
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
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Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

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FEATURES
source
1..31
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2131933"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
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/clone_lib="NCI CGAP Gas4"
/note="Organ: sfomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN
Query Match 53.8% Score 14; DB 1; Length 31;
Best Local Similarity 77.3%; Pred. No. 4.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 GAAAGCGCTAGCCATGGCGTT 25
||| ||||| ||||| |||
Db 28 GAATACGTCTACCCATTGCTTT 7

RESULT 2
A1759390 46 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-186G01-014618,
genomic survey sequence.
DEFINITION A1759390
VERSION A1759390.1 GI:21497738
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weissshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL MEDLINE 22755829
PUBMED 12874060
AUTHORS
2 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weissshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse Genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL MEDLINE 23117147
PUBMED 14756321
AUTHORS
3 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weissshaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL MEDLINE 14682050
PUBMED
4 (bases 1 to 46)
Rosso,M.G., Strizhov,N., Li,Y. and Weissshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by HAC clone
f6f22. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1..46
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/db_xref="taxon:3702"
/clone="GK-186G01-014618"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 53.1%; Score 13.8; DB 9; Length 46;
Best Local Similarity 72.0%; Pred. No. 5.9e+04;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
||||| ||||| ||||| ||||| |||||
Db 14 CAGAAAGCGCTGTCTTGGCGCTA 38

RESULT 3

AZ778581
LOCUS 29 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0013N1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0013N11 R, genomic survey sequence.

ACCESSION AZ778581
VERSION GSS.
KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weisse,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0013 row: N column: 11

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

FEATURES

Location/Qualifiers

1..29

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0013N11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.5%; Score 13.4; DB 8; Length 29;
Best Local Similarity 93.3%; Pred. No. 8.8e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTCTAGCCATGGCGT 24
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Db 5 GTCTAGCCATGGCGT 19

RESULT 4

BZ353391/c
LOCUS 45 bp DNA linear GSS 14-NOV-2002
DEFINITION SALK_120258.19.00.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_120258.19.00.x, genomic survey sequence.

ACCESSION BZ353391
VERSION BZ353391.1 GI:24944253

KEYWORDS

GSS.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 45)

REFERENCE

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

COMMENT Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies (SIGNAL)

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..45

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_120258.19.00.x"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 50.8%; Score 13.2; DB 8; Length 45;
Best Local Similarity 83.3%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAGAAAGCGTCTAGCCAT 19
||||| ||||| ||||| ||||| |||||
Db 20 CAGAAAGCATCTAGTCAT 3

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RESULT 5
AUI06301/c
LOCUS
DEFINITION
AUI06301 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00359, mRNA sequence.
ACCESSION
AUI06301
VERSION
AUI06301.1 GI:13555822
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT00359"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 50.8%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
Db 15 GCAGAGCGCGTCTAGCGTTCGCCGTTA 40
RESULT 7
AUI07861
LOCUS
DEFINITION
AUI07861 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT02084, mRNA sequence.
ACCESSION
AUI07861
VERSION
AUI07861.1 GI:13557383
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT02084"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 50.8%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
Db 17 GCAGAGCGCGTGTAGCGTTCGCCGTTA 42
RESULT 6
AUI07857
LOCUS
DEFINITION
AUI07857 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT02325, mRNA sequence.
ACCESSION
AUI07857
VERSION
AUI07857.1 GI:13557379
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

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RESULT 8
AUI07875
LOCUS
DEFINITION AUI07875 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV6C825, mRNA sequence.
ACCESSION AUI07875
VERSION AUI07875.1 GI:13557397
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Talra,H., Tsunoda,T., Mizushima-Sugano,J., Seese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 50.8%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCAGAAAGCGTCTAGCGTGGCGTTA 26
Db 15 GGAGAAGCGGTAGCGTGGCGTTA 40
RESULT 9
BH855809
LOCUS
DEFINITION BH855809 42 bp DNA linear GSS 08-JUL-2002
SALK_084531.41.35.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_084531.41.35.x, genomic
survey sequence.
ACCESSION BH855809
VERSION BH855809.1 GI:21705399
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
REFERENCE 1 (bases 1 to 42)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

```

```

Tél: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
Atlg16730 and 300 bases of the 5' end of Atlg16740.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 49.2%; Score 12.8; DB 8; Length 42;
Best Local Similarity 70.8%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 AGAAAGCGTCTAGCGTGGCGTTA 26
Db 5 AGGACAGGTGTGCATGTCATTA 28
RESULT 10
BH855815
LOCUS
DEFINITION BH855815 44 bp DNA linear GSS 08-JUL-2002
SALK_084523.40.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_084523.40.30.x, genomic
survey sequence.
ACCESSION BH855815
VERSION BH855815.1 GI:21705405
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 44)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
Atlg16730 and 300 bases of the 5' end of Atlg16740.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..44
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines

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KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 30)

AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J. and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

FEATURES
source This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g57230.
Class: TDNA tagged.
Location/Qualifiers
1..30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_104701.42.15.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN
Query Match 48.5%; Score 12.6; DB 8; Length 30;
Best Local Similarity 78.9%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 CAGAAAGCGTCTAGCCATG 20
||||| ||||| ||||| |||||
Db 19 CACAAATGCTCTAGACATG 1

RESULT 14
LOCUS BZ762449/c 30 bp DNA linear GSS 13-MAR-2003
DEFINITION SALK_104714.34.65.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_104714.34.65.x, genomic survey sequence.

ACCESSION BZ762449
VERSION BZ762449.1 GI:28935002
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 30)

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g57230.
Class: TDNA tagged.
Location/Qualifiers
1..30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_104714.34.65.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN
Query Match 48.5%; Score 12.6; DB 8; Length 30;
Best Local Similarity 78.9%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 CAGAAAGCGTCTAGCCATG 20
||||| ||||| ||||| |||||
Db 19 CACAAAGCGTCTAGACATG 1

RESULT 15
LOCUS BH915541 42 bp DNA linear GSS 12-SEP-2002
DEFINITION 3526.1.48.1.A10.2EL_x.1 3526 - RescueMu Grid K Zea mays genomic, genomic survey sequence.
ACCESSION BH915541
VERSION BH915541.1 GI:22803175
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 42)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3526.1.48.1 row: 13
Class: transposon-tagged.
Location/Qualifiers
1..42
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab host="DH10B"
/clone_lib="3526 - RescueMu Grid K"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.

ADDITIONAL	See:	Mus musculus (house mouse)
SOURCE		Mus musculus
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE		1 (bases 1 to 38)
AUTHORS		Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE		Muscle whole genome scaffolding with paired end reads from 10kb

TITLE Mouse whole genome scaffolding with paired end reads from 10kbp
Niederhausern, A. and Wright, D., Weiss, R.

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: 0 column: 13
Seq primer: GTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0062013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 47.7%; Score 12.4; DB 8; Length 38;
Best Local Similarity 92.9%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 13 TAGCCATGGCGTTA 26
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Db 37 TAGCCATGGCATT 24
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RESULT 19
AQ073861
LOCUS
DEFINITION
EP(3)3258-3prime Drosophila melanogaster EP line Drosophila melanogaster genomic sequence.
Genomic survey sequence.
AQ073861.1 GI:3403903
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 46)
Liao,G.-C., Rehm,E.J. and Rubin,G.M.
Insertion site preferences of the P transposable element in Drosophila melanogaster

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: 0 column: 13
Seq primer: GTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers
1. 38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0062013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 47.7%; Score 12.4; DB 8; Length 38;
Best Local Similarity 92.9%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 13 TAGCCATGGCGTTA 26
|||||||
Db 37 TAGCCATGGCATT 24
|||||||
RESULT 19
AQ073861
LOCUS
DEFINITION
EP(3)3258-3prime Drosophila melanogaster EP line Drosophila melanogaster genomic sequence.
Genomic survey sequence.
AQ073861.1 GI:3403903
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 46)
Liao,G.-C., Rehm,E.J. and Rubin,G.M.
Insertion site preferences of the P transposable element in Drosophila melanogaster

JOURNAL
MEDLINE
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
20202638
10716700
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P element
The P element insertion position is base 001 in the 46 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
1. 46
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single EP transposable element insertion. (The generation of these insertion strains is described in Rorth P, Szabo K, Bailey A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function genetics in Drosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."

ORIGIN
Query Match 47.7%; Score 12.4; DB 8; Length 46;
Best Local Similarity 72.7%; Pred. No. 2.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GCAGAAAGCGTCTAGCCATGCC 22
|||||||
Db 25 GCAAAAACGCTGTCCAGCGC 46
|||||||
RESULT 20
CF281394/c
LOCUS
DEFINITION
14ETL--08-G23.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--08-G23, mRNA sequence.
CF281394
CF281394.1 GI:33658781
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

```

source
1. .29
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/clone="14EFL--08-G23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14EFL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
Query Match 46.9%; Score 12.2; DB 6; Length 29;
Best Local Similarity 68.0%; Pred. No. 3.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGCTCTAGCCATGGCGTT 25
DB 26 GCTGCGGCGCTCTGCGCGCTGCTT 2

RESULT 21
LOCUS AZ959267/c 33 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0226D21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0226D21 R, genomic survey sequence.
ACCESSION AZ959267
VERSION AZ959267.1 GI:13830494
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0226 row: D column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0226D21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```

Query Match 46.9%; Score 12.2; DB 8; Length 33;
Best Local Similarity 82.4%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 5 AAGCGTCTAGCCATGG 21
DB 31 AAGTGTTTACCATGG 15

```

RESULT 22

```

LOCUS TA175A01P 48 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 175a01, forward sequence, genomic survey sequence.
ACCESSION AL475152
VERSION AL475152.1 GI:11840164
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 48)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .48

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="175a01"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

4

GAAAGCGTCTAGCCATGG 20

|||||

46.9%; Score 12.2; DB 9; Length 48;

82.4%; Pred. No. 3.7e+05;

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5

GAAAGCGTCTAGCCATGG 20

|||||

46.9%; Score 12.2; DB 9; Length 48;

82.4%; Pred. No. 3.7e+05;

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

4

GAAAGCGTCTAGCCATGG 20

|||||

46.9%; Score 12.2; DB 9; Length 48;

82.4%; Pred. No. 3.7e+05;

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

4

GAAAGCGTCTAGCCATGG 20

|||||

```

Db      13  GAAGACATTGGCCATG 29

RESULT 23
CC888361
LOCUS   48 bp  DNA  linear  GSS 31-JUL-2003
DEFINITION
Arabidopsis thaliana genomic clone SALK_151752.40.50.x, genomic
survey sequence.
ACCESSION
CC888361
VERSION
CC888361.1 GI:33364915
KEYWORDS
GSS.
SOURCE  Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 48)
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE    A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL  Arabidopsis Genome
COMMENT   Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g46430.
Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source           1..48
     /organism="Arabidopsis thaliana"
     /mol_type="genomic DNA"
     /ecotype="Col-0"
     /db_xref="taxon:3702"
     /clone="SALK_151752.40.50.x"
     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
     /note="PCR was performed on Arabidopsis thaliana lines
     each of which contains one or more TDNA insertion
     elements. The resultant fragment for each line was
     directly sequenced to determine the genomic sequence at
     the site of insertion. Details of the protocols used can
     be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      46.9%; Score 12.2; DB 9; Length 48;
Best Local Similarity 68.0%; Pred. No. 3.7e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1  GCAGAAAGCGTCTACCGCATGGCGTT 25
    |||||
Db 7  GGAGAGAGCTTCTCACCTAGACGTT 31

RESULT 24
AU104593
LOCUS   50 bp  mRNA  linear  EST 28-JAN-2004
DEFINITION
AU104593 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAE01245, mRNA sequence.
ACCESSION
AU104593
VERSION
AU104593.1 GI:13554114
KEYWORDS
EST.
SOURCE  Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="CAE01245"
     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9  CGTCTAGCCATGGCGTT 25
    |||||
Db 30 CGTCTAGGGATGGCGCT 46

RESULT 25
AU105172
LOCUS   50 bp  mRNA  linear  EST 28-JAN-2004
DEFINITION
AU105172 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS10704, mRNA sequence.
ACCESSION
AU105172
VERSION
AU105172.1 GI:13554693
KEYWORDS
EST.
SOURCE  Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="CAS10704"
     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

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Query Match 46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ACGGCTAGCCATGGCG 23
|||||
Db 6 AGCGGCCAGCCAGGGCG 22

RESULT 26
AUI06560/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI06560 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT00167, mRNA sequence.
ACCESSION AUI06560
VERSION AUI06560.1 GI:13556081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
|||||
Db 7 CACGGAGCTGCTGCCAGCGCGTTA 31

RESULT 28
AUI07873 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI07873 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION ZRV6C724, mRNA sequence.
ACCESSION AUI07873
VERSION AUI07873.1 GI:13557395
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ACGGCTAGCCATGGCG 23
|||||
Db 20 AGTGTCCAGGCATGGCG 4

RESULT 27
AUI07015 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI07015 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION REC00563, mRNA sequence.
ACCESSION AUI07015
VERSION AUI07015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
 ||||| ||||| ||||| ||||| |||||
 Db 17 GGAGAGCGCGTGTAGCGTGGCGTTA 42

RESULT 29
 AJ622111 50 bp DNA linear GSS 28-JAN-2004
 LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
 DEFINITION P[RS5]5-HA-2310, clone library P[RS5], genomic survey sequence.
 ACCESSION AJ622111 GI:41366324
 VERSION GSS; genome survey sequence.
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
 AUTHORS Ryder E.J., Ashburner M., Bagunya J., Blows F., Bucheton A.,
 Coulson D., Dickson B., Drummond J., Glover D., Gunton N.,
 Hafen E., Hall S., Heisenberg M., Lepesant J.A., Maroy P.,
 Mechler B., O'Kane C., Pflugfelder G., Rasmuson-Lestander A.,
 Reuter G., Roote J., Szidonya J., Wang S., Webster J. and
 Russell S.

TITLE Mapping of RS P element insertions in Drosophila melanogaster for
 the DrosDel second generation deficiency kit

JOURNAL Unpublished
 AUTHORS Ryder E.J.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2004) Ryder E.J., Department of Genetics,
 University of Cambridge, Downing Street, CB23EH, UNITED KINGDOM

COMMENT The insertion point of the P element is before base 1 of the
 sequence. Further information about this P element insertion line
 can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>.

FEATURES
 source
 1..50
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /chromosome="3R"
 /clone="P[RS5]5-HA-2310"
 /clone_lib="P[RS5]"
 /note="read=5' end"

misc_feature 1..50
 /note="P element insertion in the 5' to 3' orientation"

ORIGIN
 Query Match 46.9%; Score 12.2; DB 9; Length 50;
 Best Local Similarity 82.4%; Pred. No. 3.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CGTCTAGCCATGGCGTT 25
 ||||| ||||| ||||| ||||| |||||
 Db 1 CGTAAACCATGGCGTT 17

RESULT 30
 AJ622124 50 bp DNA linear GSS 28-JAN-2004
 LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
 DEFINITION P[RS5]5-HA-2407, clone library P[RS5], genomic survey sequence.
 ACCESSION AJ622124 GI:41366337
 VERSION GSS; genome survey sequence.
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
 AUTHORS Ryder E.J., Ashburner M., Bagunya J., Blows F., Bucheton A.,
 Coulson D., Dickson B., Drummond J., Glover D., Gunton N.,
 Hafen E., Hall S., Heisenberg M., Lepesant J.A., Maroy P.,
 Mechler B., O'Kane C., Pflugfelder G., Rasmuson-Lestander A.,
 Reuter G., Roote J., Szidonya J., Wang S., Webster J. and
 Russell S.

TITLE Mapping of RS P element insertions in Drosophila melanogaster for
 the DrosDel second generation deficiency kit

JOURNAL Unpublished
 AUTHORS Ryder E.J.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2004) Ryder E.J., Department of Genetics,
 University of Cambridge, Downing Street, CB23EH, UNITED KINGDOM

COMMENT The insertion point of the P element is before base 1 of the
 sequence. Further information about this P element insertion line
 can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>.

FEATURES
 Location/Qualifiers
 1..50
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /chromosome="3R"
 /clone="P[RS5]5-HA-2407"
 /clone_lib="P[RS5]"
 /note="read=5' end"

misc_feature 1..50
 /note="P element insertion in the 5' to 3' orientation"

ORIGIN
 Query Match 46.9%; Score 12.2; DB 9; Length 50;
 Best Local Similarity 82.4%; Pred. No. 3.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CGTCTAGCCATGGCGTT 25
 ||||| ||||| ||||| ||||| |||||
 Db 1 CGTAAACCATGGCGTT 17

RESULT 31
 CR014420/c 50 bp DNA linear GSS 05-JUL-2004
 LOCUS Forward strand read from insert in 5'HPRT insertion targeting and
 DEFINITION chromosome engineering clone MHPN315g04, genomic survey sequence.
 ACCESSION CR014420 GI:49747475
 VERSION GSS; genome survey sequence; MICER.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 50)
 Adams D.J., Biggs P.J., Cox A.V., Davies R.M., van der Weyden L.,
 Jonkers J., Smith J., Plumb R.W., Taylor R.G., Nishijima I., Yu Y.,
 Rogers J. and Bradley A.

TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

FEATURES
 Location/Qualifiers
 1..50
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN315g04"
 /clone_lib="MHPN"

ORIGIN
 Query Match 46.9%; Score 12.2; DB 9; Length 50;
 Best Local Similarity 82.4%; Pred. No. 3.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	2	CAGAAAGCGTCTAGCCA 18																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LHAM10979 row: p column: 23

High quality sequence start: 2

High quality sequence stop: 7

FEATURES

Location/Qualifiers

source

1..34

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NMRI"
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 /clone="IMAGE:4980358"
 /tissue_type="tumor, gross tissue"
 /dev_stages="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam4"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

ORIGIN

Query Match 46.2%; Score 12; DB 4; Length 34;

Best Local Similarity 75.0%; Pred. NO. 4.5e+05;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 AAGCGCTAGCGCGGT 24

Db 34 ACAGCGTCAGCCATCGCGT 15

RESULT 35

N49007/c

LOCUS Yy78h06.s1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA
 clone IMAGE:279707 3' similar to gb:U03626 URIDINE 5'-MONOPHOSPHATE
 SYNTHASE (HUMAN); mRNA sequence.

ACCESSION N49007

VERSION N49007.1 GI:1190173

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Ruchling,T., Soares,M., Tan,F.,
 Trevaaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project

CONTACT: Wilson RK

UNPUBLISHED (1995)

JOURNAL

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: ml3 -40 forward

High quality sequence stop: 1.

Location/Qualifiers

source

1..37

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3898083"
 /db_xref="taxon:9606"
 /clone="IMAGE:279707"
 /sex="male"
 /tissue_type="multiple sclerosis lesions"
 /dev_stages="Age 46"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares multiple sclerosis 2NBHMSF"

/note="Vector: pT7T3D (Pharmacia) with a modified

polylinker V_TYPE: phagemid; Site 1: Not I; Site 2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis

lesions from one patient was kindly provided by Dr. Kevin

G. Becker (NINDS/NIH). "

ORIGIN

Query Match 46.2%; Score 12; DB 7; Length 37;

Best Local Similarity 75.0%; Pred. NO. 4.5e+05;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATG 20

Db 33 GGAGATGGGCTTTGCCATG 14

RESULT 36

CLS28415/c

LOCUS

DEFINITION

CLS28415

ACCESSION

CLS28415.1 GI:47421626

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 38)

Mitchell,R.S., Beitzel, B.F., Schroder,A.R.W., Shinn,P., Chen,H.,

Berry, C.C., Ecker,J.R. and Bushman,F.

Retroviral DNA integration: ASLV, HIV and MLV Show Distinct Target

Site Preferences

Unpublished (2004)

Contact: Frederic Bushman

Salk Institute Infectious Disease Laboratory

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1630

Fax: 858 554 0341

Email: bushman@salk.edu

Class: PCR with specific primers.

Location/Qualifiers

1..38

FEATURES

source

1..38

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="ASV10806.fwd"

/clone_lib="ASLV-vector integration sites in human

293T-TVA cells"

/note="Human 293T cells expressing the subgroup A avian

retrovirus receptor (293T-TVA) were infected with an

ASLV-based vector. DNA was isolated and cleaved with

restriction enzymes; linkers were ligated onto the cleaved

DNA and DNAs were amplified using one primer that bound to


```

KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 41)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0541 row: 0 column: 22
              Seq primer: CACACAGGAACAGTATGACC
              Class: plasmid ends
              High quality sequence stop: 41.
              Location/Qualifiers
                1. 41
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                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adaptor DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                  inducible derivative of plasmid R1. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adaptor mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli Xli10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."

FEATURES      source
              1. 41
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
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                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli Xli10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

ORIGIN
Query Match      46.2%; Score 12; DB 8; Length 41;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCCATG 20
        |||||
Db      23 GCAGCAAGCATGTTACCATG 4

RESULT 40
AZ447207/c
LOCUS      47 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0244K09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0244K09 F, genomic survey sequence.
ACCESSION AZ447207
VERSION   AZ447207.1 GI:10598964

KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 47)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0244 row: K column: 09
              Seq primer: CGTGTAAACGACGGCCAGT
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                1. 47
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                  /lab_host="E. Coli strain Xli10-Gold, Tl-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adaptor DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                  inducible derivative of plasmid R1. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adaptor mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli Xli10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."

ORIGIN
Query Match      46.2%; Score 12; DB 8; Length 47;
Best Local Similarity 75.0%; Pred. No. 4.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCCATG 20
        |||||
Db      23 GTAGAAGCAATAGTCATG 4

Search completed: November 23, 2004, 22:23:59
Job time : 1272.54 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 38.191 Seconds
(without alignments)
614.177 Million cell updates/

Title: US-10-087-631B-5
Perfect score: 33
Sequence: 1 qccacatgactggcaaggcctctggtgataccg 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

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Minimum DB seq length: 0
Maximum DB seq length: 50
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Database : Issued Patents_NA.*
1: /cgn2_6/ptodata1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	15.4	46.7	30	4	US-09-438-954-8	Sequence 8, Appl	
2	15.4	46.7	33	3	US-09-233-493-28	Sequence 28, Appl	
C	15.4	46.7	33	3	US-09-005-476-28	Sequence 28, Appl	
C	15.4	46.7	33	3	US-09-233-492-28	Sequence 28, Appl	
C	15.4	46.7	33	3	US-09-296-280-28	Sequence 28, Appl	
C	15.4	46.7	33	4	US-09-498-074-28	Sequence 28, Appl	
C	15.4	46.7	33	4	US-09-498-074-28	Sequence 28, Appl	
C	15.4	46.7	33	5	PCT-US96-10082A-28	Sequence 28, Appl	
9	15.4	46.7	34	1	US-08-323-192D-23	Sequence 23, Appl	
10	15.4	46.7	34	1	US-08-323-192D-25	Sequence 25, Appl	
11	15.4	46.7	34	1	US-08-470-887A-22	Sequence 22, Appl	
12	15.4	46.7	34	1	US-08-470-887A-22	Sequence 24, Appl	
13	15.4	46.7	34	2	US-08-316-439A-20	Sequence 20, Appl	
14	15.4	46.7	34	2	US-08-316-439A-22	Sequence 22, Appl	
15	15.4	46.7	34	2	US-08-252-508B-22	Sequence 22, Appl	
16	15.4	46.7	34	2	US-08-252-508B-22	Sequence 24, Appl	
17	15.4	46.7	34	3	US-09-106-377-22	Sequence 22, Appl	
18	15.4	46.7	34	3	US-09-106-377-24	Sequence 24, Appl	
19	15.4	46.7	34	6	5160507-35	Patent No. 5166057	
C	15.4	46.7	38	1	US-08-323-192D-24	Sequence 24, Appl	
C	15.4	46.7	38	1	US-08-323-192D-26	Sequence 26, Appl	
C	15.4	46.7	38	1	US-08-470-887A-23	Sequence 23, Appl	
C	15.4	46.7	38	1	US-08-470-887A-25	Sequence 25, Appl	
C	15.4	46.7	38	2	US-08-316-439A-23	Sequence 23, Appl	
C	15.4	46.7	38	2	US-08-252-508B-23	Sequence 23, Appl	
C	15.4	46.7	38	2	US-08-252-508B-25	Sequence 25, Appl	
C	15.4	46.7	38	3	US-09-106-377-23	Sequence 23, Appl	

C 101	13.2	40.0	38	4	US-09-371-772B-10592	Sequence 10592, A	174	12.6	38.2	38	1	US-08-390-850-824	Sequence 824, App
C 102	13.2	40.0	39	4	US-09-002-443-7	Sequence 4, Appl	175	12.6	38.2	38	1	US-08-435-634-824	Sequence 824, App
C 103	13.2	40.0	42	2	US-08-840-887-4	Sequence 4, Appl	176	12.6	38.2	38	4	US-09-371-772B-7848	Sequence 7848, App
C 104	13.2	40.0	44	3	US-09-672-609-30	Sequence 30, Appl	177	12.6	38.2	39	2	US-08-561-521-24	Sequence 24, Appl
C 105	13.2	40.0	44	3	US-09-085-403A-30	Sequence 30, Appl	C 178	12.6	38.2	39	4	US-09-060-299-217	Sequence 217, App
C 106	13.2	40.0	45	2	US-08-379-057-34	Sequence 34, Appl	C 179	12.6	38.2	39	4	US-09-402-923A-217	Sequence 217, App
C 107	13.2	40.0	45	2	US-08-687-355A-12	Sequence 12, Appl	C 180	12.6	38.2	39	5	PCT-US95-01219-24	Sequence 24, Appl
C 108	13.2	40.0	45	4	US-09-407-367-12	Sequence 12, Appl	181	12.6	38.2	40	1	US-08-050-132A-10	Sequence 10, Appl
C 109	13.2	40.0	47	4	US-09-671-317-972	Sequence 972, App	182	12.6	38.2	40	1	US-08-815-652B-10	Sequence 10, Appl
C 110	13.2	40.0	47	4	US-09-422-978-1458	Sequence 1458, App	183	12.6	38.2	42	3	US-08-284-516C-39	Sequence 39, Appl
C 111	13	39.4	16	3	US-09-509-565-16	Sequence 16, Appl	C 184	12.6	38.2	42	3	US-08-284-516C-39	Sequence 39, Appl
C 112	13	39.4	17	3	US-09-509-565-36	Sequence 36, Appl	185	12.6	38.2	42	4	US-09-537-911A-38	Sequence 38, Appl
C 113	13	39.4	18	4	US-09-153-242-41	Sequence 41, Appl	186	12.6	38.2	42	4	US-09-537-911A-39	Sequence 39, Appl
C 114	13	39.4	22	1	US-08-433-783-23	Sequence 23, Appl	187	12.6	38.2	44	4	US-09-155-106-42	Sequence 42, Appl
C 115	13	39.4	22	1	US-08-433-783-23	Sequence 23, Appl	C 188	12.6	38.2	44	4	US-09-155-106-42	Sequence 42, Appl
C 116	13	39.4	22	5	PCT-US93-12144-23	Sequence 23, Appl	189	12.6	38.2	45	3	US-09-199-737-45	Sequence 45, Appl
C 117	13	39.4	22	5	PCT-US95-07537A-23	Sequence 23, Appl	C 190	12.6	38.2	47	4	US-09-422-978-1500	Sequence 1500, App
C 118	13	39.4	25	1	PCT-US95-07537-23	Sequence 23, Appl	191	12.6	38.2	47	4	US-09-422-978-1500	Sequence 1500, App
C 119	13	39.4	25	1	US-08-317-432A-45	Sequence 45, Appl	192	12.6	38.2	48	1	US-07-834-539A-64	Sequence 64, Appl
C 120	13	39.4	29	3	US-09-041-886-65	Sequence 65, Appl	193	12.6	38.2	48	1	US-08-053-131-112	Sequence 112, App
C 121	13	39.4	33	4	US-09-477-392-23	Sequence 23, Appl	194	12.6	38.2	48	1	US-08-645-641-112	Sequence 112, App
C 122	13	39.4	35	3	US-09-275-850-278	Sequence 278, App	195	12.6	38.2	48	1	US-07-853-408B-112	Sequence 112, App
C 123	13	39.4	38	2	US-08-460-529B-7	Sequence 7, Appl	196	12.6	38.2	48	1	US-08-096-762-112	Sequence 112, App
C 124	13	39.4	38	4	US-09-361-736B-7	Sequence 7, Appl	197	12.6	38.2	48	2	US-08-800-353-64	Sequence 64, Appl
C 125	13	39.4	39	3	US-09-423-439-4	Sequence 4, Appl	198	12.6	38.2	48	2	US-08-308-865-112	Sequence 112, App
C 126	13	39.4	41	1	US-08-317-432A-46	Sequence 46, Appl	199	12.6	38.2	48	3	US-09-042-353-305	Sequence 305, App
C 127	13	39.4	41	1	US-08-317-432A-50	Sequence 50, Appl	200	12.6	38.2	48	3	US-08-758-417A-153	Sequence 153, App
C 128	13	39.4	42	2	US-08-790-963-17	Sequence 17, Appl	201	12.6	38.2	48	5	PCT-US92-06185-64	Sequence 64, Appl
C 129	13	39.4	42	3	US-09-371-774-17	Sequence 17, Appl	202	12.6	38.2	50	1	PCT-US92-10983-112	Sequence 112, App
C 130	13	39.4	42	3	US-08-393-171-15	Sequence 15, Appl	203	12.6	38.2	50	1	US-08-171-389-494	Sequence 494, App
C 131	13	39.4	46	3	US-08-871-483-1	Sequence 1, Appl	204	12.6	38.2	50	1	US-08-123-936-494	Sequence 494, App
C 132	12.8	38.8	21	4	US-09-657-472-1010	Sequence 1010, App	205	12.6	38.2	50	1	US-08-475-228A-494	Sequence 494, App
C 133	12.8	38.8	24	3	US-09-553-231-38	Sequence 38, Appl	206	12.6	38.2	50	3	US-08-482-080A-494	Sequence 494, App
C 134	12.8	38.8	25	4	US-09-672-609-34	Sequence 34, Appl	C 207	12.6	38.2	50	3	US-09-046-247-38	Sequence 38, App
C 135	12.8	38.8	25	4	US-09-025-403A-34	Sequence 34, Appl	208	12.6	38.2	50	3	US-09-354-947-494	Sequence 494, App
C 136	12.8	38.8	29	1	US-08-356-287-22	Sequence 22, Appl	209	12.6	38.2	50	3	PCT-US93-12388-494	Sequence 494, App
C 137	12.8	38.8	29	5	PCT-US93-04863-22	Sequence 22, Appl	210	12.6	38.2	50	5	US-08-951-648-12	Sequence 12, Appl
C 138	12.8	38.8	30	2	US-08-481-658B-29	Sequence 29, Appl	211	12.4	37.6	18	3	US-09-174-437-12	Sequence 12, Appl
C 139	12.8	38.8	30	2	US-08-477-504A-29	Sequence 29, Appl	212	12.4	37.6	18	3	US-07-988-430-18	Sequence 18, Appl
C 140	12.8	38.8	30	2	US-08-486-756A-29	Sequence 29, Appl	C 213	12.4	37.6	21	4	US-09-001-052-4	Sequence 4, Appl
C 141	12.8	38.8	30	2	US-08-485-862B-29	Sequence 29, Appl	C 214	12.4	37.6	22	4	US-07-988-430-18	Sequence 18, Appl
C 142	12.8	38.8	30	3	US-08-787-739-29	Sequence 29, Appl	C 215	12.4	37.6	23	1	US-07-901-707-18	Sequence 18, Appl
C 143	12.8	38.8	30	3	US-08-487-077A-29	Sequence 29, Appl	C 216	12.4	37.6	23	1	US-07-901-707-18	Sequence 18, Appl
C 144	12.8	38.8	30	3	US-08-485-863A-29	Sequence 29, Appl	C 217	12.4	37.6	23	1	US-07-988-430-18	Sequence 18, Appl
C 145	12.8	38.8	30	3	US-08-485-863A-29	Sequence 29, Appl	C 218	12.4	37.6	25	4	PCT-US92-09487-18	Sequence 18, Appl
C 146	12.8	38.8	30	3	US-08-485-049D-29	Sequence 29, Appl	C 219	12.4	37.6	25	4	US-09-614-034-204	Sequence 204, App
C 147	12.8	38.8	30	3	US-09-178-115-29	Sequence 29, Appl	C 220	12.4	37.6	26	1	US-08-466-033-244	Sequence 244, App
C 148	12.8	38.8	30	3	US-09-177-776-29	Sequence 29, Appl	221	12.4	37.6	26	2	US-08-444-733-244	Sequence 244, App
C 149	12.8	38.8	34	3	US-09-772-719B-29	Sequence 29, Appl	222	12.4	37.6	26	2	US-08-461-134-244	Sequence 244, App
C 150	12.8	38.8	34	3	US-09-243-374-10	Sequence 10, Appl	223	12.4	37.6	26	2	US-08-461-134-244	Sequence 244, App
C 151	12.8	38.8	34	6	US-08-973-131-67	Sequence 67, Appl	224	12.4	37.6	26	2	US-08-485-910-244	Sequence 244, App
C 152	12.8	38.8	34	6	5186642-13	Patent No. 5186642	225	12.4	37.6	26	2	US-08-859-998-65	Sequence 65, Appl
C 153	12.8	38.8	35	6	5310667-16	Patent No. 5310667	226	12.4	37.6	26	3	US-09-225-928-65	Sequence 65, Appl
C 154	12.8	38.8	35	4	US-09-565-808-19	Sequence 19, Appl	227	12.4	37.6	29	1	US-09-225-928-65	Sequence 65, Appl
C 155	12.8	38.8	36	2	US-08-292-620A-846	Sequence 846, App	228	12.4	37.6	29	2	US-08-700-186-10	Sequence 10, Appl
C 156	12.8	38.8	36	3	US-09-071-845-846	Sequence 846, App	229	12.4	37.6	29	2	US-08-914-981-10	Sequence 10, Appl
C 157	12.8	38.8	38	4	US-09-371-772B-9407	Sequence 9407, App	230	12.4	37.6	29	3	US-09-116-115-10	Sequence 10, Appl
C 158	12.8	38.8	38	4	US-09-371-772B-11578	Sequence 11578, App	C 231	12.4	37.6	29	3	US-09-541-762-10	Sequence 10, Appl
C 159	12.8	38.8	39	5	US-09-371-772B-12629	Sequence 12629, A	232	12.4	37.6	29	3	US-09-304-232-91	Sequence 91, Appl
C 160	12.8	38.8	41	4	PCT-US92-10430-1	Sequence 1, Appl	233	12.4	37.6	30	3	US-08-444-818-180	Sequence 180, App
C 161	12.8	38.8	50	4	US-09-825-561A-56	Sequence 56, Appl	C 234	12.4	37.6	30	3	US-10-123-170-10	Sequence 10, Appl
C 162	12.8	38.8	50	4	US-08-956-171B-2367	Sequence 2367, App	C 235	12.4	37.6	32	4	US-09-813-781-79	Sequence 79, Appl
C 163	12.6	38.2	30	1	US-08-781-986A-2367	Sequence 2367, App	236	12.4	37.6	32	4	US-08-934-494-10	Sequence 10, Appl
C 164	12.6	38.2	30	3	US-08-384-708A-15	Sequence 15, Appl	237	12.4	37.6	33	3	US-09-143-068-10	Sequence 10, Appl
C 165	12.6	38.2	30	3	US-08-687-421-15	Sequence 15, Appl	238	12.4	37.6	33	3	US-09-143-068-10	Sequence 10, Appl
C 166	12.6	38.2	30	4	US-08-442-423-15	Sequence 15, Appl	239	12.4	37.6	33	3	US-09-202-089-10	Sequence 10, Appl
C 167	12.6	38.2	31	4	US-09-555-889A-7	Sequence 7, Appl	240	12.4	37.6	33	3	US-09-511-133-10	Sequence 10, Appl
C 168	12.6	38.2	35	3	US-09-042-353-348	Sequence 348, App	241	12.4	37.6	33	4	US-09-690-169-10	Sequence 10, Appl
C 169	12.6	38.2	36	1	US-08-758-417A-196	Sequence 196, App	242	12.4	37.6	33	4	US-09-511-631-10	Sequence 10, Appl
C 170	12.6	38.2	36	1	US-08-319-492B-261	Sequence 261, App	243	12.4	37.6	33	4	US-09-690-189-10	Sequence 10, Appl
C 171	12.6	38.2	36	1	US-08-334-847-175	Sequence 175, App	244	12.4	37.6	34	2	US-09-560-098A-36	Sequence 36, Appl
C 172	12.6	38.2	36	1	US-08-647-928-6	Sequence 6, Appl	245	12.4	37.6	39	4	US-09-396-154-85	Sequence 85, Appl
C 173	12.6	38.2	36	1	US-08-311-486C-414	Sequence 414, App	246	12.4	37.6	42	3	US-09-070-291-7	Sequence 7, Appl

C 247	12.4	37.6	43	4	US-10-001-052-18	Sequence 18, Appl	320	12.2	37.0	38	4	US-09-476-387-1324	Sequence 1324, Ap
C 248	12.4	37.6	45	3	US-08-495-695B-25	Sequence 25, Appl	C 321	12.2	37.0	40	2	US-08-425-684-98	Sequence 98, Appl
C 249	12.4	37.6	45	3	US-09-210-896-7	Sequence 7, Appl	C 322	12.2	37.0	40	2	US-08-628-422-38	Sequence 38, Appl
C 250	12.4	37.6	45	4	US-09-206-942-14	Sequence 14, Appl	C 323	12.2	37.0	40	2	US-08-675-502-98	Sequence 98, Appl
C 251	12.4	37.6	45	5	PCT-US94-14436-25	Sequence 25, Appl	C 324	12.2	37.0	40	3	US-09-411-687A-10	Sequence 10, Appl
C 252	12.2	37.0	18	2	US-08-951-648-19	Sequence 19, Appl	C 325	12.2	37.0	40	4	US-09-245-802-98	Sequence 98, Appl
C 253	12.2	37.0	18	3	US-09-280-409-134	Sequence 134, Appl	C 326	12.2	37.0	41	3	US-08-813-507-165	Sequence 165, Appl
C 254	12.2	37.0	18	3	US-09-174-437-19	Sequence 19, Appl	C 327	12.2	37.0	41	3	US-09-262-773-172	Sequence 172, Appl
C 255	12.2	37.0	18	4	US-09-686-055A-19	Sequence 19, Appl	C 328	12.2	37.0	41	3	US-09-464-453-165	Sequence 165, Appl
C 256	12.2	37.0	20	1	US-08-233-005-7	Sequence 7, Appl	C 329	12.2	37.0	43	3	US-08-983-564A-8	Sequence 8, Appl
C 257	12.2	37.0	20	1	US-08-428-943-7	Sequence 7, Appl	C 330	12.2	37.0	45	1	US-08-475-000-12	Sequence 12, Appl
C 258	12.2	37.0	20	3	US-09-016-649-7	Sequence 7, Appl	C 331	12.2	37.0	45	2	US-08-483-159-12	Sequence 12, Appl
C 259	12.2	37.0	20	3	US-09-330-330-7	Sequence 7, Appl	C 332	12.2	37.0	45	2	US-08-484-508-12	Sequence 12, Appl
C 260	12.2	37.0	20	4	US-10-044-671-10	Sequence 10, Appl	C 333	12.2	37.0	46	1	US-08-271-880A-111	Sequence 111, Appl
C 261	12.2	37.0	20	5	PCT-US95-04858-7	Sequence 7, Appl	C 334	12.2	37.0	46	2	US-08-910-408-111	Sequence 111, Appl
C 262	12.2	37.0	22	3	US-09-069-886-18	Sequence 18, Appl	C 335	12.2	37.0	46	3	US-09-249-215-111	Sequence 111, Appl
C 263	12.2	37.0	25	4	US-09-313-458-41	Sequence 41, Appl	C 336	12.2	37.0	47	4	US-09-422-978-1500	Sequence 1500, Ap
C 264	12.2	37.0	25	4	US-09-866-108A-4846	Sequence 4846, Ap	C 337	12.2	37.0	47	4	US-09-422-978-2025	Sequence 2025, Ap
C 265	12.2	37.0	26	2	US-08-859-998-530	Sequence 530, App	C 338	12.2	37.0	47	4	US-08-422-978-2025	Sequence 2025, Ap
C 266	12.2	37.0	26	2	US-08-859-998-530	Sequence 530, App	C 339	12.2	37.0	48	3	US-08-675-566-103	Sequence 103, App
C 267	12.2	37.0	26	3	US-09-092-077-53	Sequence 53, Appl	C 340	12.2	37.0	49	2	US-08-053-451B-141	Sequence 141, App
C 268	12.2	37.0	26	3	US-09-092-077-53	Sequence 54, Appl	C 341	12.2	37.0	50	2	US-08-053-451B-140	Sequence 140, App
C 269	12.2	37.0	26	3	US-09-275-850-220	Sequence 220, App	C 342	12.2	37.0	50	4	US-09-554-929-91	Sequence 91, Appl
C 270	12.2	37.0	26	3	US-09-225-928-530	Sequence 530, App	C 343	12.2	37.0	50	4	US-08-068-945A-53	Sequence 53, Appl
C 271	12.2	37.0	26	4	US-09-225-201B-530	Sequence 530, App	C 344	12.2	37.0	15	1	US-08-482-806-53	Sequence 53, Appl
C 272	12.2	37.0	27	1	US-08-468-347-5	Sequence 5, Appl	C 345	12.2	37.0	20	3	US-08-738-381-20	Sequence 20, Appl
C 273	12.2	37.0	27	1	US-08-467-389-5	Sequence 5, Appl	C 346	12.2	37.0	20	4	US-09-782-594-45	Sequence 45, Appl
C 274	12.2	37.0	27	2	US-08-779-379-5	Sequence 5, Appl	C 347	12.2	37.0	21	1	US-08-136-118-3	Sequence 3, Appl
C 275	12.2	37.0	27	2	US-08-469-219-5	Sequence 5, Appl	C 348	12.2	37.0	21	1	US-08-317-432A-23	Sequence 23, Appl
C 276	12.2	37.0	27	3	US-09-228-152-5	Sequence 5, Appl	C 349	12.2	37.0	22	4	US-08-707-938-3	Sequence 3, Appl
C 277	12.2	37.0	27	3	US-07-956-483-19	Sequence 19, Appl	C 350	12.2	37.0	24	2	US-08-572-647C-5	Sequence 5, Appl
C 278	12.2	37.0	27	3	US-08-918-148-17	Sequence 17, Appl	C 351	12.2	37.0	24	3	US-09-267-747-5	Sequence 5, Appl
C 279	12.2	37.0	27	4	US-09-184-418C-19	Sequence 19, Appl	C 352	12.2	37.0	25	4	US-09-538-709-62	Sequence 62, Appl
C 280	12.2	37.0	27	4	US-09-138-091A-17	Sequence 17, Appl	C 353	12.2	37.0	27	3	US-09-253-396A-121	Sequence 121, App
C 281	12.2	37.0	28	4	US-09-519-232-21	Sequence 21, Appl	C 354	12.2	37.0	28	4	US-09-894-799-23	Sequence 23, Appl
C 282	12.2	37.0	29	4	US-09-733-042-32	Sequence 32, Appl	C 355	12.2	37.0	29	4	US-08-260-628-3	Sequence 3, Appl
C 283	12.2	37.0	30	2	US-08-860-882A-23	Sequence 23, Appl	C 356	12.2	37.0	30	3	US-09-275-850-173	Sequence 173, App
C 284	12.2	37.0	30	3	US-08-840-466A-16	Sequence 16, Appl	C 357	12.2	37.0	31	3	US-08-586-039B-42	Sequence 42, Appl
C 285	12.2	37.0	30	4	US-09-696-188B-16	Sequence 16, Appl	C 358	12.2	37.0	31	4	US-09-699-769-42	Sequence 42, Appl
C 286	12.2	37.0	30	4	US-09-011-769A-19	Sequence 19, Appl	C 359	12.2	37.0	33	3	US-09-310-463-27	Sequence 27, Appl
C 287	12.2	37.0	31	1	US-08-647-584-22	Sequence 22, Appl	C 360	12.2	37.0	33	4	US-08-842-248A-27	Sequence 27, Appl
C 288	12.2	37.0	32	3	US-09-091-219-16	Sequence 16, Appl	C 361	12.2	37.0	34	1	US-08-347-792-22	Sequence 22, Appl
C 289	12.2	37.0	32	4	US-09-479-479-14	Sequence 14, Appl	C 362	12.2	37.0	34	1	US-08-431-357-22	Sequence 22, Appl
C 290	12.2	37.0	32	4	US-09-297-851-14	Sequence 14, Appl	C 363	12.2	37.0	34	5	PCT-US95-15353-22	Sequence 5, Appl
C 291	12.2	37.0	32	4	US-08-560-541-16	Sequence 16, Appl	C 364	12.2	37.0	36	1	US-08-433-037-5	Sequence 1, Appl
C 292	12.2	37.0	33	2	US-08-459-354-2	Sequence 2, Appl	C 365	12.2	37.0	37	4	US-09-894-799-1	Sequence 1, Appl
C 293	12.2	37.0	33	2	US-08-077-253-2	Sequence 2, Appl	C 366	12.2	37.0	38	1	US-08-390-850-805	Sequence 805, App
C 294	12.2	37.0	33	3	US-08-333-840-2	Sequence 2, Appl	C 367	12.2	37.0	38	1	US-08-373-124A-275	Sequence 275, App
C 295	12.2	37.0	35	1	US-08-347-792-34	Sequence 34, Appl	C 368	12.2	37.0	38	1	US-08-373-124A-1217	Sequence 1217, Ap
C 296	12.2	37.0	35	1	US-08-431-357-34	Sequence 34, Appl	C 369	12.2	37.0	38	1	US-08-373-124A-2320	Sequence 2320, Ap
C 297	12.2	37.0	35	5	PCT-US95-15353-34	Sequence 34, Appl	C 370	12.2	37.0	38	1	US-08-435-634-805	Sequence 805, App
C 298	12.2	37.0	36	1	US-08-291-932A-653	Sequence 653, App	C 371	12.2	37.0	38	1	US-08-435-628-375	Sequence 275, App
C 299	12.2	37.0	36	1	US-08-569-805-16	Sequence 16, Appl	C 372	12.2	37.0	38	1	US-08-435-628-1217	Sequence 1217, Ap
C 300	12.2	37.0	36	1	US-08-311-486C-409	Sequence 409, App	C 373	12.2	37.0	38	1	US-08-435-628-2320	Sequence 2320, Ap
C 301	12.2	37.0	36	2	US-08-585-684B-1453	Sequence 1453, Ap	C 374	12.2	37.0	38	4	US-09-474-432B-1260	Sequence 1260, Ap
C 302	12.2	37.0	36	2	US-08-585-684B-1891	Sequence 1891, Ap	C 375	12.2	37.0	38	4	US-09-474-432B-1452	Sequence 1452, Ap
C 303	12.2	37.0	36	2	US-08-585-684B-1892	Sequence 1892, Ap	C 376	12.2	37.0	38	4	US-09-371-772B-7428	Sequence 7428, Ap
C 304	12.2	37.0	36	2	US-08-585-684B-1893	Sequence 1893, Ap	C 377	12.2	37.0	38	4	US-09-371-772B-7681	Sequence 7681, Ap
C 305	12.2	37.0	36	3	US-09-038-073-1453	Sequence 1453, Ap	C 378	12.2	37.0	38	4	US-09-371-772B-8235	Sequence 8235, Ap
C 306	12.2	37.0	36	3	US-09-038-073-1891	Sequence 1891, Ap	C 379	12.2	37.0	38	4	US-09-371-772B-8981	Sequence 8981, Ap
C 307	12.2	37.0	36	3	US-09-038-073-1892	Sequence 1892, Ap	C 380	12.2	37.0	38	4	US-09-371-772B-9682	Sequence 9682, Ap
C 308	12.2	37.0	36	3	US-09-038-073-1893	Sequence 1893, Ap	C 381	12.2	37.0	38	4	US-09-371-772B-9776	Sequence 9776, Ap
C 309	12.2	37.0	37	4	US-08-641-294-4	Sequence 4, Appl	C 382	12.2	37.0	38	4	US-09-371-772B-10176	Sequence 10176, A
C 310	12.2	37.0	38	1	US-08-390-850-766	Sequence 766, App	C 383	12.2	37.0	38	4	US-09-371-772B-10781	Sequence 10781, A
C 311	12.2	37.0	38	1	US-08-373-124A-1242	Sequence 1242, Ap	C 384	12.2	37.0	38	4	US-09-371-772B-10781	Sequence 10781, A
C 312	12.2	37.0	38	1	US-08-435-634-766	Sequence 766, App	C 385	12.2	37.0	38	4	US-09-371-772B-10954	Sequence 10954, A
C 313	12.2	37.0	38	1	US-08-435-628-1242	Sequence 1242, Ap	C 386	12.2	37.0	38	4	US-09-371-772B-11848	Sequence 11848, A
C 314	12.2	37.0	38	4	US-09-474-432B-1325	Sequence 1325, Ap	C 387	12.2	37.0	38	4	US-09-371-772B-12036	Sequence 12036, A
C 315	12.2	37.0	38	4	US-09-371-772B-9193	Sequence 9193, Ap	C 388	12.2	37.0	38	4	US-09-371-772B-12283	Sequence 12283, A
C 316	12.2	37.0	38	4	US-09-371-772B-10032	Sequence 10032, A	C 389	12.2	37.0	38	4	US-09-371-772B-12582	Sequence 12582, A
C 317	12.2	37.0	38	4	US-09-371-772B-11410	Sequence 11410, A	C 390	12.2	37.0	38	4	US-09-371-772B-13636	Sequence 13636, A
C 318	12.2	37.0	38	4	US-09-371-772B-11852	Sequence 11852, A	C 391	12.2	37.0	38	4	US-09-476-387-1259	Sequence 1259, Ap
C 319	12.2	37.0	38	4	US-09-371-772B-11999	Sequence 11999, A	C 392	12.2	37.0	38	4	US-09-476-387-1451	Sequence 1451, Ap

C 393	12	36.4	40	2	US-08-628-422-28	Sequence 28, Appl	C 466	11.8	35.8	38	3	US-09-564-805-104	Sequence 104, App
C 394	12	36.4	40	2	US-08-483-695-20	Sequence 20, Appl	C 467	11.8	35.8	38	4	US-09-371-772B-7405	Sequence 7405, Ap
C 395	12	36.4	40	2	US-07-965-285-20	Sequence 20, Appl	C 468	11.8	35.8	38	4	US-09-371-772B-7597	Sequence 7597, Ap
C 396	12	36.4	40	2	US-08-487-231-20	Sequence 20, Appl	C 469	11.8	35.8	38	4	US-09-371-772B-10361	Sequence 10361, A
C 397	12	36.4	40	3	US-09-201-912-20	Sequence 20, Appl	C 470	11.8	35.8	38	4	US-09-371-772B-10365	Sequence 10365, A
C 398	12	36.4	41	3	US-08-864-473-69	Sequence 69, Appl	C 471	11.8	35.8	38	4	US-09-371-772B-10520	Sequence 10520, A
C 399	12	36.4	41	3	US-09-440-523-69	Sequence 69, Appl	C 472	11.8	35.8	38	4	US-09-371-772B-11889	Sequence 11889, A
C 400	12	36.4	41	4	US-09-823-823-45	Sequence 45, Appl	C 473	11.8	35.8	38	4	US-09-371-772B-12447	Sequence 12447, A
C 401	12	36.4	41	4	US-09-918-156-69	Sequence 69, Appl	C 474	11.8	35.8	38	4	US-09-371-772B-13790	Sequence 13790, A
C 402	12	36.4	42	4	US-08-749-852-12	Sequence 12, Appl	C 475	11.8	35.8	40	1	US-08-446-924-11	Sequence 11, Appl
C 403	12	36.4	42	4	US-09-459-133-19	Sequence 19, Appl	C 476	11.8	35.8	40	1	US-08-788-665-11	Sequence 11, Appl
C 404	12	36.4	45	4	US-09-079-625-21	Sequence 21, Appl	C 477	11.8	35.8	40	3	US-09-982-987A-11	Sequence 11, Appl
C 405	12	36.4	46	1	US-08-171-389-188	Sequence 188, App	C 478	11.8	35.8	40	3	US-09-363-970-14	Sequence 3, Appl
C 406	12	36.4	46	1	US-08-123-936-188	Sequence 188, App	C 479	11.8	35.8	45	4	US-08-828-592-3	Sequence 7, Appl
C 407	12	36.4	46	1	US-08-475-228A-188	Sequence 188, App	C 480	11.8	35.8	45	4	US-08-997-918-7	Sequence 1709, Ap
C 408	12	36.4	46	3	US-08-482-080A-188	Sequence 188, App	C 481	11.8	35.8	47	4	US-08-422-978-1709	Sequence 1709, Ap
C 409	12	36.4	46	3	US-09-354-947-188	Sequence 188, App	C 482	11.8	35.8	47	4	US-08-794-002-20	Sequence 96, Appl
C 410	12	36.4	46	5	PCT-US93-12388-188	Sequence 1, Appl	C 483	11.8	35.8	48	3	US-08-765-702B-21	Sequence 22, Appl
C 411	12	36.4	49	2	US-08-793-717-1	Sequence 1, Appl	C 484	11.8	35.8	50	4	US-08-317-432A-22	Sequence 3, Appl
C 412	12	36.4	50	1	US-08-171-389-478	Sequence 478, App	C 485	11.6	35.2	20	1	US-08-499-048-3	Sequence 72, Appl
C 413	12	36.4	50	1	US-08-123-936-478	Sequence 478, App	C 486	11.6	35.2	20	1	US-08-513-999C-34163	Sequence 12, Appl
C 414	12	36.4	50	2	US-08-475-228A-478	Sequence 478, App	C 487	11.6	35.2	20	1	US-08-275-893B-12	Sequence 20, Appl
C 415	12	36.4	50	3	US-08-482-080A-478	Sequence 478, App	C 488	11.6	35.2	17	3	US-08-794-002-20	Sequence 20, Appl
C 416	12	36.4	50	3	US-09-354-947-478	Sequence 478, App	C 489	11.6	35.2	17	3	US-08-854-039B-20	Sequence 20, Appl
C 417	12	36.4	50	4	US-09-605-558B-22	Sequence 22, Appl	C 490	11.6	35.2	17	4	US-08-765-702B-20	Sequence 13, Appl
C 418	12	36.4	50	4	US-09-605-558B-34	Sequence 34, Appl	C 491	11.6	35.2	18	3	US-08-275-893B-13	Sequence 21, Appl
C 419	12	36.4	50	5	PCT-US93-12388-478	Sequence 478, App	C 492	11.6	35.2	18	3	US-08-854-039B-21	Sequence 21, Appl
C 420	11.8	35.8	18	4	US-09-153-242-40	Sequence 40, Appl	C 493	11.6	35.2	20	1	US-08-794-002-21	Sequence 21, Appl
C 421	11.8	35.8	19	1	US-08-315-695-13	Sequence 13, Appl	C 494	11.6	35.2	20	1	US-08-422-978-1709	Sequence 21, Appl
C 422	11.8	35.8	20	1	US-08-484-192-71	Sequence 71, Appl	C 495	11.6	35.2	20	1	US-08-794-002-21	Sequence 21, Appl
C 423	11.8	35.8	20	1	US-08-484-192-135	Sequence 135, App	C 496	11.6	35.2	21	4	US-08-765-702B-21	Sequence 22, Appl
C 424	11.8	35.8	20	4	US-09-657-452A-46	Sequence 46, Appl	C 497	11.6	35.2	21	4	US-08-461-697-416	Sequence 416, App
C 425	11.8	35.8	20	4	US-09-866-451-45	Sequence 45, Appl	C 498	11.6	35.2	21	3	US-09-393-858-30	Sequence 30, Appl
C 426	11.8	35.8	21	2	US-08-680-326-20	Sequence 20, Appl	C 499	11.6	35.2	21	4	US-09-657-472-1731	Sequence 1731, Ap
C 427	11.8	35.8	21	3	US-09-254-325-3	Sequence 3, Appl	C 500	11.6	35.2	21	4	US-10-190-279-30	Sequence 30, Appl
C 428	11.8	35.8	21	4	US-09-657-472-1633	Sequence 1633, Ap	C 501	11.6	35.2	21	4	PCT-US94-01709-14	Sequence 14, Appl
C 429	11.8	35.8	23	4	US-10-192-369-3	Sequence 3, Appl	C 502	11.6	35.2	21	5	US-09-240-918-41	Sequence 41, Appl
C 430	11.8	35.8	24	1	US-08-337-268A-22	Sequence 22, Appl	C 503	11.6	35.2	22	3	US-09-462-606-41	Sequence 41, Appl
C 431	11.8	35.8	24	1	US-08-484-570A-22	Sequence 22, Appl	C 504	11.6	35.2	22	4	US-09-462-606-41	Sequence 41, Appl
C 432	11.8	35.8	24	1	US-09-854-140-14	Sequence 14, Appl	C 505	11.6	35.2	22	4	US-09-866-108A-15109	Sequence 45, Appl
C 433	11.8	35.8	25	1	US-08-752-238-8	Sequence 8, Appl	C 506	11.6	35.2	22	4	US-09-866-108A-15111	Sequence 45, Appl
C 434	11.8	35.8	25	3	US-09-085-603B-8	Sequence 8, Appl	C 507	11.6	35.2	25	1	US-08-317-432A-23	Sequence 43, Appl
C 435	11.8	35.8	25	4	US-09-866-108A-4847	Sequence 4847, Ap	C 508	11.6	35.2	25	4	US-09-866-108A-15107	Sequence 15107, A
C 436	11.8	35.8	25	4	US-09-866-108A-4848	Sequence 4848, Ap	C 509	11.6	35.2	25	4	US-09-866-108A-15108	Sequence 15108, A
C 437	11.8	35.8	26	1	US-08-239-256-22	Sequence 22, Appl	C 510	11.6	35.2	25	4	US-09-866-108A-15109	Sequence 15109, A
C 438	11.8	35.8	26	1	US-08-383-750-8	Sequence 8, Appl	C 511	11.6	35.2	25	4	US-09-866-108A-15111	Sequence 15111, A
C 439	11.8	35.8	26	2	US-08-225-488-8	Sequence 8, Appl	C 512	11.6	35.2	25	4	US-09-866-108A-15112	Sequence 15112, A
C 440	11.8	35.8	26	4	US-09-719-919A-8	Sequence 8, Appl	C 513	11.6	35.2	25	4	US-09-866-108A-15113	Sequence 15113, A
C 441	11.8	35.8	26	4	US-09-733-741C-5	Sequence 5, Appl	C 514	11.6	35.2	26	2	US-08-859-998-685	Sequence 685, App
C 442	11.8	35.8	27	3	US-08-985-162-1509	Sequence 1509, Ap	C 515	11.6	35.2	26	3	US-09-225-928-685	Sequence 685, App
C 443	11.8	35.8	27	4	US-09-401-063-1509	Sequence 1509, Ap	C 516	11.6	35.2	26	4	US-09-225-201B-685	Sequence 97, Appl
C 444	11.8	35.8	29	2	US-08-457-254-12	Sequence 12, Appl	C 517	11.6	35.2	27	1	US-08-399-412A-97	Sequence 87, Appl
C 445	11.8	35.8	29	4	US-07-971-834-9	Sequence 9, Appl	C 518	11.6	35.2	27	1	US-08-640-517A-97	Sequence 45, Appl
C 446	11.8	35.8	29	5	PCT-US94-08806-24	Sequence 24, Appl	C 519	11.6	35.2	27	6	US-09-689-065B-45	Sequence 45, Appl
C 447	11.8	35.8	29	5	PCT-US95-16626-12	Sequence 12, Appl	C 520	11.6	35.2	27	6	5229496-10	Patent No. 5229496
C 448	11.8	35.8	33	3	US-09-243-374-11	Sequence 11, Appl	C 521	11.6	35.2	27	6	5391485-10	Patent No. 5391485
C 449	11.8	35.8	33	4	US-09-622-439-16	Sequence 16, Appl	C 522	11.6	35.2	28	1	US-08-468-036-22	Sequence 22, Appl
C 450	11.8	35.8	34	1	US-08-091-569-24	Sequence 24, Appl	C 523	11.6	35.2	28	2	US-08-376-843-22	Sequence 22, Appl
C 451	11.8	35.8	34	1	US-08-185-232A-17	Sequence 17, Appl	C 524	11.6	35.2	28	3	US-08-590-897A-29	Sequence 29, Appl
C 452	11.8	35.8	34	1	US-08-203-676-24	Sequence 24, Appl	C 525	11.6	35.2	29	3	US-08-902-623-28	Sequence 28, Appl
C 453	11.8	35.8	34	2	US-08-416-523-17	Sequence 17, Appl	C 526	11.6	35.2	30	2	US-08-259-609-1	Sequence 1, Appl
C 454	11.8	35.8	34	3	US-08-822-238-24	Sequence 24, Appl	C 527	11.6	35.2	30	3	US-09-263-944-1	Sequence 1, Appl
C 455	11.8	35.8	34	3	US-08-789-478-17	Sequence 17, Appl	C 528	11.6	35.2	30	3	US-09-638-649-9	Sequence 9, Appl
C 456	11.8	35.8	35	3	US-09-961-083-431	Sequence 431, App	C 529	11.6	35.2	30	4	US-09-305-483-1	Sequence 1, Appl
C 457	11.8	35.8	35	4	US-09-536-784-431	Sequence 431, App	C 530	11.6	35.2	30	4	US-09-556-390A-1	Sequence 1, Appl
C 458	11.8	35.8	35	4	US-08-737-207-16	Sequence 16, App	C 531	11.6	35.2	31	2	US-08-859-998-162	Sequence 162, App
C 459	11.8	35.8	36	1	US-08-291-932A-640	Sequence 640, App	C 532	11.6	35.2	31	3	US-08-777-708C-22	Sequence 22, Appl
C 460	11.8	35.8	36	1	US-08-334-847-395	Sequence 395, App	C 533	11.6	35.2	31	3	US-09-161-466-7	Sequence 7, Appl
C 461	11.8	35.8	36	2	US-08-585-684B-1953	Sequence 1953, Ap	C 534	11.6	35.2	31	3	US-09-225-928-162	Sequence 162, App
C 462	11.8	35.8	36	2	US-08-585-684B-1954	Sequence 1954, Ap	C 535	11.6	35.2	31	4	US-09-225-201B-162	Sequence 162, App
C 463	11.8	35.8	36	3	US-09-038-073-1953	Sequence 1953, Ap	C 536	11.6	35.2	31	4	US-08-246-373-5	Sequence 5, Appl
C 464	11.8	35.8	36	3	US-08-038-073-1954	Sequence 1954, Ap	C 537	11.6	35.2	33	1	US-08-802-191-4	Sequence 4, Appl
C 465	11.8	35.8	38	2	US-08-537-811-2	Sequence 2, Appl	C 538	11.6	35.2	33	3		

539	11.6	35.2	33	4	US-09-170-496D-137	Sequence 137, App	612	11.6	35.2	40	1	US-07-714-131C-277	Sequence 277, App
c 540	11.6	35.2	33	6	5180811-8	Patent No. 5180811	613	11.6	35.2	40	1	US-07-714-131C-279	Sequence 279, App
c 541	11.6	35.2	35	1	US-07-885-970A-33	Sequence 33, Appl	614	11.6	35.2	40	1	US-08-412-110-277	Sequence 277, App
c 542	11.6	35.2	35	1	US-08-298-687A-33	Sequence 33, Appl	615	11.6	35.2	40	1	US-08-412-110-279	Sequence 279, App
c 543	11.6	35.2	35	1	US-08-298-829-33	Sequence 33, Appl	616	11.6	35.2	40	1	US-08-409-424A-277	Sequence 277, App
c 544	11.6	35.2	35	3	US-08-096-181A-5	Sequence 5, Appl	617	11.6	35.2	40	1	US-08-409-424A-279	Sequence 279, App
c 545	11.6	35.2	35	5	PCT-US94-08326-5	Sequence 5, Appl	618	11.6	35.2	40	2	US-08-469-609A-277	Sequence 277, App
546	11.6	35.2	36	1	US-08-182-530-1	Sequence 11, Appl	619	11.6	35.2	40	2	US-08-469-609A-279	Sequence 279, App
547	11.6	35.2	36	1	US-08-182-530-1	Sequence 11, Appl	620	11.6	35.2	40	3	US-09-143-190-277	Sequence 277, App
548	11.6	35.2	36	1	US-08-334-847-410	Sequence 410, App	621	11.6	35.2	40	3	US-09-143-190-279	Sequence 279, App
549	11.6	35.2	36	1	US-08-363-240A-443	Sequence 443, App	c 622	11.6	35.2	40	3	US-09-153-310-35	Sequence 35, Appl
550	11.6	35.2	36	1	US-08-050-058B-1	Sequence 1, Appl	623	11.6	35.2	40	3	US-09-502-344-277	Sequence 277, App
551	11.6	35.2	36	1	US-08-050-058B-1	Sequence 1, Appl	624	11.6	35.2	40	3	US-09-502-344-279	Sequence 279, App
552	11.6	35.2	36	1	US-08-463-587A-1	Sequence 1, Appl	625	11.6	35.2	40	4	US-09-164-714-20	Sequence 20, Appl
553	11.6	35.2	36	2	US-08-463-667A-1	Sequence 1, Appl	626	11.6	35.2	41	1	US-07-931-473B-278	Sequence 278, App
554	11.6	35.2	36	2	US-08-441-871-5	Sequence 5, Appl	627	11.6	35.2	41	1	US-07-714-131C-278	Sequence 278, App
555	11.6	35.2	36	2	US-08-441-871-15	Sequence 15, Appl	628	11.6	35.2	41	1	US-08-412-110-278	Sequence 278, App
556	11.6	35.2	36	3	US-08-923-854-1	Sequence 1, Appl	629	11.6	35.2	41	1	US-08-409-442A-278	Sequence 278, App
557	11.6	35.2	36	5	PCT-US91-09133-1	Sequence 1, Appl	c 630	11.6	35.2	41	1	US-08-317-432A-44	Sequence 44, Appl
558	11.6	35.2	36	5	PCT-US91-09133-1	Sequence 1, Appl	631	11.6	35.2	41	1	US-08-317-432A-44	Sequence 44, Appl
c 559	11.6	35.2	38	1	US-08-390-850-916	Sequence 916, App	632	11.6	35.2	41	2	US-08-469-609A-278	Sequence 278, App
c 560	11.6	35.2	38	1	US-08-390-850-917	Sequence 917, App	633	11.6	35.2	41	2	US-08-469-609A-278	Sequence 278, App
c 561	11.6	35.2	38	1	US-08-435-634-916	Sequence 916, App	634	11.6	35.2	41	3	US-09-143-190-278	Sequence 278, App
c 562	11.6	35.2	38	1	US-08-435-634-917	Sequence 917, App	635	11.6	35.2	41	3	US-09-502-344-278	Sequence 278, App
c 563	11.6	35.2	38	2	US-08-292-620A-2213	Sequence 2213, Ap	636	11.6	35.2	41	4	US-10-150-051-11	Sequence 11, Appl
564	11.6	35.2	38	2	US-08-292-620A-2304	Sequence 2304, Ap	637	11.6	35.2	42	1	US-09-938-077-3	Sequence 3, Appl
565	11.6	35.2	38	2	US-08-292-620A-2341	Sequence 2341, Ap	638	11.6	35.2	42	1	US-07-931-473B-291	Sequence 291, App
c 566	11.6	35.2	38	2	US-08-292-620A-2381	Sequence 2381, Ap	639	11.6	35.2	42	1	US-07-714-131C-291	Sequence 291, App
567	11.6	35.2	38	2	US-08-723-306-16	Sequence 16, Appl	640	11.6	35.2	42	1	US-08-412-110-291	Sequence 291, App
c 568	11.6	35.2	38	2	US-08-537-811-34	Sequence 34, Appl	641	11.6	35.2	42	1	US-08-409-442A-291	Sequence 291, App
569	11.6	35.2	38	3	US-09-071-845-2213	Sequence 2213, Ap	c 642	11.6	35.2	42	2	US-08-469-609A-291	Sequence 291, App
570	11.6	35.2	38	3	US-09-071-845-2304	Sequence 2304, Ap	643	11.6	35.2	42	3	US-08-675-566-115	Sequence 115, App
571	11.6	35.2	38	3	US-09-071-845-2341	Sequence 2341, Ap	644	11.6	35.2	42	3	US-09-502-344-291	Sequence 291, App
c 572	11.6	35.2	38	3	US-09-071-845-2381	Sequence 2381, Ap	645	11.6	35.2	43	3	US-09-526-416-12	Sequence 12, Appl
573	11.6	35.2	38	4	US-09-474-432B-1268	Sequence 1268, Ap	646	11.6	35.2	43	4	US-08-227-476-10	Sequence 10, Appl
574	11.6	35.2	38	4	US-09-474-432B-1368	Sequence 1368, Ap	647	11.6	35.2	44	1	US-08-236-311-13	Sequence 13, Appl
575	11.6	35.2	38	4	US-09-474-432B-1404	Sequence 1404, Ap	648	11.6	35.2	44	3	US-08-457-918-13	Sequence 13, Appl
576	11.6	35.2	38	4	US-09-371-772B-7327	Sequence 7327, Ap	649	11.6	35.2	44	3	US-09-355-434-6	Sequence 6, Appl
c 577	11.6	35.2	38	4	US-09-371-772B-7592	Sequence 7592, Ap	650	11.6	35.2	44	4	US-10-157-408-13	Sequence 13, Appl
c 578	11.6	35.2	38	4	US-09-371-772B-8069	Sequence 8069, Ap	651	11.6	35.2	45	1	US-08-349-696-16	Sequence 16, Appl
c 579	11.6	35.2	38	4	US-09-371-772B-8659	Sequence 8659, Ap	652	11.6	35.2	45	1	US-08-233-009-16	Sequence 16, Appl
c 580	11.6	35.2	38	4	US-09-371-772B-8813	Sequence 8813, Ap	653	11.6	35.2	45	1	US-08-560-231-16	Sequence 16, Appl
c 581	11.6	35.2	38	4	US-09-371-772B-9040	Sequence 9040, Ap	654	11.6	35.2	45	3	US-09-080-704A-16	Sequence 29, Appl
c 582	11.6	35.2	38	4	US-09-371-772B-9083	Sequence 9083, Ap	655	11.6	35.2	45	3	US-09-759-112A-29	Sequence 29, Appl
c 583	11.6	35.2	38	4	US-09-371-772B-9129	Sequence 9129, Ap	656	11.6	35.2	46	1	US-08-105-483-454	Sequence 454, App
584	11.6	35.2	38	4	US-09-371-772B-9382	Sequence 9382, Ap	657	11.6	35.2	46	1	US-08-709-209-454	Sequence 454, App
585	11.6	35.2	38	4	US-09-371-772B-9580	Sequence 9580, Ap	658	11.6	35.2	46	1	US-08-303-275-166	Sequence 166, App
c 586	11.6	35.2	38	4	US-09-371-772B-9982	Sequence 9982, Ap	659	11.6	35.2	46	1	US-08-458-101-454	Sequence 454, App
587	11.6	35.2	38	4	US-09-371-772B-10245	Sequence 10245, A	660	11.6	35.2	47	1	US-08-171-389-168	Sequence 168, App
c 588	11.6	35.2	38	4	US-09-371-772B-10514	Sequence 10514, A	661	11.6	35.2	47	1	US-08-123-936-168	Sequence 168, App
589	11.6	35.2	38	4	US-09-371-772B-10518	Sequence 10518, A	662	11.6	35.2	47	2	US-08-475-228A-168	Sequence 168, App
c 590	11.6	35.2	38	4	US-09-371-772B-10579	Sequence 10579, A	663	11.6	35.2	47	3	US-08-482-080A-168	Sequence 168, App
c 591	11.6	35.2	38	4	US-09-371-772B-10684	Sequence 10684, A	664	11.6	35.2	47	3	US-09-354-947-168	Sequence 168, App
592	11.6	35.2	38	4	US-09-371-772B-10713	Sequence 10713, A	c 665	11.6	35.2	47	4	US-09-671-317-842	Sequence 642, App
593	11.6	35.2	38	4	US-09-371-772B-11645	Sequence 11645, A	666	11.6	35.2	47	4	US-09-671-317-927	Sequence 927, App
c 594	11.6	35.2	38	4	US-09-371-772B-11820	Sequence 11820, A	667	11.6	35.2	47	4	US-09-422-978-327	Sequence 327, App
595	11.6	35.2	38	4	US-09-371-772B-11941	Sequence 11941, A	668	11.6	35.2	47	4	US-09-422-978-739	Sequence 739, App
596	11.6	35.2	38	4	US-09-371-772B-11978	Sequence 11978, A	c 669	11.6	35.2	47	4	US-09-422-978-978	Sequence 978, App
597	11.6	35.2	38	4	US-09-371-772B-13529	Sequence 13529, A	670	11.6	35.2	47	4	US-09-422-978-1425	Sequence 1425, Ap
598	11.6	35.2	38	4	US-09-371-772B-13612	Sequence 13612, A	671	11.6	35.2	47	4	US-09-422-978-1911	Sequence 1911, Ap
c 599	11.6	35.2	38	4	US-09-371-772B-13803	Sequence 13803, A	672	11.6	35.2	47	4	US-09-422-978-2519	Sequence 2519, Ap
c 600	11.6	35.2	38	4	US-09-371-772B-13975	Sequence 13975, A	673	11.6	35.2	47	4	US-09-422-978-3569	Sequence 3569, App
601	11.6	35.2	38	4	US-09-476-387-1267	Sequence 1267, Ap	674	11.6	35.2	47	5	PCT-US93-12388-168	Sequence 168, App
602	11.6	35.2	38	4	US-09-476-387-1367	Sequence 1367, Ap	675	11.6	35.2	48	3	US-08-789-333F-72	Sequence 72, Appl
603	11.6	35.2	38	4	US-09-476-387-1403	Sequence 1403, Ap	676	11.6	35.2	48	4	US-09-136-801-28	Sequence 28, Appl
c 604	11.6	35.2	38	5	PCT-US96-10041-16	Sequence 16, Appl	677	11.6	35.2	48	4	US-08-787-738B-72	Sequence 72, Appl
c 605	11.6	35.2	39	1	US-08-418-859-38	Sequence 38, Appl	678	11.6	35.2	48	4	US-09-202-088A-28	Sequence 28, Appl
c 606	11.6	35.2	39	2	US-08-643-181-38	Sequence 38, Appl	679	11.6	35.2	48	4	US-09-916-940-72	Sequence 72, Appl
607	11.6	35.2	39	2	US-08-723-306-12	Sequence 12, Appl	c 680	11.6	35.2	49	1	US-08-105-483-453	Sequence 453, App
608	11.6	35.2	39	5	PCT-US96-10041-12	Sequence 12, Appl	681	11.6	35.2	49	1	US-08-371-986-18	Sequence 18, Appl
609	11.6	35.2	39	6	5256648-32	Patent No. 5256648	c 682	11.6	35.2	49	1	US-08-709-209-453	Sequence 453, App
610	11.6	35.2	40	1	US-07-931-473B-277	Sequence 277, App	683	11.6	35.2	49	1	US-08-303-275-165	Sequence 165, App
611	11.6	35.2	40	1	US-07-931-473B-279	Sequence 279, App	c 684	11.6	35.2	49	1	US-08-458-101-453	Sequence 453, App

C 685	11.6	35.2	49	3	US-09-023-2288-63	Sequence 63, Appl	758	11.4	34.5	33	2	US-08-600-783-9	Sequence 9, Appl
C 686	11.6	35.2	49	3	US-09-163-025B-63	Sequence 63, Appl	759	11.4	34.5	33	2	US-08-985-124A-7	Sequence 7, Appl
C 687	11.6	35.2	49	3	US-09-391-104-3	Sequence 3, Appl	760	11.4	34.5	33	2	US-08-985-320A-7	Sequence 7, Appl
C 688	11.6	35.2	49	3	US-10-037-282-63	Sequence 63, Appl	761	11.4	34.5	33	3	US-08-984-732A-7	Sequence 7, Appl
C 689	11.6	35.2	50	1	US-08-236-311-20	Sequence 20, Appl	762	11.4	34.5	33	3	US-09-195-578-19	Sequence 19, Appl
C 690	11.6	35.2	50	1	US-08-171-389-433	Sequence 433, Appl	763	11.4	34.5	33	3	US-09-170-951-19	Sequence 19, Appl
C 691	11.6	35.2	50	1	US-08-171-389-477	Sequence 477, Appl	764	11.4	34.5	33	3	US-09-164-482-19	Sequence 19, Appl
C 692	11.6	35.2	50	1	US-08-123-936-433	Sequence 433, Appl	765	11.4	34.5	33	3	US-08-463-160B-42	Sequence 42, Appl
C 693	11.6	35.2	50	1	US-08-123-936-477	Sequence 477, Appl	766	11.4	34.5	33	3	US-09-332-769-14	Sequence 14, Appl
C 694	11.6	35.2	50	2	US-08-475-228A-433	Sequence 433, Appl	767	11.4	34.5	33	3	US-09-456-153-14	Sequence 14, Appl
C 695	11.6	35.2	50	2	US-08-475-228A-477	Sequence 477, Appl	768	11.4	34.5	33	3	US-09-187-180-19	Sequence 19, Appl
C 696	11.6	35.2	50	3	US-08-482-080A-433	Sequence 433, Appl	769	11.4	34.5	33	3	US-09-455-627-14	Sequence 14, Appl
C 697	11.6	35.2	50	3	US-08-482-080A-477	Sequence 477, Appl	770	11.4	34.5	33	3	US-09-426-533-14	Sequence 14, Appl
C 698	11.6	35.2	50	3	US-08-457-918-20	Sequence 20, Appl	771	11.4	34.5	33	3	US-09-609-205-15	Sequence 15, Appl
C 699	11.6	35.2	50	3	US-09-354-947-433	Sequence 433, Appl	772	11.4	34.5	33	3	US-09-516-945-14	Sequence 14, Appl
C 700	11.6	35.2	50	3	US-09-354-947-477	Sequence 477, Appl	773	11.4	34.5	33	3	US-09-757-218-15	Sequence 15, Appl
C 701	11.6	35.2	50	4	US-10-157-408-20	Sequence 20, Appl	774	11.4	34.5	33	3	US-09-516-757-14	Sequence 14, Appl
C 702	11.6	35.2	50	4	US-09-900-425B-32	Sequence 32, Appl	775	11.4	34.5	33	3	US-09-342-577-15	Sequence 15, Appl
C 703	11.6	35.2	50	5	PCT-US93-12388-433	Sequence 433, Appl	776	11.4	34.5	33	3	US-09-516-756-14	Sequence 14, Appl
C 704	11.6	35.2	50	5	PCT-US93-12388-477	Sequence 477, Appl	777	11.4	34.5	33	3	US-09-828-061A-15	Sequence 15, Appl
C 705	11.4	34.5	19	1	US-07-936-421-12	Sequence 12, Appl	778	11.4	34.5	33	3	US-09-463-917-14	Sequence 14, Appl
C 706	11.4	34.5	20	2	US-09-679-299A-21	Sequence 21, Appl	779	11.4	34.5	33	4	US-09-347-673-15	Sequence 15, Appl
C 707	11.4	34.5	20	2	US-08-697-404-8	Sequence 8, Appl	780	11.4	34.5	33	4	US-08-757-213-15	Sequence 15, Appl
C 708	11.4	34.5	21	3	US-08-545-196B-45	Sequence 45, Appl	781	11.4	34.5	33	4	US-09-656-653-14	Sequence 14, Appl
C 709	11.4	34.5	21	3	US-07-974-409C-352	Sequence 352, Appl	782	11.4	34.5	33	4	US-09-757-251-15	Sequence 15, Appl
C 710	11.4	34.5	21	4	US-08-469-260A-138	Sequence 138, Appl	783	11.4	34.5	33	4	US-09-828-259A-15	Sequence 15, Appl
C 711	11.4	34.5	21	4	US-08-469-260A-148	Sequence 148, Appl	784	11.4	34.5	33	4	US-09-719-878-15	Sequence 15, Appl
C 712	11.4	34.5	21	4	US-08-422-978-8543	Sequence 8543, Ap	785	11.4	34.5	33	4	US-09-757-217A-15	Sequence 15, Appl
C 713	11.4	34.5	21	4	US-08-488-446-138	Sequence 138, Appl	786	11.4	34.5	33	4	US-09-828-325A-15	Sequence 15, Appl
C 714	11.4	34.5	21	4	US-08-488-446-148	Sequence 148, Appl	787	11.4	34.5	33	4	US-09-756-248-14	Sequence 14, Appl
C 715	11.4	34.5	21	4	US-08-467-344A-138	Sequence 138, Appl	788	11.4	34.5	33	4	US-09-269-576G-10	Sequence 10, Appl
C 716	11.4	34.5	21	4	US-08-467-344A-148	Sequence 148, Appl	789	11.4	34.5	34	1	US-08-446-729-6	Sequence 6, Appl
C 717	11.4	34.5	21	4	US-08-424-550B-138	Sequence 138, Appl	790	11.4	34.5	35	2	US-08-455-968E-30	Sequence 30, Appl
C 718	11.4	34.5	21	4	US-08-424-550B-148	Sequence 148, Appl	791	11.4	34.5	35	3	US-09-181-183-21	Sequence 21, Appl
C 719	11.4	34.5	21	4	US-09-657-472-879	Sequence 879, Appl	792	11.4	34.5	35	3	US-08-952-793-384	Sequence 384, Appl
C 720	11.4	34.5	21	4	US-09-657-472-2154	Sequence 2154, Ap	793	11.4	34.5	35	3	US-09-280-040-21	Sequence 21, Appl
C 721	11.4	34.5	24	1	US-08-538-875-34	Sequence 34, Appl	794	11.4	34.5	35	3	US-09-277-700-21	Sequence 21, Appl
C 722	11.4	34.5	24	2	US-08-697-404-7	Sequence 7, Appl	795	11.4	34.5	35	4	US-09-849-928-384	Sequence 384, Appl
C 723	11.4	34.5	25	1	US-08-591-989-67	Sequence 67, Appl	796	11.4	34.5	35	4	US-09-874-585D-21	Sequence 21, Appl
C 724	11.4	34.5	25	2	US-08-743-637B-44	Sequence 44, Appl	797	11.4	34.5	35	4	US-09-042-460-20	Sequence 20, Appl
C 725	11.4	34.5	25	3	US-08-526-840B-44	Sequence 44, Appl	798	11.4	34.5	35	5	PCT-US96-09455A-384	Sequence 384, Appl
C 726	11.4	34.5	25	3	US-08-946-914-53	Sequence 53, Appl	799	11.4	34.5	36	3	US-09-199-637A-187	Sequence 187, Appl
C 727	11.4	34.5	25	3	US-08-946-914-60	Sequence 60, Appl	800	11.4	34.5	36	3	US-09-313-221A-103	Sequence 103, Appl
C 728	11.4	34.5	25	4	US-09-656-450-53	Sequence 53, Appl	801	11.4	34.5	36	4	US-09-589-483-2	Sequence 2, Appl
C 729	11.4	34.5	25	4	US-09-656-450-60	Sequence 60, Appl	802	11.4	34.5	36	4	US-08-726-807B-33	Sequence 33, Appl
C 730	11.4	34.5	25	4	US-09-829-855-156	Sequence 156, Appl	803	11.4	34.5	37	3	US-09-258-367-33	Sequence 33, Appl
C 731	11.4	34.5	25	4	US-09-866-108A-14605	Sequence 14605, A	804	11.4	34.5	37	3	US-09-546-550-33	Sequence 33, Appl
C 732	11.4	34.5	25	4	US-09-866-108A-14606	Sequence 14606, A	805	11.4	34.5	37	3	US-09-431-414-33	Sequence 33, Appl
C 733	11.4	34.5	25	4	US-09-866-108A-14607	Sequence 14607, A	806	11.4	34.5	37	3	US-09-225-670-33	Sequence 33, Appl
C 734	11.4	34.5	25	4	US-09-866-108A-14608	Sequence 14608, A	807	11.4	34.5	37	3	US-09-485-632B-14	Sequence 14, Appl
C 735	11.4	34.5	25	4	US-09-866-108A-14609	Sequence 14609, A	808	11.4	34.5	37	4	US-09-746-359A-48	Sequence 48, Appl
C 736	11.4	34.5	27	3	US-09-253-396A-97	Sequence 97, Appl	809	11.4	34.5	38	4	US-08-675-566-105	Sequence 105, Appl
C 737	11.4	34.5	28	1	US-08-117-364A-3	Sequence 3, Appl	810	11.4	34.5	39	4	US-09-267-311-13	Sequence 13, Appl
C 738	11.4	34.5	28	1	US-08-647-584-21	Sequence 21, Appl	811	11.4	34.5	39	4	US-08-086-428B-104	Sequence 104, Appl
C 739	11.4	34.5	28	2	US-08-457-733-3	Sequence 3, Appl	812	11.4	34.5	40	1	US-08-086-428B-106	Sequence 106, Appl
C 740	11.4	34.5	28	3	US-08-457-733-3	Sequence 3, Appl	813	11.4	34.5	40	1	US-08-086-428B-108	Sequence 108, Appl
C 741	11.4	34.5	28	4	US-09-523-849-37	Sequence 37, Appl	814	11.4	34.5	40	1	US-08-086-570-104	Sequence 104, Appl
C 742	11.4	34.5	29	4	US-09-304-232-251	Sequence 251, Appl	815	11.4	34.5	40	2	US-08-468-570-106	Sequence 106, Appl
C 743	11.4	34.5	29	4	US-09-304-232-504	Sequence 504, Appl	816	11.4	34.5	40	2	US-08-468-570-108	Sequence 108, Appl
C 744	11.4	34.5	30	2	US-08-859-998-430	Sequence 430, Appl	817	11.4	34.5	40	2	US-08-290-665A-208	Sequence 208, Appl
C 745	11.4	34.5	30	3	US-08-696-932A-40	Sequence 430, Appl	818	11.4	34.5	40	2	US-08-290-665A-210	Sequence 210, Appl
C 746	11.4	34.5	30	3	US-09-225-928-430	Sequence 430, Appl	819	11.4	34.5	40	2	US-08-290-665A-212	Sequence 212, Appl
C 747	11.4	34.5	30	4	US-09-225-201B-430	Sequence 430, Appl	820	11.4	34.5	40	2	US-09-164-714-19	Sequence 19, Appl
C 748	11.4	34.5	30	4	US-09-706-649-5	Sequence 5, Appl	821	11.4	34.5	40	4	US-09-060-299-185	Sequence 185, Appl
C 749	11.4	34.5	32	1	US-08-484-686B-26	Sequence 26, Appl	822	11.4	34.5	40	4	US-09-402-923A-185	Sequence 185, Appl
C 750	11.4	34.5	32	3	US-08-463-160B-26	Sequence 26, Appl	823	11.4	34.5	40	4	US-08-466-601A-104	Sequence 104, Appl
C 751	11.4	34.5	32	5	PCT-US91-02568-27	Sequence 27, Appl	824	11.4	34.5	40	4	US-08-466-601A-106	Sequence 106, Appl
C 752	11.4	34.5	32	5	PCT-US91-02568-29	Sequence 29, Appl	825	11.4	34.5	40	4	US-08-466-601A-108	Sequence 108, Appl
C 753	11.4	34.5	32	5	PCT-US91-02568-42	Sequence 42, Appl	826	11.4	34.5	40	4	PCT-US95-10398-208	Sequence 208, Appl
C 754	11.4	34.5	33	1	US-08-538-875-70	Sequence 70, Appl	827	11.4	34.5	40	5	PCT-US95-10398-210	Sequence 210, Appl
C 755	11.4	34.5	33	1	US-08-484-686B-42	Sequence 42, Appl	828	11.4	34.5	40			
C 756	11.4	34.5	33	2	US-08-985-337A-7	Sequence 7, Appl	829	11.4	34.5	40			
C 757	11.4	34.5	33	2	US-08-600-783-8	Sequence 8, Appl	830	11.4	34.5	40			

C 831	11.4	34.5	40	5	PCT-US95-10398-212	Sequence 212, App	C 904	11.2	33.9	21	4	US-09-657-472-2072	Sequence 2072, Ap
C 832	11.4	34.5	41	2	US-08-428-257A-57	Sequence 57, Appl	C 905	11.2	33.9	22	3	US-09-280-409-7	Sequence 7, Appl
C 833	11.4	34.5	41	4	US-08-913-370-10	Sequence 10, Appl	C 906	11.2	33.9	22	4	US-09-792-024-378	Sequence 378, App
C 834	11.4	34.5	41	4	US-09-938-077-3	Sequence 3, Appl	C 907	11.2	33.9	23	3	US-08-068-754-2	Sequence 2, Appl
C 835	11.4	34.5	43	2	US-08-714-070A-9	Sequence 9, Appl	C 908	11.2	33.9	23	3	US-09-325-926-2	Sequence 2, Appl
C 836	11.4	34.5	43	3	US-08-604-986-13	Sequence 13, Appl	C 909	11.2	33.9	24	3	US-09-035-619-3	Sequence 3, Appl
C 837	11.4	34.5	45	1	US-08-250-859-8	Sequence 8, Appl	C 910	11.2	33.9	24	3	US-09-514-006-3	Sequence 3, Appl
C 838	11.4	34.5	45	1	US-08-334-499-1	Sequence 1, Appl	C 911	11.2	33.9	24	3	US-09-423-744A-2	Sequence 2, Appl
C 839	11.4	34.5	45	1	US-08-490-803-8	Sequence 8, Appl	C 912	11.2	33.9	24	3	US-09-798-743-9	Sequence 9, Appl
C 840	11.4	34.5	45	2	US-08-464-073-35	Sequence 35, Appl	C 913	11.2	33.9	25	1	US-08-448-204-26	Sequence 26, Appl
C 841	11.4	34.5	45	2	US-08-457-254-20	Sequence 20, Appl	C 914	11.2	33.9	25	4	US-09-142-138-2	Sequence 2, Appl
C 842	11.4	34.5	45	2	US-08-484-257-8	Sequence 8, Appl	C 915	11.2	33.9	25	4	US-09-538-709-350	Sequence 350, App
C 843	11.4	34.5	45	5	PCT-US94-08806-8	Sequence 8, Appl	C 916	11.2	33.9	25	4	US-09-398-858-10	Sequence 10, Appl
C 844	11.4	34.5	45	5	PCT-US95-01775-8	Sequence 8, Appl	C 917	11.2	33.9	25	4	US-09-866-108A-4845	Sequence 4845, Ap
C 845	11.4	34.5	45	5	PCT-US95-16626-20	Sequence 20, Appl	C 918	11.2	33.9	25	4	US-09-866-108A-11254	Sequence 11254, A
C 846	11.4	34.5	46	1	US-08-403-762A-14	Sequence 14, Appl	C 919	11.2	33.9	25	4	US-09-866-108A-11255	Sequence 11255, A
C 847	11.4	34.5	46	3	US-09-164-023-8	Sequence 8, Appl	C 920	11.2	33.9	25	4	US-09-866-108A-11256	Sequence 11256, A
C 848	11.4	34.5	46	3	US-08-869-276-10	Sequence 10, Appl	C 921	11.2	33.9	25	4	US-09-866-108A-11257	Sequence 11257, A
C 849	11.4	34.5	46	3	US-09-635-344-10	Sequence 10, Appl	C 922	11.2	33.9	25	4	US-09-866-108A-11258	Sequence 11258, A
C 850	11.4	34.5	46	3	US-09-398-629-10	Sequence 10, Appl	C 923	11.2	33.9	25	4	US-09-866-108A-11259	Sequence 11259, A
C 851	11.4	34.5	46	4	US-09-799-160-10	Sequence 10, Appl	C 924	11.2	33.9	25	4	US-09-866-108A-11260	Sequence 11260, A
C 852	11.4	34.5	47	4	US-09-641-638-663	Sequence 663, App	C 925	11.2	33.9	25	4	US-09-866-108A-11261	Sequence 11261, A
C 853	11.4	34.5	47	4	US-09-641-638-1141	Sequence 1141, Ap	C 926	11.2	33.9	25	4	US-09-866-108A-11262	Sequence 11262, A
C 854	11.4	34.5	47	4	US-09-422-978-986	Sequence 986, App	C 927	11.2	33.9	25	4	US-09-866-108A-11263	Sequence 11263, A
C 855	11.4	34.5	47	4	US-09-422-978-986	Sequence 986, App	C 928	11.2	33.9	25	4	US-09-866-108A-11263	Sequence 11263, A
C 856	11.4	34.5	47	4	US-09-422-978-986	Sequence 986, App	C 929	11.2	33.9	26	2	US-08-766-439-48	Sequence 48, Appl
C 857	11.4	34.5	47	4	US-09-422-978-986	Sequence 986, App	C 930	11.2	33.9	26	2	US-08-766-439-48	Sequence 48, Appl
C 858	11.4	34.5	47	4	US-10-170-097-663	Sequence 663, App	C 931	11.2	33.9	26	2	US-09-395-017B-34	Sequence 34, Appl
C 859	11.4	34.5	47	4	US-10-170-097-663	Sequence 663, App	C 932	11.2	33.9	27	1	US-07-986-963-6	Sequence 6, Appl
C 860	11.4	34.5	48	2	US-08-896-410-26	Sequence 26, Appl	C 933	11.2	33.9	27	1	US-08-707-793A-11	Sequence 11, Appl
C 861	11.4	34.5	48	2	US-08-697-404-2	Sequence 2, Appl	C 934	11.2	33.9	27	1	US-08-707-793A-11	Sequence 11, Appl
C 862	11.4	34.5	49	2	US-08-464-073-23	Sequence 23, Appl	C 935	11.2	33.9	27	2	US-08-244-122-12	Sequence 12, Appl
C 863	11.4	34.5	49	3	US-08-428-252-23	Sequence 23, Appl	C 936	11.2	33.9	27	2	US-08-447-430A-21	Sequence 21, Appl
C 864	11.4	34.5	49	3	US-08-416-516A-23	Sequence 23, Appl	C 937	11.2	33.9	27	2	US-08-447-430A-22	Sequence 22, Appl
C 865	11.4	34.5	49	4	US-09-968-255-18	Sequence 18, Appl	C 938	11.2	33.9	27	3	US-08-985-162-844	Sequence 844, App
C 866	11.4	34.5	50	1	US-07-994-469A-37	Sequence 37, Appl	C 939	11.2	33.9	27	3	US-08-584-040-6733	Sequence 6733, Ap
C 867	11.4	34.5	50	1	US-08-688-649-19	Sequence 19, Appl	C 940	11.2	33.9	27	4	US-09-706-197-6	Sequence 6, Appl
C 868	11.4	34.5	50	2	US-08-464-073-36	Sequence 36, Appl	C 941	11.2	33.9	27	4	US-09-553-690-43	Sequence 43, Appl
C 869	11.4	34.5	50	3	US-08-377-503-3	Sequence 3, Appl	C 942	11.2	33.9	27	4	US-09-179-162A-2	Sequence 2, Appl
C 870	11.4	34.5	50	3	US-08-178-019-3	Sequence 3, Appl	C 943	11.2	33.9	27	4	US-09-342-673-21	Sequence 21, Appl
C 871	11.4	34.5	50	4	US-08-781-986A-5177	Sequence 5177, Ap	C 944	11.2	33.9	27	4	US-09-401-063-844	Sequence 22, Appl
C 872	11.2	33.9	16	1	US-08-469-802B-9	Sequence 9, Appl	C 945	11.2	33.9	27	4	US-09-401-063-844	Sequence 22, Appl
C 873	11.2	33.9	16	2	US-08-267-803B-27	Sequence 27, Appl	C 946	11.2	33.9	28	1	US-08-462-894-22	Sequence 22, Appl
C 874	11.2	33.9	17	1	US-08-373-124A-1335	Sequence 1335, Ap	C 947	11.2	33.9	28	1	US-08-206-185-22	Sequence 22, Appl
C 875	11.2	33.9	17	1	US-08-435-628-1335	Sequence 1335, Ap	C 948	11.2	33.9	28	1	US-08-183-846A-17	Sequence 17, Appl
C 876	11.2	33.9	17	2	US-08-404-531B-17	Sequence 17, Appl	C 949	11.2	33.9	28	3	US-09-267-177-6	Sequence 6, Appl
C 877	11.2	33.9	17	3	US-08-476-900A-17	Sequence 17, Appl	C 950	11.2	33.9	28	4	US-08-961-578C-17	Sequence 17, Appl
C 878	11.2	33.9	17	3	US-08-488-546A-17	Sequence 17, Appl	C 951	11.2	33.9	28	4	US-08-887-497A-72	Sequence 72, Appl
C 879	11.2	33.9	17	4	US-09-866-108A-6362	Sequence 6362, Ap	C 952	11.2	33.9	28	4	US-09-670-216-17	Sequence 17, Appl
C 880	11.2	33.9	17	4	US-09-866-108A-6363	Sequence 6363, Ap	C 953	11.2	33.9	28	4	US-08-734-443-3	Sequence 3, Appl
C 881	11.2	33.9	18	1	US-08-120-780-2	Sequence 2, Appl	C 954	11.2	33.9	29	2	US-08-829-876-20	Sequence 20, Appl
C 882	11.2	33.9	18	3	US-08-624-290B-2	Sequence 2, Appl	C 955	11.2	33.9	30	2	US-08-829-876-20	Sequence 20, Appl
C 883	11.2	33.9	19	3	US-08-851-843A-95	Sequence 95, Appl	C 956	11.2	33.9	30	3	US-08-526-840B-101	Sequence 101, App
C 884	11.2	33.9	19	3	US-08-974-549A-387	Sequence 387, App	C 957	11.2	33.9	30	3	US-08-526-840B-101	Sequence 101, App
C 885	11.2	33.9	19	3	US-08-854-050-95	Sequence 95, Appl	C 958	11.2	33.9	30	3	US-09-234-874A-20	Sequence 20, Appl
C 886	11.2	33.9	19	3	US-08-430-323-95	Sequence 95, Appl	C 959	11.2	33.9	30	4	US-09-684-385-40	Sequence 40, Appl
C 887	11.2	33.9	19	4	US-08-912-951-154	Sequence 154, App	C 960	11.2	33.9	31	6	5466668-47	Patent No. 5466668
C 888	11.2	33.9	19	4	US-09-402-181B-387	Sequence 387, App	C 961	11.2	33.9	32	1	US-08-612-895A-58	Sequence 58, Appl
C 889	11.2	33.9	19	4	US-09-721-456-387	Sequence 387, App	C 962	11.2	33.9	32	3	US-09-093-233-58	Sequence 58, Appl
C 890	11.2	33.9	19	4	US-09-696-791-3881	Sequence 3881, Ap	C 963	11.2	33.9	32	3	US-09-303-084-39	Sequence 39, Appl
C 891	11.2	33.9	20	1	US-08-531-556-53	Sequence 53, Appl	C 964	11.2	33.9	32	3	US-09-459-553-58	Sequence 58, Appl
C 892	11.2	33.9	20	1	US-08-472-416-53	Sequence 53, Appl	C 965	11.2	33.9	32	3	US-09-086-503-39	Sequence 39, Appl
C 893	11.2	33.9	20	3	US-09-428-584-12	Sequence 12, Appl	C 966	11.2	33.9	32	3	US-09-882-246-58	Sequence 58, Appl
C 894	11.2	33.9	20	3	US-09-290-640-28	Sequence 28, Appl	C 967	11.2	33.9	32	5	PCT-US94-10562A-58	Sequence 58, Appl
C 895	11.2	33.9	20	3	US-09-657-042A-33	Sequence 33, Appl	C 968	11.2	33.9	34	1	US-08-591-989-65	Sequence 65, Appl
C 896	11.2	33.9	20	3	US-09-183-636-3	Sequence 3, Appl	C 969	11.2	33.9	34	3	US-08-123-764-7	Sequence 7, Appl
C 897	11.2	33.9	20	4	US-09-422-978-5364	Sequence 5364, Ap	C 970	11.2	33.9	34	3	US-08-815-190A-7	Sequence 7, Appl
C 898	11.2	33.9	20	4	US-09-665-615B-28	Sequence 28, Appl	C 971	11.2	33.9	34	3	US-09-645-629-30	Sequence 30, Appl
C 899	11.2	33.9	21	1	US-08-290-937B-7	Sequence 7, Appl	C 972	11.2	33.9	35	1	US-08-233-030-9	Sequence 9, Appl
C 900	11.2	33.9	21	4	US-09-553-231-3	Sequence 3, Appl	C 973	11.2	33.9	35	1	US-08-361-337-17	Sequence 17, Appl
C 901	11.2	33.9	21	4	US-09-585-174-30	Sequence 30, Appl	C 974	11.2	33.9	36	1	US-07-988-194A-27	Sequence 27, Appl
C 902	11.2	33.9	21	4	US-09-194-854-202	Sequence 202, App	C 975	11.2	33.9	36	1	US-08-311-760A-146	Sequence 146, App
C 903	11.2	33.9	21	4	US-09-657-472-382	Sequence 382, App	C 976	11.2	33.9	36	1	US-08-319-492B-183	Sequence 183, App

Sequence 334, App
Sequence 637, App
Sequence 635, App
Sequence 29, App1
Sequence 159, App
Sequence 176, App
Sequence 210, App
Sequence 399, App
Sequence 860, App
Sequence 304, App
Sequence 898, App
Sequence 29, App1
Sequence 1131, App
Sequence 1442, App
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Sequence 481, App
Sequence 1028, App
Sequence 1460, App
Sequence 1555, App
Sequence 1593, App
Sequence 2005, App
Sequence 2006, App
Sequence 146, App
Sequence 1131, App

ALIGNMENTS

RESULT 1
US-09-438-954-8
; Sequence 8, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer KXD
US-09-438-954-8

Query Match 46.7%; Score 15.4; DB 4; Length 30;
Best Local Similarity 76.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 8 GAGTGGCAGCGCTCTGGTGATAC 32
DB 2 GACTGGCCAGGTTTGTGTGATACC 26
RESULT 2
US-09-233-493-28/c
; Sequence 28, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-493-28
Query Match 46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAGCGCTCTGGTGATA 30
DB 32 ATGAGTGGCAGCGCGCGGCGTAATA 8
RESULT 3
US-09-005-476-28/c
; Sequence 28, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476

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; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-005-476-28

Query Match          46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
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Db      32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 4
US-09-233-492-28/c
; Sequence 28, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-492-28

Query Match          46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
      |||||||
Db      32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 5
US-09-296-280-28/c
; Sequence 28, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
; US-09-296-280-28

Query Match          46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
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Db      32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 6
US-09-498-074-28/c
; Sequence 28, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-498-074-28

Query Match 46.7%; Score 15.4; DB 4; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
32 ATGAGTGGCAGGCGGGCGGCTAATA 8
|||||

Db

RESULT 8
PCT-US96-10082A-28/c
; Sequence 28, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
PCT-US96-10082A-28

Query Match 46.7%; Score 15.4; DB 5; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
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32 ATGAGTGGCAGGCGGGCGGCTAATA 8
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Db

RESULT 9
US-08-323-192D-23
; Sequence 23, Application US/08323192D
; Patent No. 5786199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-323-192D-23
;
Query Match 46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGGCGGGCGTAATA 31

RESULT 10
US-08-323-192D-25
; Sequence 25, Application US/08323192D
; Patent No. 5786199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
```

```
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-323-192D-25
;
Query Match 46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGGCGGGCGTAATA 31

RESULT 11
US-08-470-887A-22
; Sequence 22, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-470-887A-22
;
Query Match 46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGGCGGGCGTAATA 31

RESULT 12
US-08-470-887A-24
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us-10-087-631b-5.max.rni

Wed Nov 24 08:46:06 2004

```

; Sequence 24, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-470-887A-24

Query Match 46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
   |||||
Db 7 ATGAGTGGCAGGCGGCGGCGTAATA 31

RESULT 13
US-08-316-439A-20
; Sequence 20, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,439A

; Sequence 24, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-470-887A-24

Query Match 46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
   |||||
Db 7 ATGAGTGGCAGGCGGCGGCGTAATA 31

RESULT 14
US-08-316-439A-22
; Sequence 22, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,439A

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; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/190,678
; FILING DATE: February 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,061
; FILING DATE: August 4, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/527,237
; FILING DATE: May 22, 1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/440,053
; FILING DATE: No. 5840520ember 21, 1989
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/399,728
; FILING DATE: August 28, 1989
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CSER, LUANN
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-010/000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5165
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 22:
; LENGTH: 34 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: SYNTHETIC DNA
; US-08-316-439A-22
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Query Match 46.7%; Score 15.4; DB 2; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 6 ATGAGTGCACAGCGCTCTGGTGATA 30
|||
Db 7 ATGAGTGCACAGCGCGCGGTAATA 31
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```
RESULT 15
US-08-252-508B-22
; Sequence 22, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; REFERENCE/DOCKET NUMBER: 30,742
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-252-508B-22

Query Match 46.7%; Score 15.4; DB 2; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGCACAGCGCTCTGGTGATA 30
|||
Db 7 ATGAGTGCACAGCGCGGCGTAATA 31

RESULT 16
US-08-252-508B-24
; Sequence 24, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; REFERENCE/DOCKET NUMBER: 30,742
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-252-508B-24
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```
Query Match 46.7%; Score 15.4; DB 2; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

us-10-087-631b-5.max.rni

Wed Nov 24 08:46:06 2004

```

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/252,508
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-09-106-377-24

Query Match 46.7%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   |||||
Db 7 ATGAGTGGCAGGCGGGCGGTAATA 31

RESULT 19
5166057-35
; Patent No. 5166057
; APPLICANT: PALSESE, PETER; PARVIN, JEFFREY D.; KRYSTAL, MARK
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; EXPRESSION-SYSTEMS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/527,237
; FILING DATE: 22-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,053
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 399,728
; FILING DATE: 28-AUG-1989
; SEQ ID NO:35:
; LENGTH: 34
5166057-35

Query Match 46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   |||||
Db 7 ATGAGTGGCAGGCGGGCGGTAATA 31

RESULT 20
US-08-323-192D-24/c

```

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/ Sequence 24, Application US/08323192D
/ Patent No. 5786199
/ GENERAL INFORMATION:
/ APPLICANT: Palese, Peter
/ TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
/ REFERENCE/DOCKET NUMBER: 7682-035
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/323,192D
/ FILING DATE: 14-OCT-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7682-035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 869-9741/8864
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-08-323-192D-24

Query Match          46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db      32 ATGAGTGGCAGCGCGGGCGTAATA 8

RESULT 21
US-08-323-192D-26/c
/ Sequence 26, Application US/08323192D
/ Patent No. 5786199
/ GENERAL INFORMATION:
/ APPLICANT: Palese, Peter
/ TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
/ REFERENCE/DOCKET NUMBER: 7682-035
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/323,192D
/ FILING DATE: 14-OCT-1994
```

```
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7682-035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-08-323-192D-26

Query Match          46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db      32 ATGAGTGGCAGCGCGGGCGTAATA 8

RESULT 22
US-08-470-887A-23/c
/ Sequence 23, Application US/08470887A
/ Patent No. 5820871
/ GENERAL INFORMATION:
/ APPLICANT: Palese, Peter
/ TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
/ REFERENCE/DOCKET NUMBER: 7682-035
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,887A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7682-035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA
/ US-08-470-887A-23

Query Match          46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 23

US-08-470-887A-25/c
; Sequence 25, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-470-887A-25

Query Match 46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 24

US-08-316-439A-23/c
; Sequence 23, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GORDWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA

; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,439A
; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/190,678
; FILING DATE: February 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,061
; FILING DATE: August 4, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/527,237
; FILING DATE: May 22, 1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/440,053
; FILING DATE: No. 5840520ember 21, 1989
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/399,728
; FILING DATE: August 28, 1989
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CSERR, LUANN
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-010/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5165
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: SYNTHETIC DNA
US-08-316-439A-23

Query Match 46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 25

US-08-252-508B-23/c
; Sequence 23, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

```
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/252.508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-252-508B-23

Query Match          46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db      32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 26
US-08-252-508B-25/c
; Sequence 25, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
```

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-252-508B-25

Query Match          46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db      32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 27
US-09-106-377-23/c
; Sequence 23, Application US/09106377
; Patent No. 6001834
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/252,508
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-09-106-377-23

Query Match          46.7%; Score 15.4; DB 3; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db      32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 28
US-09-106-377-25/c
; Sequence 25, Application US/09106377
```

Patent No. 6001634
GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: Garcia-Sastre, Adolfo
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,377
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,508
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-09-106-377-25
Query Match 46.7%; Score 15.4; DB 3; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAGGCGTCTGGTATA 30
DB 32 ATGAGTGGCAGGCGGCGGTAATA 8
RESULT 29
5166057-37/c
Patent No. 5166057
APPLICANT: PALESE, PETER; PARVIN, JEFFREY D.; KRISTAL, MARK
TITLE OF INVENTION: RECOMBIANT NEGATIVE STRAND RNA VIRUS
EXPRESSION-SYSTEMS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/527,237
FILING DATE: 22-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,053
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 399,728
FILING DATE: 28-AUG-1989
SEQ ID NO: 37:
LENGTH: 38
5166057-37
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAGGCGTCTGGTATA 30
DB 32 ATGAGTGGCAGGCGGCGGTAATA 8
RESULT 30
US-09-223-139-1/c
Sequence 1, Application US/09223139
Patent No. 6441158
GENERAL INFORMATION:
APPLICANT: Dynan, William S.
APPLICANT: Yoo, Sunghan
TITLE OF INVENTION: Oligomers that Bind to KU Protein
FILE REFERENCE: MCG 102
CURRENT APPLICATION NUMBER: US/09/223,139
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: 60/070,278
EARLIER FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 40
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide
FEATURE:
NAME/KEY: misc. RNA
LOCATION: (1)..(40)
OTHER INFORMATION: oligomer SC6
US-09-223-139-1
Query Match 46.7%; Score 15.4; DB 4; Length 40;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCACATGAGTGGCAAGGCGTCTGGT 26
DB 37 CAAGACCAGTGGCAAGGCGTATGGT 13
RESULT 31
US-09-485-737B-8/c
Sequence 8, Application US/09485737B
Patent No. 6350860
GENERAL INFORMATION:
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
FILE REFERENCE: INNS-015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 40
TYPE: DNA
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: GENOMIC
US-09-485-737B-8
Query Match 44.2%; Score 14.6; DB 3; Length 40;

Best Local Similarity 69.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 9;

Qy 4 ACATGAGTGGCAAGCGCTCTGTGTATACC 32
| | | | | | | | | | | | | | | | | | | | | |
Db 37 AGATCAGCTGCAAGCGAGCGGTATACC 9
| | | | | | | | | | | | | | | | | | | | | |

RESULT 32
US-09-340-798A-39
; Sequence 39, Application US/09340798A
; Patent No. 6534312
; GENERAL INFORMATION:
; APPLICANT: SHIVER, JOHN W.
; LIU, MARGARET A.
; PERRY, HELEN C.
; DAVIES, MARY-ELLEN M.
; FREED, DANIEL C.
; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,798A
; FILING DATE: 28-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,418
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19729Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-340-798A-39

Query Match 44.2%; Score 14.6; DB 4; Length 40;
Best Local Similarity 69.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGGCAAGCGCTCTGTGTAT 29
| | | | | | | | | | | | | | | | | | | | | |
Db 8 GCTAATGGTGGCAAGTGGCCCGGCAT 36
| | | | | | | | | | | | | | | | | | | | | |

RESULT 33
US-08-053-451B-149
; Sequence 149, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.

; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-053-451B-149

Query Match 44.2%; Score 14.6; DB 2; Length 45;
Best Local Similarity 69.0%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 CATGAGTGGCAAGCGCTCTGTGTATACC 33
| | | | | | | | | | | | | | | | | | | | | |
Db 17 CATCAGCAGCCTGGAGTCTGACGATACAG 45
| | | | | | | | | | | | | | | | | | | | | |

RESULT 34
US-08-789-333F-66
; Sequence 66, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A642601DJBRMSDS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-789-333F-66

Query Match 44.2%; Score 14.6; DB 3; Length 48;

```

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-916-940-66

Query Match          44.2%; Score 14.6; DB 4; Length 48;
Best Local Similarity 69.0%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0;

Qy      1  GCACATGATGTCGCAAGGCGCTCTGGTGAT 29
Db      5  GCAAGAGAAAGGCGCACGGCGCTCTGATGCT 33

RESULT 37
US-08-053-451B-148
; Sequence 148, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Dittow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ANTHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THERE
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; COMMENT: none

```

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-053-451B-148

Query Match 44.2%; Score 14.6; DB 2; Length 50;
Best Local Similarity 69.0%; Pred.No.1.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CATGAGTGGCAAGCGCTCTGGTGATACCG 33
   ||| ||| ||| ||| ||| ||| |||
DB 22 CATCAGCAGCGCTGGAGTCTGACGATACAG 50

RESULT 38
US-09-2795-850-283/c
; Sequence 283, Application US/09275850A
; Patent No. 6261774
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Shtatland, Timur

```


APPLICANT: Javornik, Brenda
TITLE OF INVENTION: Truncation SELEX Method
FILE REFERENCE: NEX 79
CURRENT APPLICATION NUMBER: US/09/275,850A
CURRENT FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 351
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 283
LENGTH: 50
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
NAME/KEY: modified base
LOCATION: (1)..(50)
OTHER INFORMATION: All pyrimidines are 2'-F; N at positions 7, 25,
OTHER INFORMATION: and 32 are A, C, G or U.

US-09-275-850-283

Query Match 44.2%; Score 14.6; DB 3; Length 50;
Best Local Similarity 77.3%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GCGAAGGCGTCTGGTGATACG 33
|||||
DB 47 GCGGAGTCTCTGGGNATACG 26
|||||

RESULT 39

US-08-872-855-13/c
Sequence 13, Application US/08872855
Patent No. 6121045
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"

US-08-872-855-13

Query Match 43.6%; Score 14.4; DB 3; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCAAGGCGTCTGG 25
|||||
DB 19 GTGGCAAGGCGTCTGG 4
|||||
RESULT 40
US-09-422-978-2994
Sequence 2994, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2994
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-21492-310 : polymorphic base C or T
US-09-422-978-2994

Query Match 43.6%; Score 14.4; DB 4; Length 47;
Best Local Similarity 69.2%; Pred. No. 1.7e+03;
Matches 18; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 7 TGAGTGGCAAGGCGTCTGGTGATACC 32
|||||
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88	13.8	41.8	21	18	US-10-444-853A-158	Sequence 158, App	c 161	13.2	40.0	30	15	US-10-220-908-2	Sequence 2, Appl
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90	13.8	41.8	21	18	US-10-444-853A-213	Sequence 213, App	c 163	13.2	40.0	33	16	US-10-372-653-15	Sequence 15, Appl
91	13.8	41.8	21	18	US-10-667-271-1436	Sequence 1436, App	c 164	13.2	40.0	33	16	US-10-372-653-17	Sequence 17, Appl
92	13.8	41.8	21	18	US-10-667-271-1443	Sequence 1443, App	c 165	13.2	40.0	35	9	US-09-874-475-7	Sequence 7, Appl
93	13.8	41.8	21	18	US-10-667-271-1470	Sequence 1470, App	c 166	13.2	40.0	35	17	US-10-164-290A-7	Sequence 7, Appl
94	13.8	41.8	22	16	US-10-380-907-9	Sequence 9, Appl	c 167	13.2	40.0	38	10	US-09-730-289B-2420	Sequence 2420, App
95	13.8	41.8	22	16	US-10-380-907-10	Sequence 10, Appl	c 168	13.2	40.0	38	10	US-09-730-289B-2648	Sequence 2648, App
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97	13.8	41.8	25	15	US-10-098-263B-57899	Sequence 57899, A	c 170	13.2	40.0	38	10	US-09-848-754A-3788	Sequence 3788, App
98	13.8	41.8	25	15	US-10-098-263B-97710	Sequence 97710, A	c 171	13.2	40.0	38	10	US-09-776-474-1626	Sequence 1626, App
99	13.8	41.8	36	9	US-09-504-231A-2496	Sequence 2496, App	c 172	13.2	40.0	38	10	US-09-930-423-1894	Sequence 1894, App
100	13.8	41.8	36	9	US-09-774-553B-2496	Sequence 2496, App	c 173	13.2	40.0	38	10	US-09-792-818-1492	Sequence 1492, App
101	13.8	41.8	38	10	US-09-780-533A-4243	Sequence 4243, App	c 174	13.2	40.0	38	10	US-09-745-237A-1894	Sequence 1894, App
102	13.8	41.8	39	16	US-10-434-469-38	Sequence 38, Appl	c 175	13.2	40.0	38	15	US-10-156-306-893	Sequence 893, App
103	13.8	41.8	39	16	US-10-434-469-39	Sequence 39, Appl	c 176	13.2	40.0	38	15	US-10-156-306-1010	Sequence 1010, App
104	13.8	41.8	43	10	US-09-892-613C-31	Sequence 31, Appl	c 177	13.2	40.0	38	16	US-10-138-674-12869	Sequence 12869, A
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106	13.8	41.8	44	14	US-10-350-798-15	Sequence 15, Appl	c 179	13.2	40.0	38	17	US-10-712-672-2949	Sequence 2949, App
107	13.8	41.8	45	11	US-09-883-375-8	Sequence 8, Appl	c 180	13.2	40.0	39	14	US-10-147-284-7	Sequence 7, Appl
108	13.8	41.8	50	10	US-09-389-782-26	Sequence 26, Appl	c 181	13.2	40.0	41	16	US-10-035-833A-1234	Sequence 1234, App
109	13.8	41.8	50	16	US-10-131-827-5876	Sequence 5876, App	c 182	13.2	40.0	41	16	US-10-035-833A-2960	Sequence 2960, App
110	13.6	41.2	20	9	US-09-885-188-13	Sequence 13, Appl	c 183	13.2	40.0	41	16	US-10-035-833A-5123	Sequence 5123, App
111	13.6	41.2	20	9	US-09-885-189-13	Sequence 13, Appl	c 184	13.2	40.0	42	16	US-10-035-833A-7057	Sequence 7057, App
112	13.6	41.2	20	16	US-10-236-392-789	Sequence 789, App	c 185	13.2	40.0	42	16	US-10-353-678-36	Sequence 36, Appl
113	13.6	41.2	25	15	US-10-098-263B-14686	Sequence 14686, A	c 186	13.2	40.0	42	16	US-10-226-638A-11	Sequence 11, Appl
114	13.6	41.2	33	9	US-09-749-831-27	Sequence 27, Appl	c 187	13.2	40.0	44	9	US-09-025-403A-30	Sequence 30, Appl
115	13.6	41.2	33	16	US-10-321-039-266	Sequence 266, App	c 188	13.2	40.0	44	9	US-09-974-052-30	Sequence 30, Appl
116	13.6	41.2	38	10	US-09-848-754A-4463	Sequence 4463, App	c 189	13.2	40.0	44	9	US-09-974-051-30	Sequence 30, Appl
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119	13.6	41.2	38	10	US-09-827-395A-1402	Sequence 1402, App	c 192	13.2	40.0	45	11	US-09-842-776A-10	Sequence 10, Appl
120	13.6	41.2	38	10	US-09-745-237A-2474	Sequence 2474, App	c 193	13.2	40.0	45	15	US-10-188-619-12	Sequence 12, Appl
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122	13.6	41.2	38	15	US-10-430-882-1402	Sequence 1402, App	c 195	13.2	40.0	47	16	US-10-349-143-1458	Sequence 1458, App
123	13.6	41.2	38	17	US-10-712-672-3815	Sequence 3815, App	c 196	13.2	40.0	47	16	US-10-294-934-372	Sequence 972, App
124	13.6	41.2	42	11	US-09-883-375-10	Sequence 10, Appl	c 197	13	39.4	22	8	US-08-964-716-23	Sequence 23, Appl
125	13.6	41.2	44	10	US-09-942-891-4	Sequence 4, Appl	c 198	13	39.4	24	16	US-10-092-900A-454	Sequence 454, App
126	13.6	41.2	45	11	US-09-883-375-12	Sequence 12, Appl	c 199	13	39.4	25	14	US-10-215-112-13877	Sequence 13877, A
127	13.6	41.2	49	10	US-09-907-111-322	Sequence 322, App	c 200	13	39.4	26	15	US-10-094-466-95	Sequence 95, Appl
128	13.6	41.2	50	16	US-10-131-827-2244	Sequence 2244, App	c 201	13	39.4	26	15	US-10-317-444-146	Sequence 145, App
129	13.4	40.6	25	15	US-10-098-263B-71419	Sequence 71419, A	c 202	13	39.4	26	15	US-10-317-444-146	Sequence 146, App
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131	13.4	40.6	27	15	US-10-005-956-1282	Sequence 1282, App	c 204	13	39.4	30	15	US-10-283-881-56	Sequence 56, Appl
132	13.4	40.6	27	17	US-10-689-200-23	Sequence 23, Appl	c 205	13	39.4	30	15	US-10-283-881-58	Sequence 58, Appl
133	13.4	40.6	30	17	US-10-697-036-59	Sequence 59, Appl	c 206	13	39.4	35	15	US-09-907-111-278	Sequence 278, App
134	13.4	40.6	31	10	US-09-912-263-14	Sequence 14, Appl	c 207	13	39.4	35	15	US-10-377-718-18	Sequence 18, Appl
135	13.4	40.6	33	15	US-10-146-905A-2	Sequence 2, Appl	c 208	13	39.4	35	15	US-10-429-735-18	Sequence 18, Appl
136	13.4	40.6	33	17	US-10-383-135-32	Sequence 32, Appl	c 209	13	39.4	38	9	US-09-361-736-7	Sequence 7, Appl
137	13.4	40.6	34	9	US-09-874-475-9	Sequence 9, Appl	c 210	13	39.4	38	15	US-10-418-226-7	Sequence 7, Appl
138	13.4	40.6	34	17	US-10-164-290A-9	Sequence 9, Appl	c 211	13	39.4	40	15	US-10-283-881-73	Sequence 73, Appl
139	13.4	40.6	35	16	US-10-423-399-53	Sequence 53, Appl	c 212	13	39.4	41	15	US-10-283-881-74	Sequence 74, Appl
140	13.4	40.6	37	16	US-10-138-674-20361	Sequence 20361, A	c 213	13	39.4	41	16	US-10-035-833A-1399	Sequence 1399, App
141	13.4	40.6	37	17	US-10-287-949A-20361	Sequence 20361, A	c 214	13	39.4	41	16	US-10-035-833A-3867	Sequence 3867, App
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144	13.4	40.6	41	16	US-10-035-833A-217	Sequence 217, App	c 217	13	39.4	42	9	US-09-875-082-17	Sequence 17, Appl
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146	13.4	40.6	41	16	US-10-035-833A-4683	Sequence 4683, App	c 219	13	39.4	42	16	US-10-312-197-8	Sequence 8, Appl
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148	13.4	40.6	41	16	US-10-035-833A-7042	Sequence 7042, App	c 221	13	39.4	42	18	US-10-367-438-36	Sequence 36, Appl
149	13.4	40.6	50	16	US-10-131-827-5247	Sequence 5247, App	c 222	13	39.4	47	15	US-10-402-365-27	Sequence 27, Appl
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151	13.2	40.0	20	15	US-10-092-208-21	Sequence 21, Appl	c 224	13	39.4	50	16	US-10-300-236-28	Sequence 28, Appl
152	13.2	40.0	21	17	US-10-627-253A-141	Sequence 141, App	c 225	12.8	38.8	20	16	US-09-025-403A-34	Sequence 34, Appl
153	13.2	40.0	21	17	US-10-627-253A-142	Sequence 142, App	c 226	12.8	38.8	25	9	US-09-974-052-34	Sequence 34, Appl
154	13.2	40.0	22	8	US-08-259-265-3	Sequence 3, Appl	c 227	12.8	38.8	25	9	US-09-974-051-34	Sequence 34, Appl
155	13.2	40.0	25	15	US-10-098-263B-41249	Sequence 41249, A	c 228	12.8	38.8	25	10	US-09-974-498-34	Sequence 34, Appl
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157	13.2	40.0	25	17	US-10-717-597-3676	Sequence 3676, App	c 230	12.8	38.8	25	10	US-10-215-112-212	Sequence 212, App
158	13.2	40.0	28	16	US-10-401-520-109	Sequence 109, App	c 231	12.8	38.8	25	14		

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C 237	12.8	38.8	25	15	US-10-098-263B-71470	Sequence 71470, A	310	12.6	38.2	38	15	US-10-230-006-1009	Sequence 1009, Ap
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C 241	12.8	38.8	25	17	US-10-775-169-3477	Sequence 3477, Ap	314	12.6	38.2	38	17	US-10-287-949A-10125	Sequence 10125, A
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C 246	12.8	38.8	30	15	US-10-154-515-6	Sequence 6, Appli	319	12.6	38.2	39	15	US-10-331-907-217	Sequence 217, App
C 247	12.8	38.8	30	15	US-10-299-180-6	Sequence 6, Appli	320	12.6	38.2	40	15	US-10-062-809-73	Sequence 73, Appl
C 248	12.8	38.8	31	9	US-09-747-538-23	Sequence 23, Appl	321	12.6	38.2	40	17	US-10-611-527-17	Sequence 17, Appl
C 249	12.8	38.8	31	10	US-09-825-805-1520	Sequence 1520, Ap	322	12.6	38.2	41	16	US-10-035-833A-477	Sequence 477, App
C 250	12.8	38.8	34	10	US-09-852-370-67	Sequence 67, Appl	323	12.6	38.2	41	16	US-10-035-833A-720	Sequence 720, App
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C 252	12.8	38.8	35	16	US-10-422-366-23	Sequence 23, Appl	325	12.6	38.2	41	16	US-10-035-833A-3434	Sequence 3434, Ap
C 253	12.8	38.8	36	9	US-09-504-231A-1668	Sequence 1668, Ap	326	12.6	38.2	41	16	US-10-035-833A-6258	Sequence 6258, Ap
C 254	12.8	38.8	36	9	US-09-274-553D-1668	Sequence 1668, Ap	327	12.6	38.2	41	16	US-10-035-833A-6659	Sequence 6659, Ap
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C 256	12.8	38.8	38	9	US-09-864-785-1123	Sequence 1123, Ap	329	12.6	38.2	42	10	US-09-155-106-42	Sequence 42, Appl
C 257	12.8	38.8	38	10	US-09-776-474-1643	Sequence 1643, Ap	330	12.6	38.2	45	10	US-09-771-287-45	Sequence 45, Appl
C 258	12.8	38.8	38	16	US-10-138-674-11684	Sequence 11684, A	331	12.6	38.2	45	14	US-10-007-132-45	Sequence 45, Appl
C 259	12.8	38.8	38	16	US-10-138-674-13855	Sequence 13855, A	332	12.6	38.2	45	15	US-10-006-343-45	Sequence 45, Appl
C 260	12.8	38.8	38	16	US-10-138-674-14906	Sequence 14906, A	333	12.6	38.2	47	15	US-10-367-438-36	Sequence 36, Appl
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C 263	12.8	38.8	38	17	US-10-287-949A-14906	Sequence 14906, A	336	12.6	38.2	50	10	US-09-993-346-494	Sequence 494, App
C 264	12.8	38.8	38	17	US-10-679-620-45	Sequence 45, Appl	337	12.6	38.2	50	16	US-10-131-827-2269	Sequence 2269, Ap
C 265	12.8	38.8	39	15	US-10-314-861-14	Sequence 14, Appl	338	12.6	38.2	50	16	US-10-131-827-3168	Sequence 3168, Ap
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C 267	12.8	38.8	41	14	US-10-109-812-35	Sequence 35, Appl	340	12.6	38.2	50	16	US-10-131-827-4900	Sequence 4900, Ap
C 268	12.8	38.8	45	16	US-10-474-832-28	Sequence 28, Appl	341	12.6	38.2	50	16	US-10-131-827-8054	Sequence 8054, Ap
C 269	12.8	38.8	48	9	US-09-822-698A-56	Sequence 56, Appl	342	12.4	37.6	22	15	US-10-440-998-12	Sequence 12, Appl
C 270	12.8	38.8	49	10	US-09-990-586-42	Sequence 42, Appl	343	12.4	37.6	22	15	US-10-204-884-105	Sequence 105, App
C 271	12.8	38.8	49	15	US-10-310-113-38	Sequence 38, Appl	344	12.4	37.6	22	16	US-10-001-052-4	Sequence 4, Appli
C 272	12.8	38.8	49	15	US-10-230-880-42	Sequence 42, Appl	345	12.4	37.6	23	16	US-10-280-183A-417	Sequence 417, App
C 273	12.8	38.8	50	8	US-08-781-986A-2367	Sequence 2367, Ap	346	12.4	37.6	25	10	US-09-847-102A-18	Sequence 18, Appl
C 274	12.8	38.8	50	16	US-10-131-827-92	Sequence 92, Appl	347	12.4	37.6	25	14	US-10-215-112-213	Sequence 213, App
C 275	12.8	38.8	50	16	US-10-131-827-1443	Sequence 1443, Ap	348	12.4	37.6	25	14	US-10-215-112-9912	Sequence 9912, App
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C 286	12.6	38.2	28	17	US-10-312-197-9	Sequence 9, Appli	359	12.4	37.6	25	15	US-10-308-503-204	Sequence 204, App
C 287	12.6	38.2	28	17	US-10-276-050-9	Sequence 9, Appli	360	12.4	37.6	25	17	US-10-775-169-3968	Sequence 3968, App
C 288	12.6	38.2	30	17	US-10-220-481-251	Sequence 251, App	361	12.4	37.6	29	9	US-09-952-663-10	Sequence 10, Appl
C 289	12.6	38.2	32	15	US-10-322-656-47	Sequence 47, Appl	362	12.4	37.6	29	15	US-10-171-452A-4	Sequence 4, Appli
C 290	12.6	38.2	36	9	US-09-504-231A-1784	Sequence 1784, Ap	363	12.4	37.6	29	15	US-10-336-638-91	Sequence 91, Appl
C 291	12.6	38.2	36	9	US-09-504-231A-1750	Sequence 1750, Ap	364	12.4	37.6	29	15	US-10-353-708-4	Sequence 4, Appli
C 292	12.6	38.2	36	9	US-09-274-553D-1784	Sequence 1784, Ap	365	12.4	37.6	29	17	US-10-731-984-38	Sequence 38, Appl
C 293	12.6	38.2	36	9	US-09-274-553D-2750	Sequence 2750, Ap	366	12.4	37.6	30	14	US-10-423-170-10	Sequence 10, Appl
C 294	12.6	38.2	36	9	US-09-274-553D-2750	Sequence 2750, Ap	367	12.4	37.6	31	15	US-10-100-294A-66	Sequence 66, Appl
C 295	12.6	38.2	36	9	US-09-966-955A-50	Sequence 50, Appl	368	12.4	37.6	31	15	US-10-085-388-1	Sequence 1, Appli
C 296	12.6	38.2	37	9	US-09-504-231A-3167	Sequence 3167, Ap	369	12.4	37.6	32	9	US-09-813-781-79	Sequence 79, Appl
C 297	12.6	38.2	38	9	US-09-864-785-825	Sequence 825, App	370	12.4	37.6	32	10	US-09-747-377-467	Sequence 467, App
C 298	12.6	38.2	38	9	US-09-864-785-1314	Sequence 1314, Ap	371	12.4	37.6	32	14	US-10-105-613-467	Sequence 467, App
C 299	12.6	38.2	38	10	US-09-730-289B-2863	Sequence 2863, Ap	372	12.4	37.6	33	15	US-10-289-498-10	Sequence 10, Appl
C 300	12.6	38.2	38	10	US-09-780-533A-3865	Sequence 3865, Ap	373	12.4	37.6	33	15	US-10-289-527-10	Sequence 10, Appl
C 301	12.6	38.2	38	10	US-09-877-478-2776	Sequence 2776, Ap	374	12.4	37.6	33	17	US-10-383-135-33	Sequence 33, Appl
C 302	12.6	38.2	38	10	US-09-877-478-3470	Sequence 3470, Ap	375	12.4	37.6	36	15	US-10-424-233-69	Sequence 69, Appl
C 303	12.6	38.2	38	10	US-09-848-754A-4719	Sequence 4719, Ap	376	12.4	37.6	36	16	US-10-423-399-54	Sequence 54, Appl
C 304	12.6	38.2	38	10	US-09-848-754A-4930	Sequence 4930, Ap	377	12.4	37.6	37	10	US-09-848-754A-6147	Sequence 6147, Ap

378	12.4	37.6	37	10	US-09-848-754A-6152	Sequence 6152, Ap	c 451	12.2	37.0	36	9	US-09-504-231A-1865	Sequence 1865, Ap
379	12.4	37.6	37	10	US-09-848-754A-6272	Sequence 6272, Ap	452	12.2	37.0	36	9	US-09-504-231A-1897	Sequence 1897, Ap
380	12.4	37.6	37	10	US-09-848-754A-6427	Sequence 6427, Ap	c 453	12.2	37.0	36	9	US-09-274-5530-1865	Sequence 1865, Ap
381	12.4	37.6	39	15	US-10-378-168-85	Sequence 85, Appl	c 454	12.2	37.0	36	9	US-09-274-5530-1897	Sequence 1897, Ap
382	12.4	37.6	39	16	US-10-252-155-775	Sequence 775, Appl	c 455	12.2	37.0	36	14	US-10-056-41A-653	Sequence 653, Appl
383	12.4	37.6	41	16	US-10-035-833A-2713	Sequence 2713, Ap	c 456	12.2	37.0	36	15	US-10-440-850-1676	Sequence 1676, Ap
384	12.4	37.6	41	16	US-10-035-833A-6140	Sequence 6140, Ap	c 457	12.2	37.0	36	16	US-10-420-194-602	Sequence 602, Appl
385	12.4	37.6	43	15	US-10-032-585-1869	Sequence 1869, Ap	c 458	12.2	37.0	38	10	US-09-825-805-1324	Sequence 1324, Ap
386	12.4	37.6	43	16	US-10-001-052-18	Sequence 18, Appl	c 459	12.2	37.0	38	10	US-09-780-533A-2883	Sequence 2883, Ap
387	12.4	37.6	45	11	US-09-883-375-7	Sequence 7, Appl	c 460	12.2	37.0	38	10	US-09-927-046-2208	Sequence 2208, Ap
388	12.4	37.6	45	11	US-10-193-764-14	Sequence 14, Appl	c 461	12.2	37.0	38	10	US-09-927-046-2208	Sequence 2208, Ap
389	12.4	37.6	46	14	US-10-125-789A-2	Sequence 2, Appl	c 462	12.2	37.0	38	10	US-09-927-046-2208	Sequence 2208, Ap
390	12.4	37.6	46	15	US-10-199-820-157	Sequence 157, Appl	c 463	12.2	37.0	38	10	US-09-927-046-2208	Sequence 2208, Ap
391	12.4	37.6	50	15	US-10-422-934-61	Sequence 61, Appl	c 464	12.2	37.0	38	10	US-09-927-046-2208	Sequence 2208, Ap
392	12.4	37.6	50	16	US-10-131-827-1219	Sequence 1219, Ap	c 465	12.2	37.0	38	10	US-09-927-046-2208	Sequence 2208, Ap
393	12.4	37.6	50	16	US-10-131-827-2375	Sequence 2375, Ap	c 466	12.2	37.0	38	10	US-09-927-046-2208	Sequence 2208, Ap
394	12.2	37.0	17	10	US-09-877-478-2405	Sequence 2405, Ap	c 467	12.2	37.0	38	10	US-09-848-754A-4249	Sequence 4249, Ap
395	12.2	37.0	17	10	US-09-930-423-1556	Sequence 1556, Ap	c 468	12.2	37.0	38	10	US-09-848-754A-4630	Sequence 4630, Ap
396	12.2	37.0	17	10	US-09-745-237A-1556	Sequence 1556, Ap	c 469	12.2	37.0	38	10	US-09-848-754A-5233	Sequence 5233, Ap
397	12.2	37.0	17	16	US-10-342-902-2405	Sequence 2405, Ap	c 470	12.2	37.0	38	10	US-09-848-754A-5552	Sequence 5552, Ap
398	12.2	37.0	17	17	US-10-669-841-2208	Sequence 2208, Ap	c 471	12.2	37.0	38	10	US-09-930-423-1877	Sequence 1877, Ap
399	12.2	37.0	18	15	US-10-044-998-19	Sequence 19, Appl	c 472	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
400	12.2	37.0	20	13	US-10-044-671-10	Sequence 10, Appl	c 473	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
401	12.2	37.0	20	15	US-10-174-465-25	Sequence 25, Appl	c 474	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
402	12.2	37.0	20	15	US-10-174-465-58	Sequence 58, Appl	c 475	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
403	12.2	37.0	20	15	US-10-348-431-25	Sequence 25, Appl	c 476	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
404	12.2	37.0	20	15	US-10-348-431-58	Sequence 58, Appl	c 477	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
405	12.2	37.0	20	15	US-10-236-392-72	Sequence 72, Appl	c 478	12.2	37.0	38	10	US-10-156-306-2056	Sequence 2056, Ap
406	12.2	37.0	20	17	US-10-303-633-72	Sequence 72, Appl	c 479	12.2	37.0	38	15	US-10-430-882-1134	Sequence 1134, Ap
407	12.2	37.0	20	17	US-10-416-530-11	Sequence 11, Appl	c 480	12.2	37.0	38	15	US-10-191-540-95	Sequence 95, Appl
408	12.2	37.0	20	17	US-10-317-248-22	Sequence 22, Appl	c 481	12.2	37.0	38	15	US-10-453-483-74	Sequence 74, Appl
409	12.2	37.0	20	17	US-10-317-248-98	Sequence 98, Appl	c 482	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
410	12.2	37.0	22	15	US-10-296-995-97	Sequence 97, Appl	c 483	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
411	12.2	37.0	24	10	US-09-992-665-333	Sequence 333, Appl	c 484	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
412	12.2	37.0	24	10	US-09-940-188-2764	Sequence 2764, Ap	c 485	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
413	12.2	37.0	25	9	US-09-866-108-4846	Sequence 4846, Ap	c 486	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
414	12.2	37.0	25	9	US-09-866-108-15114	Sequence 15114, A	c 487	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
415	12.2	37.0	25	15	US-10-098-263B-12001	Sequence 12001, A	c 488	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
416	12.2	37.0	25	15	US-10-098-263B-23699	Sequence 23699, A	c 489	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
417	12.2	37.0	25	15	US-10-098-263B-24966	Sequence 24966, A	c 490	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
418	12.2	37.0	25	15	US-10-098-263B-29509	Sequence 29509, A	c 491	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
419	12.2	37.0	25	15	US-10-098-263B-31484	Sequence 31484, A	c 492	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
420	12.2	37.0	25	15	US-10-098-263B-35724	Sequence 35724, A	c 493	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
421	12.2	37.0	25	15	US-10-098-263B-35954	Sequence 35954, A	c 494	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
422	12.2	37.0	25	15	US-10-098-263B-49008	Sequence 49008, A	c 495	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
423	12.2	37.0	25	15	US-10-098-263B-97709	Sequence 97709, A	c 496	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
424	12.2	37.0	25	15	US-10-098-263B-99425	Sequence 99425, A	c 497	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
425	12.2	37.0	25	15	US-10-098-263B-100962	Sequence 100962, A	c 498	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
426	12.2	37.0	25	15	US-10-098-263B-108332	Sequence 108332, A	c 499	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
427	12.2	37.0	25	15	US-10-098-263B-119973	Sequence 119973, A	c 500	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
428	12.2	37.0	25	15	US-10-321-163-41	Sequence 41, Appl	c 501	12.2	37.0	40	9	US-09-245-802-98	Sequence 98, Appl
429	12.2	37.0	25	15	US-10-413-661-41	Sequence 41, Appl	c 502	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
430	12.2	37.0	25	15	US-10-084-839-3305	Sequence 3305, Ap	c 503	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
431	12.2	37.0	25	17	US-10-723-361-4846	Sequence 4846, Ap	c 504	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
432	12.2	37.0	25	17	US-10-723-361-15114	Sequence 15114, A	c 505	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
433	12.2	37.0	25	17	US-10-789-129-41	Sequence 41, Appl	c 506	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
434	12.2	37.0	25	17	US-10-789-251-41	Sequence 41, Appl	c 507	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
435	12.2	37.0	25	17	US-10-789-968-41	Sequence 41, Appl	c 508	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
436	12.2	37.0	25	17	US-10-748-484-41	Sequence 41, Appl	c 509	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
437	12.2	37.0	25	17	US-10-907-111-220	Sequence 220, Appl	c 510	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
438	12.2	37.0	26	15	US-10-290-579-19	Sequence 19, Appl	c 511	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
439	12.2	37.0	28	9	US-09-733-042-32	Sequence 32, Appl	c 512	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
440	12.2	37.0	29	16	US-08-837-459-16	Sequence 2, Appl	c 513	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
441	12.2	37.0	30	8	US-08-837-459-16	Sequence 16, Appl	c 514	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
442	12.2	37.0	30	15	US-10-150-058-16	Sequence 16, Appl	c 515	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
443	12.2	37.0	31	9	US-09-801-274-1768	Sequence 1768, Ap	c 516	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
444	12.2	37.0	31	9	US-09-747-538-23	Sequence 23, Appl	c 517	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
445	12.2	37.0	31	9	US-09-783-504-2	Sequence 2, Appl	c 518	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
446	12.2	37.0	33	16	US-10-336-672-2	Sequence 2, Appl	c 519	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
447	12.2	37.0	33	16	US-10-459-729-1	Sequence 1, Appl	c 520	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
448	12.2	37.0	33	16	US-10-459-729-1	Sequence 1, Appl	c 521	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
449	12.2	37.0	33	9	US-09-987-456-139	Sequence 139, Appl	c 522	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
450	12.2	37.0	35	10	US-09-921-819-47	Sequence 47, Appl	c 523	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl

524	12.2	37.0	47	16	US-10-349-143-2025	Sequence 2025, Ap	597	12.	36.4	38	10	US-09-780-533A-4033	Sequence 4033, Ap
525	12.2	37.0	47	16	US-10-349-143-2249	Sequence 2249, Ap	598	12.	36.4	38	10	US-09-780-533A-4116	Sequence 4116, Ap
526	12.2	37.0	50	15	US-10-218-567-99	Sequence 89, Appl	599	12.	36.4	38	10	US-09-780-533A-4186	Sequence 4186, Ap
527	12.2	37.0	50	15	US-10-322-360-91	Sequence 91, Appl	600	12.	36.4	38	10	US-09-927-046-2416	Sequence 2416, Ap
528	12.2	37.0	50	16	US-10-131-827-2960	Sequence 2960, Ap	601	12.	36.4	38	10	US-09-927-046-3146	Sequence 3146, Ap
529	12.2	37.0	50	16	US-10-131-827-4355	Sequence 4355, Ap	602	12.	36.4	38	10	US-09-927-046-3360	Sequence 3360, Ap
530	12	36.4	20	16	US-10-187-659A-69	Sequence 69, Appl	603	12	36.4	38	10	US-09-877-478-2770	Sequence 2770, Ap
531	12	36.4	20	16	US-10-187-659A-126	Sequence 126, Appl	604	12	36.4	38	10	US-09-877-478-3210	Sequence 3210, Ap
532	12	36.4	22	9	US-09-803-687-1	Sequence 1, Appl	605	12	36.4	38	10	US-09-877-478-3408	Sequence 3408, Ap
533	12	36.4	23	14	US-10-146-574-10	Sequence 10, Appl	606	12	36.4	38	10	US-09-877-478-3446	Sequence 3446, Ap
534	12	36.4	24	15	US-10-117-109-21	Sequence 21, Appl	607	12	36.4	38	10	US-09-877-478-3481	Sequence 3481, Ap
535	12	36.4	24	15	US-10-117-109-22	Sequence 22, Appl	608	12	36.4	38	10	US-09-877-478-3611	Sequence 3611, Ap
536	12	36.4	24	15	US-10-117-109-23	Sequence 23, Appl	609	12	36.4	38	10	US-09-877-478-3657	Sequence 3657, Ap
537	12	36.4	24	15	US-10-117-109-24	Sequence 24, Appl	610	12	36.4	38	10	US-09-877-478-3761	Sequence 3761, Ap
538	12	36.4	24	15	US-10-407-078-21	Sequence 21, Appl	611	12	36.4	38	10	US-09-877-478-4230	Sequence 4230, Ap
539	12	36.4	24	15	US-10-407-078-22	Sequence 22, Appl	612	12	36.4	38	10	US-09-877-478-4504	Sequence 4504, Ap
540	12	36.4	24	15	US-10-407-078-23	Sequence 23, Appl	613	12	36.4	38	10	US-09-848-754A-3897	Sequence 3897, Ap
541	12	36.4	24	15	US-10-407-078-24	Sequence 24, Appl	614	12	36.4	38	10	US-09-848-754A-4001	Sequence 4001, Ap
542	12	36.4	24	16	US-10-332-553-1	Sequence 1, Appl	615	12	36.4	38	10	US-09-848-754A-4623	Sequence 4623, Ap
543	12	36.4	25	15	US-10-098-263B-2237	Sequence 2237, Ap	616	12	36.4	38	10	US-09-848-754A-5057	Sequence 5057, Ap
544	12	36.4	25	15	US-10-098-263B-2238	Sequence 2238, Ap	617	12	36.4	38	10	US-09-848-754A-5081	Sequence 5081, Ap
545	12	36.4	25	15	US-10-098-263B-2270	Sequence 2270, Ap	618	12	36.4	38	10	US-09-848-754A-5798	Sequence 5798, Ap
546	12	36.4	25	15	US-10-098-263B-2565	Sequence 2565, Ap	619	12	36.4	38	10	US-09-776-474-1329	Sequence 1329, Ap
547	12	36.4	25	15	US-10-098-263B-3254	Sequence 3254, Ap	620	12	36.4	38	10	US-09-930-423-2214	Sequence 2214, Ap
548	12	36.4	25	15	US-10-098-263B-5554	Sequence 5554, Ap	621	12	36.4	38	10	US-09-930-423-2648	Sequence 2648, Ap
549	12	36.4	25	15	US-10-098-263B-14685	Sequence 14685, A	622	12	36.4	38	10	US-09-930-423-3152	Sequence 3152, Ap
550	12	36.4	25	15	US-10-098-263B-32209	Sequence 32209, A	623	12	36.4	38	10	US-09-780-164-1096	Sequence 1096, Ap
551	12	36.4	25	15	US-10-098-263B-35648	Sequence 35648, A	624	12	36.4	38	10	US-09-780-164-1156	Sequence 1156, Ap
552	12	36.4	25	15	US-10-098-263B-74471	Sequence 74471, A	625	12	36.4	38	10	US-09-827-395A-1104	Sequence 1104, Ap
553	12	36.4	25	15	US-10-098-263B-104126	Sequence 104126, A	626	12	36.4	38	10	US-09-827-395A-1239	Sequence 1239, Ap
554	12	36.4	25	15	US-10-098-263B-107584	Sequence 107584, A	627	12	36.4	38	10	US-09-827-395A-1275	Sequence 1275, Ap
555	12	36.4	25	15	US-10-098-263B-108927	Sequence 108927, A	628	12	36.4	38	10	US-09-827-395A-1370	Sequence 1370, Ap
556	12	36.4	25	15	US-10-098-263B-108928	Sequence 108928, A	629	12	36.4	38	10	US-09-792-818-1315	Sequence 1315, Ap
557	12	36.4	25	17	US-10-775-169-3476	Sequence 3476, Ap	630	12	36.4	38	10	US-09-792-818-1554	Sequence 1554, Ap
558	12	36.4	28	10	US-09-894-799-23	Sequence 23, Appl	631	12	36.4	38	10	US-09-745-237A-2214	Sequence 2214, Ap
559	12	36.4	28	16	US-10-648-584-23	Sequence 23, Appl	632	12	36.4	38	10	US-09-745-237A-2648	Sequence 2648, Ap
560	12	36.4	29	13	US-10-146-221-3	Sequence 3, Appl	633	12	36.4	38	10	US-09-745-237A-3152	Sequence 3152, Ap
561	12	36.4	29	15	US-10-104-473A-4	Sequence 4, Appl	634	12	36.4	38	15	US-10-156-306-4565	Sequence 4565, Ap
562	12	36.4	29	15	US-10-104-473A-6	Sequence 6, Appl	635	12	36.4	38	15	US-10-156-306-4572	Sequence 4572, Ap
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564	12	36.4	30	10	US-09-844-861A-70	Sequence 70, Appl	637	12	36.4	38	15	US-10-230-006-1004	Sequence 1004, Ap
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568	12	36.4	31	16	US-10-198-447A-11	Sequence 11, Appl	641	12	36.4	38	15	US-10-430-882-1104	Sequence 1104, Ap
569	12	36.4	33	14	US-10-139-662-27	Sequence 27, Appl	642	12	36.4	38	15	US-10-430-882-1239	Sequence 1239, Ap
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571	12	36.4	33	15	US-10-143-618-27	Sequence 27, Appl	644	12	36.4	38	15	US-10-430-882-1370	Sequence 1370, Ap
572	12	36.4	33	17	US-10-745-034-27	Sequence 27, Appl	645	12	36.4	38	16	US-10-342-902-2770	Sequence 2770, Ap
573	12	36.4	34	17	US-10-641-001-11	Sequence 11, Appl	646	12	36.4	38	16	US-10-342-902-3210	Sequence 3210, Ap
574	12	36.4	37	10	US-09-894-799-1	Sequence 1, Appl	647	12	36.4	38	16	US-10-342-902-3408	Sequence 3408, Ap
575	12	36.4	37	10	US-09-848-754A-6415	Sequence 6415, Ap	648	12	36.4	38	16	US-10-342-902-3446	Sequence 3446, Ap
576	12	36.4	37	15	US-10-156-306-6231	Sequence 6231, Ap	649	12	36.4	38	16	US-10-342-902-3481	Sequence 3481, Ap
577	12	36.4	37	15	US-10-156-306-6231	Sequence 28, Appl	650	12	36.4	38	16	US-10-342-902-3611	Sequence 3611, Ap
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586	12	36.4	38	9	US-09-864-785-835	Sequence 835, App	659	12	36.4	38	16	US-10-138-674-11959	Sequence 11959, A
587	12	36.4	38	9	US-09-864-785-1023	Sequence 1023, Ap	660	12	36.4	38	16	US-10-138-674-12053	Sequence 12053, A
588	12	36.4	38	9	US-09-864-785-1026	Sequence 1026, Ap	661	12	36.4	38	16	US-10-138-674-12453	Sequence 12453, A
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590	12	36.4	38	10	US-09-825-805-1451	Sequence 1451, Ap	663	12	36.4	38	16	US-10-138-674-13231	Sequence 13231, A
591	12	36.4	38	10	US-09-998-425-59	Sequence 59, Appl	664	12	36.4	38	16	US-10-138-674-14125	Sequence 14125, A
592	12	36.4	38	10	US-09-997-623-17	Sequence 17, Appl	665	12	36.4	38	16	US-10-138-674-14313	Sequence 14313, A
593	12	36.4	38	10	US-09-997-623-18	Sequence 18, Appl	666	12	36.4	38	16	US-10-138-674-14560	Sequence 14560, A
594	12	36.4	38	10	US-09-997-977-59	Sequence 59, Appl	667	12	36.4	38	16	US-10-138-674-14859	Sequence 14859, A
595	12	36.4	38	10	US-09-978-917A-17	Sequence 17, Appl	668	12	36.4	38	16	US-10-138-674-15913	Sequence 15913, A
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670	12	36.4	38	17	US-10-287-949A-9958	Sequence 9958, Ap	743	12	36.4	50	16	US-10-144-094-34	Sequence 34, Appl
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672	12	36.4	38	17	US-10-287-949A-11258	Sequence 11258, A	745	12	36.4	50	17	US-10-702-676A-34	Sequence 34, Appl
673	12	36.4	38	17	US-10-287-949A-11959	Sequence 11959, A	746	12	36.4	50	18	US-10-360-141-24	Sequence 24, Appl
674	12	36.4	38	17	US-10-287-949A-12053	Sequence 12053, A	747	11.8	35.8	17	16	US-10-380-334-6	Sequence 6, Appl
675	12	36.4	38	17	US-10-287-949A-12453	Sequence 12453, A	748	11.8	35.8	19	15	US-10-084-839-3306	Sequence 3306, Ap
676	12	36.4	38	17	US-10-287-949A-13058	Sequence 13058, A	749	11.8	35.8	20	10	US-09-966-451-45	Sequence 45, Appl
677	12	36.4	38	17	US-10-287-949A-13231	Sequence 13231, A	750	11.8	35.8	20	15	US-10-128-560-49	Sequence 49, Appl
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707	12	36.4	42	15	US-10-033-024A-33	Sequence 33, Appl	780	11.8	35.8	25	15	US-10-098-263B-101436	Sequence 101436, A
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710	12	36.4	43	15	US-10-156-995-150	Sequence 150, Appl	783	11.8	35.8	25	15	US-10-098-263B-124821	Sequence 124821, A
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712	12	36.4	45	10	US-08-911-824-109	Sequence 109, Appl	785	11.8	35.8	25	17	US-10-723-361-4848	Sequence 4848, Ap
713	12	36.4	46	8	US-10-251-085B-52	Sequence 52, Appl	786	11.8	35.8	25	17	US-10-775-169-1152	Sequence 1152, Ap
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717	12	36.4	48	17	US-10-737-252-53	Sequence 53, Appl	790	11.8	35.8	26	9	US-10-010-476-76	Sequence 76, Appl
718	12	36.4	49	13	US-10-006-009-7	Sequence 7, Appl	791	11.8	35.8	26	15	US-10-317-444-59	Sequence 59, Appl
719	12	36.4	49	13	US-10-006-009-18	Sequence 18, Appl	792	11.8	35.8	26	15	US-10-317-444-60	Sequence 60, Appl
720	12	36.4	49	15	US-10-310-677-160	Sequence 160, Appl	793	11.8	35.8	26	15	US-10-738-455-8	Sequence 8, Appl
721	12	36.4	49	17	US-10-471-136-10	Sequence 6, Appl	794	11.8	35.8	26	17	US-10-229-834A-25	Sequence 25, Appl
722	12	36.4	50	10	US-09-993-346-478	Sequence 478, Appl	795	11.8	35.8	27	15	US-10-204-889-3	Sequence 3, Appl
723	12	36.4	50	13	US-10-006-009-22	Sequence 22, Appl	796	11.8	35.8	27	16	US-10-829-430-3	Sequence 3, Appl
724	12	36.4	50	15	US-10-144-094-22	Sequence 22, Appl	797	11.8	35.8	27	17	US-10-829-430-3	Sequence 3, Appl
725	12	36.4	50	15	US-10-131-827-1384	Sequence 1384, Ap	798	11.8	35.8	28	16	US-10-401-520-126	Sequence 126, Appl
726	12	36.4	50	16	US-10-131-827-2208	Sequence 2208, Ap	799	11.8	35.8	31	9	US-09-801-274-593	Sequence 593, Appl
727	12	36.4	50	16	US-10-131-827-4257	Sequence 4257, Ap	800	11.8	35.8	31	9	US-09-801-274-845	Sequence 845, Appl
728	12	36.4	50	16	US-10-131-827-5603	Sequence 5603, Ap	801	11.8	35.8	31	9	US-09-801-274-1699	Sequence 1699, Ap
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733	12	36.4	50	16	US-10-144-094-22	Sequence 22, Appl	806	11.8	35.8	35	9	US-09-864-785-3849	Sequence 3849, Ap
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737	12	36.4	50	16			810	11.8	35.8	36	9	US-09-274-5530-2281	Sequence 2281, Ap
738	12	36.4	50	16			811	11.8	35.8	36	14	US-10-056-414-640	Sequence 640, Appl
739	12	36.4	50	16			812	11.8	35.8	36	15	US-10-331-446-1	Sequence 1, Appl
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741	12	36.4	50	16			814	11.8	35.8	36	15	US-10-129-422-10	Sequence 10, Appl
742	12	36.4	50	16			815	11.8	35.8	36	15		

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C 817	11.8	35.8	37	9	US-09-860-996-3	Sequence 3, Appl	C 890	11.8	35.8	47	16	US-10-349-143-1709	Sequence 1709, Ap
C 818	11.8	35.8	37	9	US-09-864-785-2001	Sequence 2001, Ap	C 891	11.8	35.8	47	16	US-10-349-143-3761	Sequence 3761, Ap
C 819	11.8	35.8	37	9	US-09-864-785-3850	Sequence 3850, Ap	C 892	11.8	35.8	48	10	US-09-893-512-6	Sequence 6, Appl
C 820	11.8	35.8	37	10	US-09-927-046-3744	Sequence 3744, Ap	C 893	11.8	35.8	49	10	US-09-405-032-96	Sequence 96, Appl
C 821	11.8	35.8	37	10	US-09-848-754A-5950	Sequence 5950, Ap	C 894	11.8	35.8	50	16	US-10-131-827-1542	Sequence 1542, Ap
C 822	11.8	35.8	37	10	US-09-848-754A-6451	Sequence 6451, Ap	C 895	11.8	35.8	50	16	US-10-131-827-1793	Sequence 1793, Ap
C 823	11.8	35.8	37	10	US-09-827-395A-1579	Sequence 1579, Ap	C 896	11.8	35.8	50	16	US-10-131-827-2438	Sequence 2438, Ap
C 824	11.8	35.8	37	10	US-09-827-395A-1809	Sequence 1809, Ap	C 897	11.8	35.8	50	16	US-10-131-827-6152	Sequence 6152, Ap
C 825	11.8	35.8	37	15	US-10-156-306-2516	Sequence 2516, Ap	C 898	11.8	35.8	50	16	US-10-035-833A-7114	Sequence 7114, Ap
C 826	11.8	35.8	37	15	US-10-430-882-1579	Sequence 1579, Ap	C 899	11.8	35.8	50	16	US-10-343-319-47	Sequence 47, Appl
C 827	11.8	35.8	37	15	US-10-430-882-1809	Sequence 1809, Ap	C 900	11.8	35.8	50	16	US-10-343-319-64	Sequence 64, Appl
C 828	11.8	35.8	37	16	US-10-138-674-18481	Sequence 18481, A	C 901	11.8	35.8	50	16	US-10-343-319-65	Sequence 65, Appl
C 829	11.8	35.8	37	16	US-10-138-674-18682	Sequence 18682, A	C 902	11.8	35.8	50	16	US-10-343-319-67	Sequence 67, Appl
C 830	11.8	35.8	37	16	US-10-138-674-20240	Sequence 20240, A	C 903	11.8	35.8	50	16	US-10-343-319-68	Sequence 68, Appl
C 831	11.8	35.8	37	16	US-10-138-674-20261	Sequence 20261, A	C 904	11.6	35.2	17	9	US-09-865-018-20	Sequence 20, Appl
C 832	11.8	35.8	37	16	US-10-138-674-20545	Sequence 20545, A	C 905	11.6	35.2	18	9	US-09-865-018-21	Sequence 21, Appl
C 833	11.8	35.8	37	16	US-10-138-674-20575	Sequence 20575, A	C 906	11.6	35.2	20	15	US-10-027-983-72	Sequence 72, Appl
C 834	11.8	35.8	37	16	US-10-138-674-20771	Sequence 20771, A	C 907	11.6	35.2	20	15	US-10-148-835-88	Sequence 88, Appl
C 835	11.8	35.8	37	17	US-10-287-949A-18481	Sequence 18481, A	C 908	11.6	35.2	20	15	US-10-148-835-89	Sequence 89, Appl
C 836	11.8	35.8	37	17	US-10-287-949A-18682	Sequence 18682, A	C 909	11.6	35.2	20	15	US-10-448-753-72	Sequence 72, Appl
C 837	11.8	35.8	37	17	US-10-287-949A-20240	Sequence 20240, A	C 910	11.6	35.2	20	15	US-10-160-787-37	Sequence 37, Appl
C 838	11.8	35.8	37	17	US-10-287-949A-20261	Sequence 20261, A	C 911	11.6	35.2	20	15	US-10-160-787-106	Sequence 106, App
C 839	11.8	35.8	37	17	US-10-287-949A-20545	Sequence 20545, A	C 912	11.6	35.2	20	16	US-10-190-366-115	Sequence 115, App
C 840	11.8	35.8	37	17	US-10-287-949A-20575	Sequence 20575, A	C 913	11.6	35.2	20	16	US-10-190-366-312	Sequence 312, App
C 841	11.8	35.8	37	17	US-10-287-949A-20771	Sequence 20771, A	C 914	11.6	35.2	20	16	US-10-272-810-43	Sequence 43, Appl
C 842	11.8	35.8	38	9	US-09-864-785-1134	Sequence 1134, Ap	C 915	11.6	35.2	20	16	US-10-273-070-43	Sequence 43, Appl
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C 844	11.8	35.8	38	10	US-09-988-687-104	Sequence 104, App	C 917	11.6	35.2	20	18	US-10-604-944-23	Sequence 23, Appl
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RESULT 3

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/ APPLICANT: Kevin P. Baker
/ APPLICANT: David A. Bolstein
/ APPLICANT: Luc Desnoyers
/ APPLICANT: Dan L. Eaton
/ APPLICANT: Napoleone Ferrara
/ APPLICANT: Sherman Fong
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/ APPLICANT: Timothy A. Stewart
/ APPLICANT: Daniel Tumas
/ APPLICANT: Colin K. Watanabe
/ APPLICANT: P. Mickey Williams
/ APPLICANT: William I. Wood
/ APPLICANT: Zemin Zang
/ TITLE OF INVENTION: SECRETED AND TITLED
/ TITLE OF INVENTION: ACIDS ENCODING
/ FILE REFERENCE: P31301C17
/ CURRENT APPLICATION NUMBER: US/10/0002-02-01
/ CURRENT FILING DATE: 2002-02-01
/ PRIOR APPLICATION NUMBER: 10/002,700
/ PRIOR FILING DATE: 2001-11-15
/ PRIOR APPLICATION NUMBER: 60/056970

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; Sequence 61, Application US/10002796
; Publication No. US20030032057A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
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; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C1
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Query Match 49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGAGTGGCAAGGCGTCTGCT 26
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Db 43 GCCACAGTTGTGGCAAGATGTGTGCT 18

RESULT 5

US-10-066-273-61/c
; Sequence 61, Application US/10066273
; Publication No. US20030032062A1

GENERAL INFORMATION:

; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C2
; CURRENT APPLICATION NUMBER: US/10/066,273
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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Query Match          49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 43 GCCACAGTGTGGCAAGATGTGCT 18

RESULT 6
US-10-066-494-61/c
; Sequence 61, Application US/10066494
; Publication No. US20030032063A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
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; APPLICANT: Daniel Tunas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C9
; CURRENT APPLICATION NUMBER: US/10/066,494
; PRIOR FILING DATE: 2002-02-01
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Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGCACAGGGCTCTGGT 26
Db 43 GCCACATGAGTGCACAGGGCTCTGGT 18

RESULT 7

US-10-066-269-61/c
; Sequence 61, Application US/10066269
; Publication No. US20030040014A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
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; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C4
; CURRENT APPLICATION NUMBER: US/10/066,269
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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Query Match 49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;

;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/095998
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;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/139695
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;; PRIOR APPLICATION NUMBER: 60/145070
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;; PRIOR APPLICATION NUMBER: 09/136828
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;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 09/202088
;; PRIOR FILING DATE: 1998-12-08
;; PRIOR APPLICATION NUMBER: 09/254311
;; PRIOR FILING DATE: 1999-03-03
;; PRIOR APPLICATION NUMBER: 09/254460
;; PRIOR FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: 09/254465
;; PRIOR FILING DATE: 1999-03-05
;; PRIOR APPLICATION NUMBER: 09/284663
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: 09/332928
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: 09/332929
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;; PRIOR APPLICATION NUMBER: 09/333075
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: 09/333077
;; PRIOR FILING DATE: 1999-06-14
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;; PRIOR FILING DATE: 1999-08-25

;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380139
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/403296
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/423844
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 09/522342
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: 09/548815
;; PRIOR FILING DATE: 2000-04-13
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;; PRIOR FILING DATE: 2000-09-18
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;; PRIOR FILING DATE: 2000-09-18
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;; PRIOR FILING DATE: 2001-01-22
;; PRIOR APPLICATION NUMBER: 09/802706
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;; PRIOR APPLICATION NUMBER: 09/808689
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;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/870574
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/886342
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: PCT/US98/14552
;; PRIOR FILING DATE: 1998-07-14
;; PRIOR APPLICATION NUMBER: PCT/US98/18824
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/US98/19093
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: 1998-09-16
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;; PRIOR APPLICATION NUMBER: PCT/US98/24855
;; PRIOR FILING DATE: 1998-11-20
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: 1998-12-01
;; PRIOR APPLICATION NUMBER: PCT/US98/25190
;; PRIOR FILING DATE: 1998-11-25
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGGCAAGCGCTGTGT 26
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Db 43 GCCACAGTTGTGGCAGATGTGTGT 18
|||||

RESULT 8
US-10-066-211-61/c
; Sequence 61, Application US/10066211
; Publication No. US2003004844A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C8
; CURRENT APPLICATION NUMBER: US/10/066,211
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGATGGCAAGCGTGTGT 26
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Db 43 GCCACAGTTGTGGCAAGATGTGTGT 18

RESULT 9
US-10-066-193-61/c
; Sequence 61, Application US/10066193
; Publication No. US20030044902A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker

; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C3
; CURRENT APPLICATION NUMBER: US/10/066.193
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002.796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1998-02-09
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; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/099601
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812

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US-10-226-739-61/c
; Sequence 61, Application US/10226739
; Publication No. US20030104558A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi
; APPLICANT: Baker
; APPLICANT: Botstein
; APPLICANT: Desnovers
; APPLICANT: Eaton
; APPLICANT: Ferrara
; APPLICANT: Fong
; APPLICANT: Gao
; APPLICANT: Gerber, Gerritsen

```

APPLICANT: Goddard
APPLICANT: Godowski
APPLICANT: Gurney
APPLICANT: Kijavin
APPLICANT: Mather
APPLICANT: Napier
APPLICANT: Pan
APPLICANT: Paoni
APPLICANT: Roy
APPLICANT: Stewart
APPLICANT: Tamas
APPLICANT: Watanabe
APPLICANT: Williams
APPLICANT: Wood
APPLICANT: Zang

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

FILE REFERENCE: P3130R1C10

CURRENT APPLICATION NUMBER: US/10/226,739

PRIOR FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: US 10/002,796

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: PCT/US99/20111

PRIOR FILING DATE: 1999-09-01

PRIOR APPLICATION NUMBER: US 09/403,297

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US 60/106,032

PRIOR FILING DATE: 1998-10-28

NUMBER OF SEQ ID NOS: 151

SEQ ID NO 61

LENGTH: 43

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-226-739-61

Query Match 49.7%; Score 16.4; DB 15; Length 43;

Best Local Similarity 76.9%; Pred. No. 1.6e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 GCCACATGAGTGGCAAGCGCTGCTGT 26

||||| ||||| ||||| |||||

Db 43 GCCACAGTTGTGGCAAGATGCTGCT 18

RESULT 11

US-10-066-198-61/c

Sequence 61, Application US/10066198

Publication No. US20030170721A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi

APPLICANT: Kevin P. Baker

APPLICANT: David A. Botstein

APPLICANT: Luc Desnoyers

APPLICANT: Dan L. Eaton

APPLICANT: Napoleone Ferrara

APPLICANT: Sherman Fong

APPLICANT: Wei-Qiang Gao

APPLICANT: Hanspeter Gerber

APPLICANT: Mary E. Gerritsen

APPLICANT: Audrey Goddard

APPLICANT: Paul J. Godowski

APPLICANT: Austin L. Gurney

APPLICANT: Ivar J. Kijavin

APPLICANT: Jennie P. Mather

APPLICANT: Mary A. Napier

APPLICANT: James Pan

APPLICANT: Nicholas F. Paoni

APPLICANT: Margaret Ann Roy

APPLICANT: Timothy A. Stewart

APPLICANT: Daniel Tamas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

FILE REFERENCE: P3130R1C6

CURRENT APPLICATION NUMBER: US/10/066,198

PRIOR FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 10/002,796

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059588

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PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/081049

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PRIOR FILING DATE: 1998-09-24

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PRIOR APPLICATION NUMBER: 60/145070

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/145698

PRIOR FILING DATE: 1999-07-26

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;
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 08/918874
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 08/933821
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 08/960507
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 09/114844
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: 09/136801
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/136804
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/136828
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/158342
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/202088
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: 09/254311
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/254460
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/254465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 09/284663
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 09/332928
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/332929
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/333075
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; PRIOR FILING DATE: 1999-06-14
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; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/403296
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
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; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 09/522342
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 09/548815
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 09/664610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/665350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/709238
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; PRIOR APPLICATION NUMBER: 09/767609
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; PRIOR FILING DATE: 2001-03-09
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; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/866028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/870574
; PRIOR FILING DATE: 2001-05-30

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; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/886342
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: PCT/US98/14552
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/19093
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: PCT/US98/25190
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
;
Query Match 49.7%; Score 16.4; DB 15; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGGCGAAGCGTCTGGT 26
DB 43 GCCACAGTTGTGGCAAGATGTGGT 18

RESULT 12
US-10-066-203-61/c
; Sequence 61, Application US/10066203
; Publication No. US20030180796A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleon Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Geixtsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3130RLCS
CURRENT APPLICATION NUMBER: US/10/066,203
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066840
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/095998
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/097000
PRIOR FILING DATE: 1998-08-18
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PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
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PRIOR FILING DATE: 1998-10-28
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PRIOR FILING DATE: 1998-11-20
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PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 60/139695
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/145070
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1998-07-26
PRIOR APPLICATION NUMBER: 60/149396
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1998-12-07
PRIOR APPLICATION NUMBER: 08/918874
PRIOR FILING DATE: 1997-08-26
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PRIOR APPLICATION NUMBER: 08/960507
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PRIOR FILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: 09/136828
PRIOR FILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: 09/158342
PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/202088
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: 09/254311
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/254460
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 09/254465
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PRIOR APPLICATION NUMBER: 09/284663
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PRIOR APPLICATION NUMBER: 09/33075
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/33077
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1999-08-25
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PRIOR FILING DATE: 1999-10-18
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PRIOR FILING DATE: 1999-11-10
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PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 09/522342
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
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PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/767609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/808689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/866028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/870574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/886342
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: PCT/US98/14552
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: PCT/US98/18824

Qy	Db	Sequence	Score	DB 15;	Length	DB 15;	Length	DB 15;	Length	DB 15;	Length
1	43	GCACATGAGTGGCAGGCGTCTGGT 26	49.7%;	Score 16.4;	DB 15;	Length 43;					
		Best Local Similarity 76.9%;	Pred. No. 1.6e+03;								
		Matches 20;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;					
1	43	GCACATGAGTGGCAGGCGTCTGGT 18									
<p>RESULT 13</p> <p>US-10-098-263B-65283/G</p> <p>Sequence 65283, Application US/10098263B</p> <p>Publication No. US20030104410A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Mittman, Michael</p> <p>TITLE OF INVENTION: Human Microarray</p> <p>FILE REFERENCE: 3118.1</p> <p>CURRENT APPLICATION NUMBER: US/10/098,263B</p> <p>CURRENT FILING DATE: 2003-01-08</p> <p>PRIOR APPLICATION NUMBER: 60/276,759</p> <p>PRIOR FILING DATE: 2001-03-16</p> <p>NUMBER OF SEQ ID NOS: 131066</p> <p>SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1</p> <p>SEQ ID NO 65283</p> <p>LENGTH: 25</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapien</p> <p>US-10-098-263B-65283</p>											
1	22	GCACATGAGTGGCAGGCGTCT 22	47.3%;	Score 15.6;	DB 15;	Length 25;					
		Best Local Similarity 81.8%;	Pred. No. 3.5e+03;								
		Matches 18;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;					
1	22	GCACATGAGTGGCAGGCGTCT 1									
<p>RESULT 14</p> <p>US-10-667-271-1525</p> <p>Sequence 1525, Application US/10667271</p> <p>Publication No. US20040209831A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Sirna Therapeutics</p> <p>APPLICANT: McSwiggen, James</p> <p>APPLICANT: Macejak, Dennis</p> <p>APPLICANT: Beigelman, Leonid</p> <p>APPLICANT: Moxizesev, David</p>											


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; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal
US-10-667-271-1525

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Query Match 46.7%; Score 15.4; DB 18; Length 21;
Best Local Similarity 76.5%; Pred. No. 4.3e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GGCAAGGCGTCTGGTGA 28
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Db 3 GCCAAGGCGUCUGGUGA 19

RESULT 15
US-10-667-271-1537/c
Sequence 1537, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/129 (MBHB02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIORITY APPLICATION NUMBER: US 10/444,853
PRIORITY FILING DATE: 2003-05-23
PRIORITY APPLICATION NUMBER: PCT / US03/05043
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: PCT / US02/09187
PRIORITY FILING DATE: 2002-03-26
PRIORITY APPLICATION NUMBER: USSN 60/401,104
PRIORITY FILING DATE: 2002-08-05
PRIORITY APPLICATION NUMBER: USSN 60/358,580
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: USSN 60/363,124
PRIORITY FILING DATE: 2002-03-11
PRIORITY APPLICATION NUMBER: USSN 60/386,782
PRIORITY FILING DATE: 2002-06-06
PRIORITY APPLICATION NUMBER: USSN 60/406,784
PRIORITY FILING DATE: 2002-08-29
PRIORITY APPLICATION NUMBER: USSN 60/408,378
PRIORITY FILING DATE: 2002-09-05
PRIORITY APPLICATION NUMBER: USSN 60/409,293
PRIORITY FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1537
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(2)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:

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; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1582
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
; US-10-667-271-1582
;
; Query Match 46.7%; Score 15.4; DB 18; Length 21;
; Best Local Similarity 76.5%; Pred. No. 4.3e+03;
; Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 GCCAAGGCGCTGCTGTA 28
; DB 3 GCCAAGGCGCUCUGGUGA 19
;
; RESULT 17
; US-10-667-271-1594/c
; Sequence 1594, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
;
; Query Match 46.7%; Score 15.4; DB 18; Length 21;
; Best Local Similarity 94.1%; Pred. No. 4.3e+03;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 GCCAAGGCGCTGCTGTA 28
; DB 17 GCCAAGGCGCTGCTGTA 1
;
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1594
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; US-10-667-271-1594
;
; Query Match 46.7%; Score 15.4; DB 18; Length 21;
; Best Local Similarity 94.1%; Pred. No. 4.3e+03;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 GCCAAGGCGCTGCTGTA 28
; DB 17 GCCAAGGCGCTGCTGTA 1
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RESULT 18
US-10-098-263B-57900
; Sequence 57900, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 57900
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-57900

Query Match          46.7%; Score 15.4; DB 15; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CACATGACTGGCAAGCGCTCTGGTG 27
Db 1 CACATGAGGGTCAAGTCTGCCGAG 25

RESULT 19
US-10-233-996-8
; Sequence 8, Application US/10233996
; Publication No. US20030096976A1
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES LB-00503 AND LB-00506 SPECIFIC FOR HUMAN 4-1
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING SAID HUMANIZED ANTIBODIES
; FILE REFERENCE: 4363-0102P
; CURRENT APPLICATION NUMBER: US/10/233,996
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer KXD
US-10-233-996-8

Query Match          46.7%; Score 15.4; DB 14; Length 30;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 8 GAGTGGCAAGCGCTCTGGTGATACC 32
Db 2 GACTGCCCAGGTTTGTGTATACC 26

RESULT 20
US-09-855-797A-28/c
; Sequence 28, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
US-09-855-797A-28/c

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 21
US-09-907-900-28/c
; Sequence 28, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942-2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-907-900-28/c

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 22
US-09-907-719-28/c
; Sequence 28, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
US-09-907-719-28/c

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8
```

```
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942-2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-855-797A-28

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8
```

```
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-907-719-28

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 ATGAGTGGCAAGCGCTCTGCTGATA 30
        |||||||
Db      32 ATGAGTGGCAGCGGGCGGCGTAATA 8

RESULT 23
US-09-432-085-28/c
; Sequence 28, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
```

```
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-28

Query Match          46.7%; Score 15.4; DB 10; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 ATGAGTGGCAAGCGCTCTGCTGATA 30
        |||||||
Db      32 ATGAGTGGCAGCGGGCGGCGTAATA 8

RESULT 24
US-09-985-448-28/c
; Sequence 28, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-985-448-28

Query Match          46.7%; Score 15.4; DB 10; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 ATGAGTGGCAAGCGCTCTGCTGATA 30
        |||||||
Db      32 ATGAGTGGCAGCGGGCGGCGTAATA 8

RESULT 25
US-10-058-292-28/c
; Sequence 28, Application US/10058292
; Publication No. US2003005452A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-058-292-28

Query Match      46.7%; Score 15.4; DB 14; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGCGGCGTAATA 8

RESULT 26
US-10-058-291-28/c
Sequence 28, Application US/10058291
Publication No. US20030064515A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,291
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-058-291-28

Query Match      46.7%; Score 15.4; DB 14; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGCGGCGTAATA 8

RESULT 27
US-10-162-879-28/c
Sequence 28, Application US/10162879
Publication No. US20030068799A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
```

```
;
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-162-879-28
Query Match 46.7%; Score 15.4; DB 14; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 ATGAGTGGCAGGCGCGGGCGTAATA 8

RESULT 28
US-10-300-892-28/c
; Sequence 28, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-300-892-28

Query Match 46.7%; Score 15.4; DB 15; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 ATGAGTGGCAGGCGCGGGCGTAATA 8

RESULT 29
US-10-680-316-28/c
; Sequence 28, Application US/10680316
; Publication No. US20040063207A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/680,316
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28

;
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-680-316-28

Query Match 46.7%; Score 15.4; DB 16; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 ATGAGTGGCAGGCGCGGGCGTAATA 8

RESULT 30
US-10-815-730-28/c
; Sequence 28, Application US/10815730
; Publication No. US20040171156A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/815,730
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-815-730-28

Query Match 46.7%; Score 15.4; DB 17; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 ATGAGTGGCAGGCGCGGGCGTAATA 8

RESULT 31
US-10-820-133-28/c
; Sequence 28, Application US/10820133
; Publication No. US20040171157A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/820,133
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
```

```
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-820-133-28

Query Match          46.7%; Score 15.4; DB 17; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 32
US-10-796-868A-28/c
; Sequence 28, Application US/10796868A
; Publication No. US20040219673A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
; FILE REFERENCE: 0942.285000K
; CURRENT APPLICATION NUMBER: US/10/796,868A
; CURRENT FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 09/498,074
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/005,476
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 08/663,002
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/486,139
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA/RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CAT right PCR primer
US-10-796-868A-28

Query Match          46.7%; Score 15.4; DB 18; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 33
US-10-430-984-1
; Sequence 1, Application US/10430984
; Publication No. US20040225112A1
; GENERAL INFORMATION:
; APPLICANT: Crew, Mark D
; APPLICANT: The Board of Trustees of the University of Arkansas
; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen B (HLA-E)
; TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
; FILE REFERENCE: 8793-53098
; CURRENT APPLICATION NUMBER: US/10/430,984
; CURRENT FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 1
```

```
; LENGTH: 44
; TYPE: DNA
; ORGANISM: human leukocyte antigen E
US-10-430-984-1

Query Match          46.7%; Score 15.4; DB 18; Length 44;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGCAAGGCGCTCTGGTGATACCG 33
Db 11 GCGACATGGGTGGTGGCGGTTCTGGTGGCG 43

RESULT 34
US-10-411-954-85/c
; Sequence 85, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 85
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-85

Query Match          46.1%; Score 15.2; DB 15; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 AGTGGCAAGGCGTCTGGTGA 28
Db 37 AGTGGCAGGGGCGCTGGTGA 18

RESULT 35
US-10-411-954-282/c
; Sequence 282, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 282
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-282

Query Match          46.1%; Score 15.2; DB 15; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 9 AGTGGCAAGGCGCTCTGGTGA 28
||||||| ||| |||||
Db 37 AGTGGCAGGGCGCTGGTGA 18

RESULT 36
US-10-617-070-85/c
; Sequence 85, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-85

Query Match 46.1%; Score 15.2; DB 16; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAAGGCGCTCTGGTGA 28
||||||| ||| |||||
Db 37 AGTGGCAGGGCGCTGGTGA 18

RESULT 37
US-10-617-070-282/c
; Sequence 282, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 282
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-282

Query Match 46.1%; Score 15.2; DB 16; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAAGGCGCTCTGGTGA 28
||||||| ||| |||||
Db 37 AGTGGCAGGGCGCTGGTGA 18

RESULT 39
US-10-191-540-87/c
; Sequence 87, Application US/10191540
; Publication No. US20030224494A1
; GENERAL INFORMATION:
; APPLICANT: Tsuyoshi Nomoto, Tetsuya Yano, Shinya Kozaki and Tsutomu Honma
; APPLICANT: Polyhydroxyalkanoate-containing structure and manufacturing method
; TITLE OF INVENTION: thereof
; FILE REFERENCE: CFI016534
; CURRENT APPLICATION NUMBER: US/10/191,540
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: JP P2001-210052
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: JP P2002-172978
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for PCR multiplication
US-10-191-540-87


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Query Match      45.5%; Score 15; DB 15; Length 38;
Best Local Similarity 67.7%; Pred. No. 6.8e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGGCAAGGCGTCTGGTGATACC 32
Db 38 CAACGTGACCAGCACCGCGTTTATTGATACC 8

RESULT 40
US-10-453-483-66/c
; Sequence 66, Application US/10453483
; Publication No. US20040005638A1
; GENERAL INFORMATION:
; APPLICANT: Tetsuya Yano
; APPLICANT: Tutomu Honma
; APPLICANT: Tsuyoshi No. US20040005638A1oto
; APPLICANT: Shinya Kozaki
; TITLE OF INVENTION: Immunoassay, reagent for immunoassay, and production method of th
; FILE REFERENCE: CF017318
; CURRENT APPLICATION NUMBER: US/10/453,483
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: JP P2002-173027
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: JP P2003-127099
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: complementary to 65
US-10-453-483-66

Query Match      45.5%; Score 15; DB 16; Length 38;
Best Local Similarity 67.7%; Pred. No. 6.8e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGGCAAGGCGTCTGGTGATACC 32
Db 38 CAACGTGACCAGCACCGCGTTTATTGATACC 8

Search completed: November 24, 2004, 03:42:34
Job time : 163.842 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1582.15 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-5

Perfect score: 33

Sequence: 1 gccacatgagtggaaggcgtcgtggtacaccg 33

Scoring table: IDENTITY NUC

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Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	15	45.5	50	1	AU103463
6	14.6	44.2	36	8	AZ481987
7	14.4	43.6	34	8	AZ329468
8	14.4	43.6	34	8	AZ480659
9	14.4	43.6	38	8	AZ818206
10	14.2	43.0	50	1	AU103440
11	14.2	43.0	50	1	AU103448
12	14	42.4	36	8	AZ783989
13	14	42.4	40	7	T51935
14	14	42.4	47	8	AZ490009
15	14	42.4	49	4	BG489537
16	13.8	41.8	49	2	BF578678
17	13.8	41.8	43	8	AZ664916
18	13.8	41.8	50	1	AA206278
19	13.8	41.8	50	9	BX289625
20	13.6	41.2	58	1	AU105625
21	13.4	40.6	28	1	A1419869
22	13.4	40.6	44	8	AZ990977
23	13.4	40.6	46	8	BH853635
24	13.4	40.6	50	1	AU103740

98	12	36.4	34	8	BZ762058	SALK 0855	171	11.6	35.2	40	8	AZ610675	AZ610675	1M0436H12
99	12	36.4	36	8	AZ659063	1M0536N10	172	11.6	35.2	40	8	AZ835260	AZ835260	2M0129H20
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101	12	36.4	36	8	BH902764	SALK 0990	174	11.6	35.2	42	4	BI665361	BI665361	603288R93
102	12	36.4	37	1	AI721492	IC28d01.x	175	11.6	35.2	42	4	BM400471	BM400471	5009-0-73
103	12	36.4	39	8	AZ478568	1M0298P09	176	11.6	35.2	42	8	AZ806216	AZ806216	2M0068D09
104	12	36.4	40	8	AZ952424	2M0217B17	c 177	11.6	35.2	43	1	AA534781	AA534781	nf1e01.s
105	12	36.4	43	8	CC053600	SALK 0455	178	11.6	35.2	44	2	BE536392	BE536392	601062593
106	12	36.4	44	8	AQ073165	EP(X)0371	179	11.6	35.2	44	9	TA294F02P	TA294F02P	T. brucei
107	12	36.4	45	6	CB074815	EST00060	180	11.6	35.2	44	9	AG221236	AG221236	Lotus cor
108	12	36.4	47	8	AZ815240	2M0083C19	181	11.6	35.2	46	2	BE884491	BE884491	601510781
109	12	36.4	49	1	AI495587	sa99g08.y	182	11.6	35.2	47	7	H39179	H39179	Ym48401.r1
110	12	36.4	50	1	AU102519	AU102519	c 183	11.6	35.2	49	1	AA775622	AA775622	zf30f12.s
111	12	36.4	50	1	AU105486	AU105486	184	11.6	35.2	49	7	W80511	W80511	zh50h08.s1
112	12	36.4	50	1	AU105487	AU105487	c 185	11.6	35.2	50	1	AU103479	AU103479	AU103479
113	12	36.4	50	1	AU105488	AU105488	186	11.6	35.2	50	1	AU103627	AU103627	AU103627
114	12	36.4	50	1	AU105490	AU105490	187	11.6	35.2	50	1	AU104211	AU104211	AU104211
115	12	36.4	50	1	AU105492	AU105492	c 188	11.6	35.2	50	1	AU105624	AU105624	AU105624
116	12	36.4	50	1	AU1056583	AU1056583	189	11.6	35.2	50	1	AU105861	AU105861	AU105861
117	12	36.4	50	9	BE58968	ArabiDops	c 190	11.6	35.2	50	1	AU106866	AU106866	AU106866
118	11.8	35.8	23	8	AZ447157	1M0243G22	191	11.6	35.2	50	1	AU106914	AU106914	AU106914
119	11.8	35.8	27	8	AZ468814	1M0282G02	192	11.6	35.2	50	1	AU106915	AU106915	AU106915
120	11.8	35.8	31	9	AJ596088	ArabiDops	193	11.6	35.2	50	1	AU106917	AU106917	AU106917
121	11.8	35.8	33	8	BZ770289	SALK 1432	194	11.6	35.2	50	1	AU106918	AU106918	AU106918
122	11.8	35.8	33	8	BZ770290	SALK 1432	195	11.6	35.2	50	1	AU106920	AU106920	AU106920
123	11.8	35.8	34	1	AI047833	ud64C05.x	196	11.6	35.2	50	1	AU106922	AU106922	AU106922
124	11.8	35.8	34	1	AI132658	ue33b11.x	c 197	11.6	35.2	50	1	AU107349	AU107349	AU107349
125	11.8	35.8	36	8	AZ583007	1M0376N11	198	11.6	35.2	50	2	AW248122	AW248122	2819697.5
126	11.8	35.8	37	1	AA423390	ve39C02.r	c 199	11.6	35.2	50	8	AF087243	AF087243	AF087243
127	11.8	35.8	38	1	AI182596	ud73C09.x	200	11.6	35.2	50	8	AZ921706	AZ921706	1006031E1
128	11.8	35.8	38	1	AI255273	ui90a03.x	201	11.6	35.2	50	8	BH902336	BH902336	SALK 0916
129	11.8	35.8	38	1	AI255816	ui89e11.x	c 202	11.6	35.2	50	9	TA179D03P	TA179D03P	TA179D03P
130	11.8	35.8	38	1	AI256061	ui94F01.x	203	11.4	34.5	22	8	AZ588797	AZ588797	1M0397D21
131	11.8	35.8	38	1	AI256061	ui94F01.x	204	11.4	34.5	28	8	AZ410454	AZ410454	1M0182K16
132	11.8	35.8	38	1	AI786184	uj52C08.x	205	11.4	34.5	29	8	AZ658502	AZ658502	1M0535M12
133	11.8	35.8	38	1	AI875207	ul30H03.x	206	11.4	34.5	32	8	AZ799831	AZ799831	2M0057G03
134	11.8	35.8	38	1	AA619263	vo50G04.r	207	11.4	34.5	34	5	EX557840	EX557840	EX557840
135	11.8	35.8	39	1	AI256185	ui96a06.x	208	11.4	34.5	35	6	CA585970	CA585970	CA585970
136	11.8	35.8	39	9	DME545087	Drosophila	209	11.4	34.5	35	6	BG914491	BG914491	602813233
137	11.8	35.8	40	7	N95034	zb32b05.r1	210	11.4	34.5	36	4	BI154838	BI154838	602902820
138	11.8	35.8	40	7	N98542	za69e06.r1	211	11.4	34.5	36	4	BI251361	BI251361	602994578
139	11.8	35.8	40	8	AZ762374	1M0557H22	212	11.4	34.5	39	1	AJ790274	AJ790274	AJ790274
140	11.8	35.8	40	9	AX891603	ArabiDops	c 213	11.4	34.5	39	8	BZ357110	BZ357110	SALK 1302
141	11.8	35.8	40	9	TA96H01Q	T. brucei	214	11.4	34.5	40	1	AA976421	AA976421	Oq51b07.s
142	11.8	35.8	41	8	AZ580746	1M036911	c 215	11.4	34.5	40	1	AI084761	AI084761	Oz79h04.x
143	11.8	35.8	42	8	AQ939867	hmbxgs13	216	11.4	34.5	41	9	BX289962	BX289962	ArabiDops
144	11.8	35.8	42	8	AZ586799	1M0394F04	217	11.4	34.5	41	9	CNS078R1	CNS078R1	Anopheles
145	11.8	35.8	42	8	BH800878	100802B80	218	11.4	34.5	43	8	AZ512618	AZ512618	1M0358P17
146	11.8	35.8	44	8	BZ377472	SALK 0828	c 219	11.4	34.5	43	8	BH644282	BH644282	1008043D0
147	11.8	35.8	44	9	AG198602	Pan trogl	220	11.4	34.5	43	8	BH905069	BH905069	SALK 1055
148	11.8	35.8	46	7	R66026	Yp12f04.r1	221	11.4	34.5	44	8	AZ639684	AZ639684	1M0501L13
149	11.8	35.8	46	9	TA314C05P	T. brucei	c 222	11.4	34.5	45	8	AZ412102	AZ412102	1M0185Q24
150	11.8	35.8	47	8	BG777442	602664745	c 223	11.4	34.5	45	9	CG806284	CG806284	1118067G1
151	11.8	35.8	47	8	AZ832536	2M0113E05	c 224	11.4	34.5	46	1	AA834374	AA834374	Oq51b07.s
152	11.8	35.8	49	1	AI188352	qd08B06.x	c 225	11.4	34.5	46	1	AA501996	AA501996	ne53g01.s
153	11.8	35.8	49	8	AZ487139	1M0316D04	c 226	11.4	34.5	46	1	AV833431	AV833431	Danio rer
154	11.8	35.8	49	8	AZ658888	1M035J021	227	11.4	34.5	46	9	BX125933	BX125933	BX125933
155	11.8	35.8	50	1	AU102388	AU102388	228	11.4	34.5	47	8	BZ768669	BZ768669	SALK 1405
156	11.8	35.8	50	1	AU102540	AU102540	c 229	11.4	34.5	49	9	AZ830102	AZ830102	2M0109E11
157	11.8	35.8	50	1	AU105049	AU105049	230	11.4	34.5	49	9	HSWC33G02	HSWC33G02	X88144 H sapiens D
158	11.8	35.8	50	1	AU105075	AU105075	c 231	11.4	34.5	49	9	TA119E02Q	TA119E02Q	AL463249 T. brucei
159	11.8	35.8	50	1	AU105083	AU105083	232	11.4	34.5	50	1	AU103895	AU103895	CG723151 1119074H1
160	11.8	35.8	50	1	AU107689	AU107689	233	11.4	34.5	50	1	AU104715	AU104715	AU104715
161	11.8	35.8	50	4	BG370398	nai33a04.	234	11.4	34.5	50	1	AU105169	AU105169	AU105169
162	11.8	35.8	50	4	BG721131	602692987	235	11.4	34.5	50	1	AU105170	AU105170	AU105170
163	11.8	35.8	50	7	CN936328	000304AVB	236	11.4	34.5	50	1	AU105174	AU105174	AU105174
164	11.6	35.2	24	8	AZ813254	2M0080M21	237	11.4	34.5	50	1	AU105175	AU105175	AU105175
165	11.6	35.2	30	8	AZ666375	1M0548C20	238	11.4	34.5	50	1	AU105176	AU105176	AU105176
166	11.6	35.2	33	2	BE539711	601059362	239	11.4	34.5	50	1	AU105644	AU105644	AU105644
167	11.6	35.2	34	1	AA707874	zh25g10.s	240	11.4	34.5	50	1	AU105646	AU105646	AU105646
168	11.6	35.2	34	8	AZ787308	2M0033B21	241	11.4	34.5	50	1	AU105648	AU105648	AU105648
169	11.6	35.2	40	1	AI499289	1009C08.x	242	11.4	34.5	50	1	AU105651	AU105651	AU105651
170	11.6	35.2	40	4	BM394053	50072-2-1	243	11.4	34.5	50	1	AU105651	AU105651	AU105651

244	11.4	34.5	50	1	AU105653	AU105653	317	11.2	33.9	50	1	AU103059	AU103059
245	11.4	34.5	50	1	AU105654	AU105654	318	11.2	33.9	50	1	AU103789	AU103789
246	11.4	34.5	50	1	AU106240	AU106240	319	11.2	33.9	50	1	AU103799	AU103799
247	11.4	34.5	50	1	AU106872	AU106872	320	11.2	33.9	50	1	AU103805	AU103805
248	11.4	34.5	50	1	AU108081	AU108081	321	11.2	33.9	50	1	AU103868	AU103868
249	11.4	34.5	50	1	AU108081	AU108081	322	11.2	33.9	50	1	AU104730	AU104730
250	11.4	34.5	50	2	AU108536	AU108536	323	11.2	33.9	50	1	AU105060	AU105060
251	11.4	34.5	19	8	B2425239	B2425239	324	11.2	33.9	50	1	AU105482	AU105482
252	11.2	33.9	21	8	A2862876	A2862876	325	11.2	33.9	50	1	AU105483	AU105483
253	11.2	33.9	24	8	A2993498	A2993498	326	11.2	33.9	50	1	AU106250	AU106250
254	11.2	33.9	25	1	A1594892	A1594892	327	11.2	33.9	50	1	AU106295	AU106295
255	11.2	33.9	26	8	A2389492	A2389492	328	11.2	33.9	50	1	AU106296	AU106296
256	11.2	33.9	27	5	BQ584417	BQ584417	329	11.2	33.9	50	1	AU106597	AU106597
257	11.2	33.9	28	8	A2831000	A2831000	330	11.2	33.9	50	1	AU106915	AU106915
258	11.2	33.9	29	8	TA320F03Q	TA320F03Q	331	11.2	33.9	50	1	AU107298	AU107298
259	11.2	33.9	29	1	AJ807265	AJ807265	332	11.2	33.9	50	1	AU107300	AU107300
260	11.2	33.9	31	1	AJ807265	AJ807265	333	11.2	33.9	50	1	AU107302	AU107302
261	11.2	33.9	31	9	EX535270	EX535270	334	11.2	33.9	50	1	AU107308	AU107308
262	11.2	33.9	33	8	A2805273	A2805273	335	11.2	33.9	50	1	AU107309	AU107309
263	11.2	33.9	34	9	TA244E09Q	TA244E09Q	336	11.2	33.9	50	1	AU107311	AU107311
264	11.2	33.9	35	4	BI769066	BI769066	337	11.2	33.9	50	1	AU107313	AU107313
265	11.2	33.9	35	4	BI906671	BI906671	338	11.2	33.9	50	1	AU107315	AU107315
266	11.2	33.9	36	1	AJ652672	AJ652672	339	11.2	33.9	50	1	AU107316	AU107316
267	11.2	33.9	36	8	AJ581836	AJ581836	340	11.2	33.9	50	1	AU107317	AU107317
268	11.2	33.9	37	4	BI766183	BI766183	341	11.2	33.9	50	1	AU107318	AU107318
269	11.2	33.9	37	7	H40236	H40236	342	11.2	33.9	50	1	AU107319	AU107319
270	11.2	33.9	37	8	A2782753	A2782753	343	11.2	33.9	50	1	AU107321	AU107321
271	11.2	33.9	37	9	AG217884	AG217884	344	11.2	33.9	50	1	AU107326	AU107326
272	11.2	33.9	38	8	A2499479	A2499479	345	11.2	33.9	50	1	AU107330	AU107330
273	11.2	33.9	39	2	B8874819	B8874819	346	11.2	33.9	50	1	AU107332	AU107332
274	11.2	33.9	39	4	BI1818665	BI1818665	347	11.2	33.9	50	1	AU107741	AU107741
275	11.2	33.9	39	8	A2576137	A2576137	348	11.2	33.9	50	8	AZ402001	1M0169809
276	11.2	33.9	39	8	A2601737	A2601737	349	11.2	33.9	50	8	AZ666374	1M0548C19
277	11.2	33.9	39	9	CG730671	CG730671	350	11.2	33.9	50	8	AZ803049	2M0063A17
278	11.2	33.9	40	1	AJ939192	AJ939192	351	11.2	33.9	50	8	BH913380	3526_1_39
279	11.2	33.9	40	8	A490455	A490455	352	11.2	33.9	50	8	CC456525	SALK_0989
280	11.2	33.9	40	8	BH848043	BH848043	353	11.2	33.9	50	9	AG215560	Drosophila
281	11.2	33.9	40	8	BH856887	BH856887	354	11.2	33.9	23	8	AZ783394	2M0025L06
282	11.2	33.9	40	8	BH856881	BH856881	355	11.2	33.9	24	8	AZ610568	1M0435K21
283	11.2	33.9	40	8	BH856929	BH856929	356	11.2	33.9	25	8	AZ346741	1M0082C11
284	11.2	33.9	40	8	BH856978	BH856978	357	11.2	33.9	26	1	AU258271	AU258271
285	11.2	33.9	40	8	BZ383943	BZ383943	358	11.2	33.9	27	8	AZ978415	2M0254D15
286	11.2	33.9	40	9	TA274D05Q	TA274D05Q	359	11.2	33.9	28	8	AZ822723	2M0096009
287	11.2	33.9	41	8	A2844720	A2844720	360	11.2	33.9	30	1	AA976515	Q330505_8
288	11.2	33.9	42	8	AQ026474	AQ026474	361	11.2	33.9	30	8	AZ318355	1M0037D20
289	11.2	33.9	42	8	A236078	A236078	362	11.2	33.9	32	8	AZ618214	1M0449016
290	11.2	33.9	43	1	AA907625	AA907625	363	11.2	33.9	33	8	AZ319143	1M0038B12
291	11.2	33.9	43	8	BH902270	BH902270	364	11.2	33.9	34	7	T72000	ye07e08.r1
292	11.2	33.9	43	9	CG709706	CG709706	365	11.2	33.9	34	8	AZ427682	1M0209115
293	11.2	33.9	44	4	BI518751	BI518751	366	11.2	33.9	34	8	BZ595388	SALK_0869
294	11.2	33.9	44	8	AZ322603	AZ322603	367	11.2	33.9	34	9	TA102C06P	AL462338
295	11.2	33.9	44	8	BZ354782	BZ354782	368	11.2	33.9	35	7	R84783	vt66c02.r1
296	11.2	33.9	45	6	CA586746	CA586746	369	11.2	33.9	37	7	AA1032109	O875a01.s
297	11.2	33.9	45	8	A2592599	A2592599	370	11.2	33.9	37	1	AI148862	qc70b01.x
298	11.2	33.9	45	8	BH757973	BH757973	371	11.2	33.9	37	1	AV833600	AV833600
299	11.2	33.9	46	1	AA758346	AA758346	372	11.2	33.9	37	1	AV844566	AV844566
300	11.2	33.9	46	1	AA758346	AA758346	373	11.2	33.9	37	1	AV851317	AV851317
301	11.2	33.9	46	1	AI941237	AI941237	374	11.2	33.9	37	2	BE548155	BE548155
302	11.2	33.9	46	8	A2992697	A2992697	375	11.2	33.9	37	6	CF063618	QC24b07.
303	11.2	33.9	46	9	CG780494	CG780494	376	11.2	33.9	37	8	N83014	TGESTy57g1
304	11.2	33.9	46	9	CG805368	CG805368	377	11.2	33.9	37	8	AZ769896	1M0571E03
305	11.2	33.9	47	4	BI916743	BI916743	378	11.2	33.9	38	8	AZ447531	1M0244C15
306	11.2	33.9	47	7	CK446591	CK446591	379	11.2	33.9	38	8	BH130009	G-6f16.f
307	11.2	33.9	47	9	CG804917	CG804917	380	11.2	33.9	38	8	BH791568	BH791568
308	11.2	33.9	48	9	AG201231	AG201231	381	11.2	33.9	39	8	BZ354203	BZ354203
309	11.2	33.9	49	1	AI766723	AI766723	382	11.2	33.9	40	1	AA162748	AA162748
310	11.2	33.9	49	1	AA569919	AA569919	383	11.2	33.9	40	8	AZ595949	1M0408124
311	11.2	33.9	49	4	BI523939	BI523939	384	11.2	33.9	41	1	AJ656445	AJ656445
312	11.2	33.9	49	9	CL256784	CL256784	385	11.2	33.9	41	7	CO788347	CO788347
313	11.2	33.9	50	1	AU102247	AU102247	386	11.2	33.9	41	8	AZ848135	2M0149A09
314	11.2	33.9	50	1	AU102389	AU102389	387	11.2	33.9	41	8	BH905776	SALK_1077
315	11.2	33.9	50	1	AU102759	AU102759	388	11.2	33.9	42	6	CF307497	HD11--06-
316	11.2	33.9	50	1	AU102868	AU102868	389	11.2	33.9	42	8	AZ467316	1M0278B08

c 390	11	33.3	42	9	CL640531	CL640531 G076C11 G	c 463	10.8	32.7	37	9	AG216758	AG216758 Drosophil
391	11	33.3	43	1	AA256343	AA256343 zr79h08.s	c 464	10.8	32.7	37	9	AG217821	AG217821 Drosophil
c 392	11	33.3	43	7	D67714	D67714 CELK076HF	c 465	10.8	32.7	37	9	AG217899	AG217899 Drosophil
c 393	11	33.3	44	8	AZ940577	AZ940577 2M0200E06	c 466	10.8	32.7	38	8	AZ811077	AZ811077 2M0077K02
394	11	33.3	44	8	AG193375	AG193375 Pan trogl	467	10.8	32.7	38	9	CL436882	CL436882 EST4020-N
395	11	33.3	44	8	AZ453471	AZ453471 1M0254F17	468	10.8	32.7	39	4	BG968413	BG968413 602835A16
c 396	11	33.3	45	9	DM854484	AJ545484 Drosophil	469	10.8	32.7	39	8	AZ804350	AZ804350 2M0065M24
397	11	33.3	45	9	TA329607Q	AL492426 T. brucei	470	10.8	32.7	39	9	CT976635	CT976635 SALK 1362
398	11	33.3	46	1	AI006377	AI006377 ua71c10.r	471	10.8	32.7	40	1	AI189771	AI189771 qd33508.x
c 399	11	33.3	46	1	AI023393	AI023393 ow70a11.s	472	10.8	32.7	40	2	BE902785	BE902785 601676114
c 400	11	33.3	46	1	AJ789455	AJ789455 AJ789455	c 473	10.8	32.7	40	8	AZ806050	AZ806050 2M0067B22
c 401	11	33.3	46	7	D19556	D19556 MUSGS00956	474	10.8	32.7	40	9	AJ592673	AJ592673 Arabidops
c 402	11	33.3	46	8	AZ666500	AZ666500 1M0548K12	c 475	10.8	32.7	40	9	TA339H05P	TA339H05P T. brucei
403	11	33.3	46	9	CL307788	CL307788 02S0135-1	c 476	10.8	32.7	41	5	BP069327	BP069327 BP069327
404	11	33.3	46	9	CL347041	CL347041 PST4371-N	c 477	10.8	32.7	41	9	CG773749	CG773749 1123014D0
c 405	11	33.3	47	7	R55441	R55441 YJ79d08.r1	c 478	10.8	32.7	42	6	CA587667	CA587667 LBEL4p25P
c 406	11	33.3	47	8	AZ488215	AZ488215 1M0318D20	479	10.8	32.7	42	8	AQ024965	AQ024965 EP(2)0822
407	11	33.3	47	8	BZ662640	BZ662640 SALK 0261	c 480	10.8	32.7	42	8	AZ452625	AZ452625 1M0252O02
408	11	33.3	47	9	BX658228	BX658228 Arabidops	481	10.8	32.7	42	8	BH804014	BH804014 100809780
c 409	11	33.3	48	1	AU012741	AU012741 AU012741	482	10.8	32.7	43	1	AA663711	AA663711 ae71a03.s
410	11	33.3	48	1	AA429295	AA429295 zw07a04.r	483	10.8	32.7	43	1	AJ364636	AJ364636 qw39e05.x
411	11	33.3	48	2	BF032107	BF032107 601559702	c 484	10.8	32.7	43	1	AA075270	AA075270 zm84d05.s
c 412	11	33.3	48	8	AZ390229	AZ390229 1M0515B06	c 485	10.8	32.7	43	1	AI687911	AI687911 tp80h05.x
c 413	11	33.3	48	9	BX661183	BX661183 Arabidops	c 486	10.8	32.7	43	4	BJ065096	BJ065096 BJ065096
414	11	33.3	49	6	CA965896	CA965896 CcLX05a20	487	10.8	32.7	43	8	BH895175	BH895175 3526_1_33
415	11	33.3	49	8	AZ836991	AZ836991 2M0132P04	c 488	10.8	32.7	43	8	BZ584220	BZ584220 3590_1_55
416	11	33.3	50	1	AU102449	AU102449 AU102449	c 489	10.8	32.7	44	2	BE967336	BE967336 601649333
417	11	33.3	50	1	AU102450	AU102450 AU102450	c 490	10.8	32.7	44	4	BG779515	BG779515 602666932
c 418	11	33.3	50	1	AU103692	AU103692 AU103692	c 491	10.8	32.7	44	8	AZ428590	AZ428590 1M0212H09
419	11	33.3	50	1	AU103793	AU103793 AU103793	492	10.8	32.7	44	8	AZ451728	AZ451728 1M0251D14
c 420	11	33.3	50	1	AU103820	AU103820 AU103820	493	10.8	32.7	44	8	AZ474015	AZ474015 1M0290A13
c 421	11	33.3	50	1	AU104378	AU104378 AU104378	494	10.8	32.7	44	8	BH611429	BH611429 SALK 0309
422	11	33.3	50	1	AU104857	AU104857 AU104857	495	10.8	32.7	45	8	AZ413281	AZ413281 1M0197M16
423	11	33.3	50	1	AU104860	AU104860 AU104860	c 496	10.8	32.7	46	1	AA001102	AA001102 zh82e02.r
424	11	33.3	50	1	AU104961	AU104961 AU104961	c 497	10.8	32.7	46	1	AI744320	AI744320 tr09d05.x
c 425	11	33.3	50	1	AU104968	AU104968 AU104968	c 498	10.8	32.7	46	8	BZ289563	BZ289563 SALK_0229
c 426	11	33.3	50	1	AU104969	AU104969 AU104969	c 499	10.8	32.7	46	9	CG778195	CG778195 112302660
c 427	11	33.3	50	1	AU105087	AU105087 AU105087	c 500	10.8	32.7	47	4	BG484978	BG484978 602503986
c 428	11	33.3	50	1	AU105484	AU105484 AU105484	501	10.8	32.7	47	8	AZ369672	AZ369672 1M0120E21
c 429	11	33.3	50	1	AU105491	AU105491 AU105491	c 502	10.8	32.7	47	9	CR327908	CR327908 Medicago
c 430	11	33.3	50	1	AU105493	AU105493 AU105493	c 503	10.8	32.7	47	9	DR4D108	DR4D108 Danio rer
c 431	11	33.3	50	1	AU106599	AU106599 AU106599	c 504	10.8	32.7	48	1	AV950291	AV950291 AV950291
c 432	11	33.3	50	1	AU107088	AU107088 AU107088	c 505	10.8	32.7	48	8	BH614033	BH614033 SALK_0353
c 433	11	33.3	50	1	AU107637	AU107637 AU107637	c 506	10.8	32.7	48	8	BZ663678	BZ663678 SALK_0272
434	11	33.3	50	2	AW630853	AW630853 hh88e07.y	507	10.8	32.7	48	8	BZ762629	BZ762629 SALK_1059
435	11	33.3	50	5	BG662220	BG662220 cl83a07.z	c 508	10.8	32.7	48	9	AL946210	AL946210 Arabidops
c 436	11	33.3	50	8	AZ627991	AZ627991 1M0476A10	c 509	10.8	32.7	49	1	AA927087	AA927087 oi58a06.s
c 437	11	33.3	50	8	AZ638664	AZ638664 1M0498L07	c 510	10.8	32.7	49	7	N51399	N51399 yz16h06.sl
438	11	33.3	50	8	BZ662269	BZ662269 SALK_0257	c 511	10.8	32.7	49	8	AZ514447	AZ514447 1M0361M14
c 439	10.8	32.7	22	7	CO784859	CO784859 BL281D.E1	512	10.8	32.7	49	8	AZ821504	AZ821504 2M0094K14
c 440	10.8	32.7	23	9	TA78E03P	AL461956 T. brucei	513	10.8	32.7	49	8	BH889223	BH889223 3526_1_32
441	10.8	32.7	24	8	AZ451051	AZ451051 1M0250D12	514	10.8	32.7	49	8	BH903159	BH903159 SALK_1021
442	10.8	32.7	27	8	AZ951944	AZ951944 2M0216O04	515	10.8	32.7	50	1	AI066783	AI066783 ov17b03.x
c 443	10.8	32.7	27	8	AZ966603	AZ966603 2M0337J12	c 516	10.8	32.7	50	1	AU102283	AU102283 AU102283
c 444	10.8	32.7	27	8	BH910341	BH910341 SALK_0590	c 517	10.8	32.7	50	1	AU102387	AU102387 AU102387
445	10.8	32.7	29	8	AZ345823	AZ345823 1M0080M09	518	10.8	32.7	50	1	AU103057	AU103057 AU103057
446	10.8	32.7	29	8	AZ829296	AZ829296 2M0106E22	c 519	10.8	32.7	50	1	AU103582	AU103582 AU103582
447	10.8	32.7	30	8	AZ810546	AZ810546 2M0076F10	c 520	10.8	32.7	50	1	AU103659	AU103659 AU103659
448	10.8	32.7	31	4	BI154913	BI154913 602902712	521	10.8	32.7	50	1	AU103734	AU103734 AU103734
c 449	10.8	32.7	31	7	U44252	U44252 ENU44252.As	522	10.8	32.7	50	1	AU103738	AU103738 AU103738
450	10.8	32.7	33	4	BM401378	BM401378 5009-0-9	523	10.8	32.7	50	1	AU103741	AU103741 AU103741
c 451	10.8	32.7	33	8	AZ304883	AZ304883 1M0005L23	524	10.8	32.7	50	1	AU103743	AU103743 AU103743
c 452	10.8	32.7	34	2	BE748594	BE748594 601571567	525	10.8	32.7	50	1	AU103747	AU103747 AU103747
c 453	10.8	32.7	34	8	AZ419323	AZ419323 1M0195H17	526	10.8	32.7	50	1	AU103754	AU103754 AU103754
454	10.8	32.7	35	9	AG204326	AG204326 Pan trogl	527	10.8	32.7	50	1	AU103760	AU103760 AU103760
c 455	10.8	32.7	36	8	AZ427281	AZ427281 1M0209H10	528	10.8	32.7	50	1	AU103769	AU103769 AU103769
456	10.8	32.7	37	1	AA961266	AA961266 on96a05.s	529	10.8	32.7	50	1	AU103771	AU103771 AU103771
c 457	10.8	32.7	37	9	AJ599517	AJ599517 Arabidops	530	10.8	32.7	50	1	AU103776	AU103776 AU103776
c 458	10.8	32.7	37	9	AG215935	AG215935 Drosophil	531	10.8	32.7	50	1	AU103787	AU103787 AU103787
c 459	10.8	32.7	37	9	AG216163	AG216163 Drosophil	532	10.8	32.7	50	1	AU103792	AU103792 AU103792
c 460	10.8	32.7	37	9	AG216196	AG216196 Drosophil	533	10.8	32.7	50	1	AU103797	AU103797 AU103797
c 461	10.8	32.7	37	9	AG216210	AG216210 Drosophil	534	10.8	32.7	50	1	AU103800	AU103800 AU103800
c 462	10.8	32.7	37	9	AG216512	AG216512 Drosophil	535	10.8	32.7	50	1	AU103801	AU103801 AU103801

682	10.6	32.1	50	1	AUI02809	AUI02809	AUI02809	755	10.4	31.5	38	2	BE788802	601475711
C 683	10.6	32.1	50	1	AUI03011	AUI03011	AUI03011	756	10.4	31.5	38	8	AZ779310	2M0015M05
684	10.6	32.1	50	1	AUI03019	AUI03019	AUI03019	C 757	10.4	31.5	38	8	BZ765588	SALK_1318
685	10.6	32.1	50	1	AUI03020	AUI03020	AUI03020	758	10.4	31.5	39	2	BE878080	601487463
C 686	10.6	32.1	50	1	AUI03688	AUI03688	AUI03688	759	10.4	31.5	39	4	BJ063766	BJ063766
C 687	10.6	32.1	50	1	AUI03691	AUI03691	AUI03691	C 760	10.4	31.5	39	7	N93435	ZB52906.s1
C 688	10.6	32.1	50	1	AUI03698	AUI03698	AUI03698	761	10.4	31.5	39	9	AZ807468	2M0070A21
C 689	10.6	32.1	50	1	AUI03816	AUI03816	AUI03816	762	10.4	31.5	39	9	CG718595	1119053G0
C 690	10.6	32.1	50	1	AUI03863	AUI03863	AUI03863	C 763	10.4	31.5	40	1	AA209583	AA209583
C 691	10.6	32.1	50	1	AUI03864	AUI03864	AUI03864	C 764	10.4	31.5	40	8	AZ942732	2M0203E02
C 692	10.6	32.1	50	1	AUI03865	AUI03865	AUI03865	765	10.4	31.5	40	8	CC022664	3591_1_30
C 693	10.6	32.1	50	1	AUI03867	AUI03867	AUI03867	766	10.4	31.5	40	8	EX214592	Dan10_rer
C 694	10.6	32.1	50	1	AUI03869	AUI03869	AUI03869	C 767	10.4	31.5	40	9	CL682702	PR10134d
C 695	10.6	32.1	50	1	AUI03870	AUI03870	AUI03870	C 768	10.4	31.5	41	8	AZ576478	AST-3T008
C 696	10.6	32.1	50	1	AUI03874	AUI03874	AUI03874	C 769	10.4	31.5	41	8	AZ776137	2M0009K06
C 697	10.6	32.1	50	1	AUI03875	AUI03875	AUI03875	C 770	10.4	31.5	41	8	AZ868204	2M0179P14
C 698	10.6	32.1	50	1	AUI03885	AUI03885	AUI03885	771	10.4	31.5	41	8	AZ868204	2M0179P14
C 699	10.6	32.1	50	1	AUI03886	AUI03886	AUI03886	C 772	10.4	31.5	42	8	AZ458289	1M0262D14
C 700	10.6	32.1	50	1	AUI03892	AUI03892	AUI03892	C 773	10.4	31.5	42	8	AZ799728	2M0057A20
C 701	10.6	32.1	50	1	AUI04027	AUI04027	AUI04027	C 774	10.4	31.5	42	9	AL939024	ArabiDops
C 702	10.6	32.1	50	1	AUI04813	AUI04813	AUI04813	C 775	10.4	31.5	43	8	AZ621196	1M0454H17
C 703	10.6	32.1	50	1	AUI04814	AUI04814	AUI04814	776	10.4	31.5	43	8	AZ621196	1M0454H17
C 704	10.6	32.1	50	1	AUI04966	AUI04966	AUI04966	777	10.4	31.5	43	8	AZ658528	1M0535C14
C 705	10.6	32.1	50	1	AUI04967	AUI04967	AUI04967	778	10.4	31.5	43	8	BZ353665	SALK_1210
C 706	10.6	32.1	50	1	AUI05294	AUI05294	AUI05294	C 779	10.4	31.5	43	8	BZ662712	SALK_0262
C 707	10.6	32.1	50	1	AUI06329	AUI06329	AUI06329	C 780	10.4	31.5	43	9	CL520077	DAH8G05_F
C 708	10.6	32.1	50	1	AUI06633	AUI06633	AUI06633	C 781	10.4	31.5	43	9	AG214307	Oryza sat
C 709	10.6	32.1	50	1	AUI06927	AUI06927	AUI06927	782	10.4	31.5	44	4	BJ030340	BJ030340
C 710	10.6	32.1	50	1	AUI07987	AUI07987	AUI07987	783	10.4	31.5	44	8	AZ7373192	1M0125D21
C 711	10.6	32.1	50	8	AZ322785	1M0043D12	AZ322785	784	10.4	31.5	44	8	AZ997640	2M0284D18
C 712	10.6	32.1	50	8	BH644632	1008053H0	BH644632	C 785	10.4	31.5	44	8	BH635563	100805G0
C 713	10.6	32.1	50	8	CC459066	SALK_1242	CC459066	C 786	10.4	31.5	44	9	BM6558969	ArabiDops
C 714	10.6	32.1	50	9	EX980763	Forward_8	EX980763	C 787	10.4	31.5	45	2	DM250942	Drosophila
C 715	10.6	32.1	50	9	CR181440	Forward_8	CR181440	C 788	10.4	31.5	45	2	AW250942	Drosophila
C 716	10.6	32.1	50	9	CS165338	CH240_362	CS165338	C 789	10.4	31.5	45	8	AZ434327	2M0238E01
C 717	10.4	31.5	19	8	AZ789827	2M0038C02	AZ789827	790	10.4	31.5	45	8	BH790030	SALK_0543
C 718	10.4	31.5	22	8	AZ627938	1M0469A24	AZ627938	791	10.4	31.5	45	8	BH810609	ArabiDops
C 719	10.4	31.5	24	8	BZ230658	SALK_0908	BZ230658	C 792	10.4	31.5	45	9	EX287762	ArabiDops
C 720	10.4	31.5	25	8	AZ307549	1M0009J24	AZ307549	C 793	10.4	31.5	46	1	AA906453	oj94g12.s
C 721	10.4	31.5	25	8	AZ376766	1M0130113	AZ376766	C 794	10.4	31.5	46	1	AA929076	om77f07.s
C 722	10.4	31.5	25	8	AZ781174	2M0019007	AZ781174	795	10.4	31.5	46	1	AA929076	om77f07.s
C 723	10.4	31.5	25	8	AZ304003	1M0003K22	AZ304003	796	10.4	31.5	46	2	BE209004	SWOVIMCAR
C 724	10.4	31.5	27	8	AZ465567	2M0175C17	AZ465567	C 797	10.4	31.5	46	8	BH641999	1008052B0
C 725	10.4	31.5	27	8	AZ864233	2M0173P12	AZ864233	C 798	10.4	31.5	46	9	AL759390	ArabiDops
C 726	10.4	31.5	27	8	AZ970627	2M0243O14	AZ970627	C 799	10.4	31.5	46	9	AL759390	ArabiDops
C 727	10.4	31.5	27	8	AZ598779	1M0413G16	AZ598779	800	10.4	31.5	47	4	BI156866	602921488
C 728	10.4	31.5	29	8	AZ828747	2M0105J21	AZ828747	C 801	10.4	31.5	47	5	BM504334	BM504334
C 729	10.4	31.5	30	8	AZ463319	1M0272M03	AZ463319	802	10.4	31.5	47	5	CL519316	DAG1H09_F
C 730	10.4	31.5	31	1	AI795030	6D75C08.Y	AI795030	803	10.4	31.5	47	9	CL519316	DAG1H09_F
C 731	10.4	31.5	31	2	BE299821	600944283	BE299821	C 804	10.4	31.5	48	8	AZ408184	1M0442C22
C 732	10.4	31.5	31	8	BH792555	SALK_0647	BH792555	805	10.4	31.5	48	9	AL948370	ArabiDops
C 733	10.4	31.5	32	1	AJ672813	AJ672813	AJ672813	806	10.4	31.5	49	1	AA782046	ai48d07.s
C 734	10.4	31.5	32	8	AZ346256	1M0081P12	AZ346256	807	10.4	31.5	49	1	AA835093	ak83b06.s
C 735	10.4	31.5	32	9	EX287654	ArabiDops	EX287654	808	10.4	31.5	49	1	AA835093	ak83b06.s
C 736	10.4	31.5	33	1	AU006896	ArabiDops	AU006896	809	10.4	31.5	49	1	AI312023	qp78b08.x
C 737	10.4	31.5	33	9	AL766917	ArabiDops	AL766917	C 810	10.4	31.5	49	1	AI312023	qp78b08.x
C 738	10.4	31.5	33	9	AL766996	ArabiDops	AL766996	C 811	10.4	31.5	49	1	AJ649956	AJ649956
C 739	10.4	31.5	34	4	BI143747	602907208	BI143747	C 812	10.4	31.5	49	1	AA204601	mu25C05.r
C 740	10.4	31.5	35	1	AL644522	AL644522	AL644522	813	10.4	31.5	49	7	W52971	zc97d11.r1
C 741	10.4	31.5	35	4	BI823435	603041176	BI823435	814	10.4	31.5	49	8	AZ423083	1M0202101
C 742	10.4	31.5	35	6	CA913569	EScherich	CA913569	815	10.4	31.5	49	8	AZ776551	2M0010G15
C 743	10.4	31.5	35	9	AG613319	EScherich	AG613319	C 816	10.4	31.5	49	8	AZ971265	2M0244N12
C 744	10.4	31.5	35	9	BX289041	ArabiDops	BX289041	817	10.4	31.5	50	1	BH626797	1007065C0
C 745	10.4	31.5	35	9	CC798057	SALK_1457	CC798057	818	10.4	31.5	50	1	AUI02219	AUI02219
C 746	10.4	31.5	36	9	AJ598616	ArabiDops	AJ598616	C 819	10.4	31.5	50	1	AUI02317	AUI02317
C 747	10.4	31.5	36	9	TAZ5811P	T. brucei	TAZ5811P	C 820	10.4	31.5	50	1	AUI02391	AUI02391
C 748	10.4	31.5	37	1	AA681821	vb6SH03.r	AA681821	C 821	10.4	31.5	50	1	AUI02664	AUI02664
C 749	10.4	31.5	37	1	AI444289	fb47e01.Y	AI444289	822	10.4	31.5	50	1	AUI02727	AUI02727
C 750	10.4	31.5	37	8	AZ320555	1M0040J09	AZ320555	823	10.4	31.5	50	1	AUI02837	AUI02837
C 751	10.4	31.5	37	8	AZ789783	2M0037H19	AZ789783	824	10.4	31.5	50	1	AUI02958	AUI02958
C 752	10.4	31.5	37	8	AZ808191	2M0071C18	AZ808191	825	10.4	31.5	50	1	AUI03148	AUI03148
C 753	10.4	31.5	37	8	CG707109	1119001B1	CG707109	826	10.4	31.5	50	1	AUI03167	AUI03167
C 754	10.4	31.5	37	9	CL528315	ASV13A03.	CL528315	C 827	10.4	31.5	50	1	AUI03949	AUI03949

755	10.4	31.5	38	2	BE788802	601475711
756	10.4	31.5	38	8	AZ779310	2M0015M05
C 757	10.4	31.5	38	8	BZ765588	SALK_1318
758	10.4	31.5	39	2	BE878080	601487463
759	10.4	31.5	39	4	BJ063766	BJ063766
C 760	10.4	31.5	39	7	N93435	ZB52906.s1
761	10.4	31.5	39	9	AZ807468	2M0070A21
762	10.4	31.5	39	9	CG718595	1119053G0
C 763	10.4	31.5	40	1	AA209583	AA209583
C 764	10.4	31.5	40	8	AZ769030	1M0569M13
765	10.4	31.5	40	8	AZ942732	2M0203E02
766	10.4	31.5	40	8	CC022664	3591_1_30
C 767	10.4	31.5	40	9	EX214592	Dan10_rer
C 768	10.4	31.5	40	9	CL682702	PR10134d
C 769	10.4	31.5	41	8	AZ576478	AST-3T008
C 770	10.4	31.5	41	8	AZ776137	2M0009K06
771	10.4	31.5	41	8	AZ868204	2M0179P14
C 772	10.4	31.5	42	8	AZ458289	1M0262D14
C 773	10.4	31.5	42	8	AZ799728	2M0057A20
C 774	10.4	31.5	42	9	AL939024	ArabiDops
C 775	10.4	31.5	43	1	AI080022	Oz50F06.x
776	10.4	31.5	43	8	AZ621196	1M0454H17
777	10.4	31.5	43	8	AZ658528	1M0535C14
778	10.4	31.5	43	8	BZ353665	SALK_1210
C 779	10.4	31.5	43	9	BZ662712	SALK_0262
C 780	10.4	31.5	43	9	CL520077	DAH8G05_F
C 781	10.4	31.5	43	9	AG214307	Oryza sat
782	10.4	31.5	44	4	BJ030340	BJ030340
783	10.4	31.5	44	8	AZ7373192	1M0125D21
784	10.4	31.5	44	8	AZ997640	2M0284D18
C 785	10.4	31.5	44	8	BH635563	100805G0
C 786	10.4	31.5	44	9	BM655896	ArabiDops
C 787	10.4	31.5	44	9	DM250942	Drosophila
C 788	10.4	31.5	45	2	AW250942	Drosophila
C 789	10.4	31.5	45	8	AZ434327	2M0238E01
790	10.4	31.5	45	8	AZ803772	2M0064P15
C 791	10.4	31.5	45	8	BH790030	SALK_0543
C 792	10.4	31.5	45	8	BH810609	ArabiDops
793	10.4	31.5	45	9	EX287762	ArabiDops
C 794	10.4	31.5	46	1	AA906453	oj94g12.s
795	10.4	31.5	46	1	AA929076	om77f07.s
796	10.4	31.5	46	2	BE209004	SWOVIMCAR
797	10.4	31.5	46	8	BH641999	1008052B0
C 798	10.4	31.5	46	9	AL759390	ArabiDops
C 799	10.4	31.5	46	9	AL759390	ArabiDops
800	10.4	31.5	47	5	BI156866	602921A88
C 801	10.4	31.5	47	5	BW504334	BW504334
C 802	10.4	31.5	47	9	CL519316	DAGIH09_F
803	10.4	31.5	48	8	AZ408184	1M0179F15
C 804	10.4	31.5	48	8	AZ614159	ArabiDops
805	10.4	31.5	48	9	AL948370	ArabiDops
806	10.4	31.5	49	1	AA835093	ak63b06.s
807	10.4	31.5	49	1	AA897888	als1a10.s
808	10.4	31.5	49	1	AI312023	qp78b08.x
809	10.4	31.5	49	1	AJ649956	AJ649956
C 810	10.4	31.5	49	1	AA204601	mu25c05.r
C 811	10.4	31.5	49	7	W52971	zc97d11.r1
812	10.4	31.5	49	8	AZ432083	2M0202I01
813	10.4	31.5	49	8	AZ776551	2M0010G15
814	10.4	31.5	49	8	AZ971265	2M0244N12
815	10.4	31.5	49	8	BH626797	1007065C0
C 816	10.4	31.5	50	1	AU102219	AU102219
817	10.4	31.5	50	1	AU102317	AU102317
818	10.4	31.5	50	1	AU102391	AU102391
C 819	10.4	31.5	50	1	AU102664	AU102664
C 820	10.4	31.5	50	1	AU102727	AU102727
C 821	10.4	31.5	50	1	AU102837	AU102837
822	10.4	31.5	50	1	AU102837	AU102837
823	10.4	31.5	50	1	AU102958	AU102958
824	10.4	31.5	50	1	AU103148	AU103148
825	10.4	31.5	50	1	AU103167	AU103167
826	10.4	31.5	50	1	AU103949	AU103949
C 827	10.4	31.5	50	1	AU103949	AU103949

c 828	10.4	31.5	50	1	AUI03955	AUI03955	AUI03955	c 901	10.2	30.9	33	8	BH790108	BH790108	SALK 0545
c 829	10.4	31.5	50	1	AUI03962	AUI03962	AUI03962	c 902	10.2	30.9	34	1	A1381014	tg20e10.x	A1381014
c 830	10.4	31.5	50	1	AUI04742	AUI04742	AUI04742	c 903	10.2	30.9	34	1	BI553461	603193222	BI553461
c 831	10.4	31.5	50	1	AUI04973	AUI04973	AUI04973	c 904	10.2	30.9	34	8	AZ421063	1M0199009	AZ421063
c 832	10.4	31.5	50	1	AUI05057	AUI05057	AUI05057	c 905	10.2	30.9	34	8	AZ856275	2M0160812	AZ856275
c 833	10.4	31.5	50	1	AUI05073	AUI05073	AUI05073	c 906	10.2	30.9	34	8	BZ358990	SALK 1336	BZ358990
c 834	10.4	31.5	50	1	AUI06586	AUI06586	AUI06586	c 907	10.2	30.9	34	8	BZ665782	KG10553-5	BZ665782
c 835	10.4	31.5	50	1	AUI06618	AUI06618	AUI06618	c 908	10.2	30.9	35	2	BE542178	601066507	BE542178
c 836	10.4	31.5	50	1	AUI06769	AUI06769	AUI06769	c 909	10.2	30.9	35	8	AZ428773	1M0212123	AZ428773
c 837	10.4	31.5	50	1	AUI06822	AUI06822	AUI06822	c 910	10.2	30.9	35	8	BH814760	SALK 0669	BH814760
c 838	10.4	31.5	50	1	AUI06970	AUI06970	AUI06970	c 911	10.2	30.9	36	1	AV680090	AV680090	AV680090
c 839	10.4	31.5	50	1	AUI07138	AUI07138	AUI07138	c 912	10.2	30.9	36	5	EX621489	EX621489	EX621489
c 840	10.4	31.5	50	1	AUI07354	AUI07354	AUI07354	c 913	10.2	30.9	36	7	H71797	YB05909.B1	H71797
c 841	10.4	31.5	50	1	AUI07355	AUI07355	AUI07355	c 914	10.2	30.9	36	7	R85295	YQ24e08.B1	R85295
c 842	10.4	31.5	50	1	AUI07356	AUI07356	AUI07356	c 915	10.2	30.9	36	8	AZ797263	2M0053G23	AZ797263
c 843	10.4	31.5	50	1	AUI07358	AUI07358	AUI07358	c 916	10.2	30.9	36	8	AZ797263	2M0053G23	AZ797263
c 844	10.4	31.5	50	1	AUI07359	AUI07359	AUI07359	c 917	10.2	30.9	36	8	AZ834877	2M0117L15	AZ834877
c 845	10.4	31.5	50	1	AUI07361	AUI07361	AUI07361	c 918	10.2	30.9	36	8	AZ983835	2M0265E10	AZ983835
c 846	10.4	31.5	50	1	AUI07365	AUI07365	AUI07365	c 919	10.2	30.9	36	9	CG179378	1119057D0	CG179378
c 847	10.4	31.5	50	1	AUI07366	AUI07366	AUI07366	c 920	10.2	30.9	37	1	AA873768	0106F01.S	AA873768
c 848	10.4	31.5	50	1	AUI07369	AUI07369	AUI07369	c 921	10.2	30.9	37	8	AZ312666	1M0028L14	AZ312666
c 849	10.4	31.5	50	1	AUI07370	AUI07370	AUI07370	c 922	10.2	30.9	37	8	AZ800309	2M0058F15	AZ800309
c 850	10.4	31.5	50	1	AUI07371	AUI07371	AUI07371	c 923	10.2	30.9	37	8	AZ809839	2M0074G05	AZ809839
c 851	10.4	31.5	50	1	AUI07372	AUI07372	AUI07372	c 924	10.2	30.9	37	8	AZ809839	2M0074G05	AZ809839
c 852	10.4	31.5	50	1	AUI07373	AUI07373	AUI07373	c 925	10.2	30.9	37	8	AZ960486	2M0228L01	AZ960486
c 853	10.4	31.5	50	1	AUI07375	AUI07375	AUI07375	c 926	10.2	30.9	37	8	BH791796	SALK 0613	BH791796
c 854	10.4	31.5	50	1	AUI07376	AUI07376	AUI07376	c 927	10.2	30.9	38	1	AA035969	mi70H01.r	AA035969
c 855	10.4	31.5	50	1	AUI07377	AUI07377	AUI07377	c 928	10.2	30.9	38	4	BJ034631	BJ034631	BJ034631
c 856	10.4	31.5	50	1	AUI07378	AUI07378	AUI07378	c 929	10.2	30.9	38	7	H30464	Y058a02.r1	H30464
c 857	10.4	31.5	50	2	BH76895	BH76895	BH76895	c 930	10.2	30.9	38	8	AZ975236	2M0250B17	AZ975236
c 858	10.4	31.5	50	5	CP00960	CP00960	CP00960	c 931	10.2	30.9	38	8	BH848869	SALK 0689	BH848869
c 859	10.4	31.5	50	6	CP00960	CP00960	CP00960	c 932	10.2	30.9	38	8	CG178161	1119051H0	CG178161
c 860	10.4	31.5	50	7	CP00960	CP00960	CP00960	c 933	10.2	30.9	38	9	AZ217395	Drosophila	AZ217395
c 861	10.4	31.5	50	8	CP00960	CP00960	CP00960	c 934	10.2	30.9	39	8	AZ307710	1M0009L01	AZ307710
c 862	10.4	31.5	50	8	CP00960	CP00960	CP00960	c 935	10.2	30.9	39	8	AZ416776	1M0192J07	AZ416776
c 863	10.4	31.5	50	9	CP00960	CP00960	CP00960	c 936	10.2	30.9	39	8	AZ659033	1M0536109	AZ659033
c 864	10.4	31.5	50	9	CP00960	CP00960	CP00960	c 937	10.2	30.9	39	9	TA100F02Q	T. brucei	TA100F02Q
c 865	10.4	31.5	50	9	CP00960	CP00960	CP00960	c 938	10.2	30.9	39	9	TA100F02Q	T. brucei	TA100F02Q
c 866	10.4	31.5	50	9	CP00960	CP00960	CP00960	c 939	10.2	30.9	39	9	TA100F02Q	T. brucei	TA100F02Q
c 867	10.2	30.9	20	8	AZ366535	AZ366535	AZ366535	c 940	10.2	30.9	40	1	AA456867	aa38b02.r	AA456867
c 868	10.2	30.9	20	8	CP533377	CP533377	CP533377	c 941	10.2	30.9	40	1	AA456867	aa38b02.r	AA456867
c 869	10.2	30.9	22	8	AZ623338	AZ623338	AZ623338	c 942	10.2	30.9	40	8	AZ454771	1M0256C22	AZ454771
c 870	10.2	30.9	23	1	AJ791120	AJ791120	AJ791120	c 943	10.2	30.9	40	8	AZ786213	2M0031F04	AZ786213
c 871	10.2	30.9	23	7	L32034	L32034	L32034	c 944	10.2	30.9	40	9	CR405146	Arabidops	CR405146
c 872	10.2	30.9	24	8	AU205942	AU205942	AU205942	c 945	10.2	30.9	40	9	TA14B10Q	CL266024	TA14B10Q
c 873	10.2	30.9	25	1	AU254095	AU254095	AU254095	c 946	10.2	30.9	40	9	CL266024	03S3081-1	CL266024
c 874	10.2	30.9	25	8	AZ324338	AZ324338	AZ324338	c 947	10.2	30.9	40	9	AG260533	Lotus cor	AG260533
c 875	10.2	30.9	25	8	AZ764603	AZ764603	AZ764603	c 948	10.2	30.9	40	4	BJ046937	BJ046937	BJ046937
c 876	10.2	30.9	25	9	TA28C08P	TA28C08P	TA28C08P	c 949	10.2	30.9	41	6	CB305228	3'EST-NF1	CB305228
c 877	10.2	30.9	27	7	D19150	D19150	D19150	c 950	10.2	30.9	41	7	D74277	CELK079AXF	D74277
c 878	10.2	30.9	27	8	AZ303969	AZ303969	AZ303969	c 951	10.2	30.9	41	8	AZ758979	1M0551D18	AZ758979
c 879	10.2	30.9	27	8	AZ367484	AZ367484	AZ367484	c 952	10.2	30.9	41	9	TA90D03Q	T. brucei	TA90D03Q
c 880	10.2	30.9	27	8	BH907088	BH907088	BH907088	c 953	10.2	30.9	41	9	CL525893	BY04451-5	CL525893
c 881	10.2	30.9	28	1	AA936125	AA936125	AA936125	c 954	10.2	30.9	42	4	BG252356	602365945	BG252356
c 882	10.2	30.9	28	1	AJ799189	AJ799189	AJ799189	c 955	10.2	30.9	42	8	AZ499983	1M0338P02	AZ499983
c 883	10.2	30.9	28	1	AZ412849	AZ412849	AZ412849	c 956	10.2	30.9	42	8	AZ579550	1M0367K02	AZ579550
c 884	10.2	30.9	28	8	AZ463714	AZ463714	AZ463714	c 957	10.2	30.9	42	8	BZ288809	SALK 0221	BZ288809
c 885	10.2	30.9	28	8	AZ840409	AZ840409	AZ840409	c 958	10.2	30.9	42	9	AL947757	Arabidops	AL947757
c 886	10.2	30.9	29	8	AZ808606	AZ808606	AZ808606	c 959	10.2	30.9	42	9	CH360039	Arabidops	CH360039
c 887	10.2	30.9	29	8	AZ871142	AZ871142	AZ871142	c 960	10.2	30.9	42	9	TA92F10Q	T. brucei	TA92F10Q
c 888	10.2	30.9	30	2	BF209105	BF209105	BF209105	c 961	10.2	30.9	43	1	AI492250	tf59a03.x	AI492250
c 889	10.2	30.9	30	4	BG772537	BG772537	BG772537	c 962	10.2	30.9	43	1	AJ660103	AJ660103	AJ660103
c 890	10.2	30.9	30	8	AZ451718	AZ451718	AZ451718	c 963	10.2	30.9	43	1	AA522067	v108H03.r	AA522067
c 891	10.2	30.9	30	8	BH740820	BH740820	BH740820	c 964	10.2	30.9	43	4	BG250039	602362124	BG250039
c 892	10.2	30.9	31	1	AI140482	AI140482	AI140482	c 965	10.2	30.9	43	4	BG259962	602371733	BG259962
c 893	10.2	30.9	31	1	BG284226	BG284226	BG284226	c 966	10.2	30.9	43	4	BI094800	EST-CD34N	BI094800
c 894	10.2	30.9	31	8	AZ844531	AZ844531	AZ844531	c 967	10.2	30.9	43	4	BI453108	603170093	BI453108
c 895	10.2	30.9	31	9	CL436258	CL436258	CL436258	c 968	10.2	30.9	43	7	H09843	Ym01D05.x1	H09843
c 896	10.2	30.9	32	4	BG545479	BG545479	BG545479	c 969	10.2	30.9	43	7	H14006	EST00032 Ch	H14006
c 897	10.2	30.9	32	9	CR397869	CR397869	CR397869	c 970	10.2	30.9	43	8	AZ789239	2M0036A23	AZ789239
c 898	10.2	30.9	32	9	CG721758	CG721758	CG721758	c 971	10.2	30.9	43	8	BH792796	SALK 0650	BH792796
c 899	10.2	30.9	32	9	AG203845	AG203845	AG203845	c 972	10.2	30.9	43	8	BH813587	SALK 0644	BH813587
c 900	10.2	30.9	33	4	BI656215	BI656215	BI656215	c 973	10.2	30.9	43	9	CL520645	DAI7F12 F	CL520645

c 974 10.2 30.9 44 8 A2347569 1M0083P11
975 10.2 30.9 44 8 A2579383 1M0363013
976 10.2 30.9 44 8 A2766302 1M0563H15
977 10.2 30.9 44 8 A2956563 2M0223B12
978 10.2 30.9 44 8 B2358244 SALK 1321
979 10.2 30.9 45 1 A1968998 w68a08.x
980 10.2 30.9 45 2 BF688559 60184873
981 10.2 30.9 45 2 AW719230 LJNESTle1
982 10.2 30.9 45 4 B1218941 G02938541
983 10.2 30.9 45 5 BX621624 BX621624
984 10.2 30.9 45 8 A2451564 1M0251801
985 10.2 30.9 45 8 A2453471 1M0254F17
986 10.2 30.9 45 8 BH810080 SALK 0406
987 10.2 30.9 45 8 BX894755 Arabidops
988 10.2 30.9 45 9 TA388A10Q
989 10.2 30.9 45 9 CL439197 PST8831-N
990 10.2 30.9 45 1 AA983189 am18b12.s
991 10.2 30.9 46 1 AA980407 ua52b05.r
992 10.2 30.9 46 1 AA137422 mq85d12.r
993 10.2 30.9 46 1 AJ673709 AJ673709
994 10.2 30.9 46 1 B1646968 603278737
995 10.2 30.9 46 4 R72707 YJ95a01.r1
996 10.2 30.9 46 7 W89968 mf64g11.r1
997 10.2 30.9 46 7 W89968
998 10.2 30.9 46 8 AZ628883 1M0481A22
999 10.2 30.9 46 8 AZ665608 1M0547G11
1000 10.2 30.9 46 8 BH895155 3526_1_33

ALIGNMENTS

RESULT 1
AA615310 50 bp mRNA linear EST 07-OCT-1997
LOCUS V001h08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:1040223 5', mRNA sequence.

ACCESSION AA615310.1 GI:2502538
VERSION V001h08.r1
KEYWORDS Mus musculus (house mouse)
SOURCE EST.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 50)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:580247
Seq primer: -28m13 rev1 ET from Amersham.

FEATURES
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1040223"
/sex="females"
/tissue type="whole skin"
/dev_stage="11 weeks old"

ORIGIN
Query Match 48.5%; Score 16; DB 1; Length 50;
Best Local Similarity 79.2%; Pred. No. 4.1e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 GCCACATGAGTGCACAGGCGTCTG 24
Db 24 GCCACATGAGTGCACAGGCTTCTG 47
sequence: 5' CTCGAGTGTGTTTTTTTTTTTTTTT 3'

RESULT 2
AUI03444/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03444 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03841, mRNA sequence.
ACCESSION AUI03444
VERSION AUI03444.1 GI:13552965
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03841"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 47.3%; Score 15.6; DB 1; Length 50;
Best Local Similarity 81.8%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 8 GAGTGGCAGGCGCTCTGGTGTAT 29
Db 39 GAGTGGCAGGCGGATGGTGT 18
sequence: 5' CTCGAGTGTGTTTTTTTTTTTTTTT 3'

RESULT 3
AUI03445/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03445 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03842, mRNA sequence.
ACCESSION AUI03445

FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03841"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 47.3%; Score 15.6; DB 1; Length 50;
Best Local Similarity 81.8%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 8 GAGTGGCAGGCGCTCTGGTGTAT 29
Db 39 GAGTGGCAGGCGGATGGTGT 18
sequence: 5' CTCGAGTGTGTTTTTTTTTTTTTTT 3'

RESULT 3
AUI03445/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03445 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03842, mRNA sequence.
ACCESSION AUI03445

FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03841"
/clone_lib="Sugano Homo sapiens cDNA library"

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VERSION AU103445.1 GI:13552966
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 47.3%; Score 15.6; DB 1; Length 50;
Best Local Similarity 81.8%; Pred No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 GAGTGGCAAGCGCTGCTGGTGT 29
Db 34 GAGTGGCAAGCGGCGATGGTGT 13

RESULT 4
AZ582580/c
LOCUS 25 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0376N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0376N05 F, genomic survey sequence.
ACCESSION AZ582580
VERSION AZ582580.1 GI:11701604
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0376 row: N column: 05
Seq primer: CGTTGTAACACGACGCCGAGT

FEATURES
source Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0376N05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (Gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.5%; Score 15; DB 8; Length 25;
Best Local Similarity 78.3%; Pred No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGGCAAGCGCTGTG 24
Db 23 CCCCATGAGCGCCAGCGCGCAG 1

RESULT 5
AU103463/c
LOCUS 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU103463 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP15715, mRNA sequence.
ACCESSION AU103463
VERSION AU103463.1 GI:13552984
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source Location/Qualifiers

```

Wed Nov 24 08:46:07 2004

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP15715"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 45.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 8 GAGTGGCAAGCGCTCTGGTGATA 30
|||||
DB 49 GAGTGGCAAGCGGCGATGGTCTTA 27
|||||

RESULT 6
AZ481987/c 36 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0306M08R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGCLM0306M08 R, genomic survey sequence.

ACCESSION AZ481987
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 36)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: M column: 08
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 36.

FEATURES

Location/Qualifiers
1. .36
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0306M08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

ORIGIN

Query Match 44.2%; Score 14.6; DB 8; Length 36;
Best Local Similarity 69.0%; Pred. No. 1.6e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 4 ACATGAGTGGCAAGCGCTCTGGTGATACC 32
|||||
DB 34 AAAAGATGAATAGTGTGTGTGACACC 6
|||||

RESULT 7
AZ329468 34 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0053B14R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGCLM0053B14 R, genomic survey sequence.

ACCESSION AZ329468
VERSION
KEYWORDS GSS.
SOURCE AZ329468.1 GI:10390209
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 34)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: B column: 14
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.

FEATURES

Location/Qualifiers
1. .34
/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGCLM0053B14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

RESULT 11	
AUI03448/c	
LOCUS	50 bp mRNA linear EST 28-JAN-2004
DEFINITION	Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION	HEP05740, mRNA sequence.
VERSION	AUI03448
KEYWORDS	AUI03448.1 GI:13552969
	EST.

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Fax: 801 585 1177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: N column: 11
Seq primer: GCTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 36.

FEATURES
source

Location/Qualifiers
1. .36
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0026N11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.4%; Score 14; DB 8; Length 36;
Best Local Similarity 77.3%; Pred. No. 2.9e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CACATGATGGCAAGCGCTCTG 24
||||| ||||| ||||| |||||
Db 1 CACATGTGTGACATGCCCTCTG 22

RESULT 13
T51935/c

LOCUS 40 bp mRNA linear EST 06-FEB-1995
DEFINITION yb28c09.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA
clone IMAGE:72496 3' similar to contains PTR7 repetitive element,
mRNA sequence.

ACCESSION T51935 GI:653795
VERSION T51935.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)

REFERENCE
AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Travaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
and Maria, M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

MEDLINE
PUBMED

8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the

FEATURES
source

IMAGE Consortium (infoimage.llnl.gov) for further information.
Seq primer: -21m13
High quality sequence stop: 41.
Location/Qualifiers
1. .40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:494161"
/db_xref="taxon:9606"
/clone="IMAGE:72496"
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene fetal spleen (#937205)"
/note="Organ: spleen; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

ORIGIN

Query Match 42.4%; Score 14; DB 7; Length 40;
Best Local Similarity 73.9%; Pred. No. 2.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGATGGCAAGCGCTCT 23
||||| ||||| ||||| |||||
Db 24 GCCACAGAGCGACATCCGCTCT 2

RESULT 14

AZ490009

LOCUS

DEFINITION 1M0322F22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0322F22 R, genomic survey sequence.

ACCESSION AZ490009 GI:10660508

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0322 row: F column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 47.

FEATURES

source

1. .47
Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0322F22"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.4%; Score 14; DB 8; Length 47;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCACATGCTGGCAAGCGTCTGGTGATAC 31
|||||
DB 17 CCACATGCTGTGAATGTGGTGACATAC 46
|||||

RESULT 15

BG489537
LOCUS 602517943F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4636427 5',
DEFINITION mRNA sequence.

ACCESSION BG489537.1 GI:13451047

VERSION BG489537

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 49)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTD/DTF/Gazdar

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM1395 row: f column: 12

High quality sequence stop: 49.

Location/Qualifiers

1..49

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4636427"

/tissue_type="large cell carcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_18"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dt priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACGAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Query Match 42.4%; Score 14; DB 4; Length 49;
Best Local Similarity 77.3%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GGCAAGCGCTCTGTGATACCG 33
|||||
DB 1 GGCTAACCGCTCTGTGATCTCG 22
|||||

RESULT 16

BF578678
LOCUS 602093151F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4207477 5',
DEFINITION mRNA sequence.

ACCESSION BF578678

VERSION BF578678.1 GI:11652299

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 45)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM9770 row: e column: 14

High quality sequence stop: 45.

Location/Qualifiers

1..45

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4207477"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 41.8%; Score 13.8; DB 2; Length 45;
Best Local Similarity 88.2%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GAGTGGCAAGCGCTCTG 24
|||||
DB 26 GGGTGGCAAGCGGCTG 42
|||||

RESULT 17

AZ664916
LOCUS 1M0545N04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0545N04 R, genomic survey sequence.

ACCESSION AZ664916

VERSION AZ664916.1 GI:11802062

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 49)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, H., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0545 row: N column: 04
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 49.

FEATURES
 Location/Qualifiers
 1..49
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0545N04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWP42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 41.8%; Score 13.8; DB 8; Length 49;
 Best Local Similarity 72.0%; Pred. No. 3.6e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CACATGAGTGGCAAGGCGTCTGGTG 27
 ||||| ||||| ||||| ||||| |||||
 Db 24 CACATGAGTGGCAAGGCGTCTGGTG 48

RESULT 18
 AA206278 50 bp mRNA linear EST 12-MAR-1998
 zq77g10.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
DEFINITION IMAGE:647682 3' similar to gb:X75042 C-REL PROTO-ONCOGENE PROTEIN (HUMAN); contains element MER4 repetitive element ;, mRNA sequence.

ACCESSION AA206278
VERSION AA206278.1 GI:1801665
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 50)

REFERENCE
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Lucca, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE WashU-NCI human EST Project

JOURNAL Unpublished (1997)

COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: polyT not found
 Insert Length: 1217 Std Error: 0.00
 Seq primer: -40M13 fwd. from Amersham
 High quality sequence stop: 1.

FEATURES
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5217934"
 /db_xref="taxon:9606"
 /clone="IMAGE:647682"
 /dev_stage="hNT neurons"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene hNT neuron (#937233)"
 /note="Vector: phluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGACGAG 3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"

ORIGIN
 Query Match 41.8%; Score 13.8; DB 1; Length 50;
 Best Local Similarity 69.2%; Pred. No. 3.6e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CACATGAGTGGCAAGGCGTCTGGTGA 28
 ||||| ||||| ||||| ||||| |||||
 Db 22 CACCTGATGTCAAGGAGTTTNAAGA 47

RESULT 19
 EX289625 50 bp DNA linear GSS 02-APR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-428G07-018097,
DEFINITION Genomic survey sequence.
ACCESSION BX289625
VERSION BX289625.1 GI:28888621
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

TITLE Weisshaar, B.
JOURNAL An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
MEDLINE flanking sequence tag-based reverse genetics
PUBMED Plant Mol. Biol. 53 (1-2), 247-259 (2003)
REFERENCE 23117147
AUTHORS 14756321
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
 Weisshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
JOURNAL mutagenized Arabidopsis thaliana lines
PUBMED Biotechniques 35 (6), 1164-1168 (2003)
REFERENCE 14682050
 4 (bases 1 to 50)
AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion close to or within gene At4g24760.
 Details on the protocols used for generation of the sequence are
 described in References 1-3. The sequences are generated at the MPI
 for Plant Breeding Research in the context of the GABI-Kat project.
 GABI-Kat is part of the German Plant Genomics program designated
 'GABI'. Information on line availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
 source
 1..50
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-428G07-018097"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /notes="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector pAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."
ORIGIN
 Query Match 41.8%; Score 13.8; DB 9; Length 50;
 Best Local Similarity 72.0%; Pred. No. 3.6e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 5 CATGACTGGCAAGGCGTCTGGTGAT 29
 ||||| | |||||
 Db 21 CATGAGCAGACGACGCGGTGGTGAT 45
 ||||| | |||||
RESULT 20
 AU105625/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU105625 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HS107037, mRNA sequence.
ACCESSION AU105625
VERSION AU105625.1 GI:13555146
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072

PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997)
FEATURES Location/Qualifiers
 source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS107037"
 /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
 Query Match 41.2%; Score 13.6; DB 1; Length 50;
 Best Local Similarity 67.9%; Pred. No. 4.4e+05;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 GCCACATGAGTGGCAAGCGCTCTGGTGA 28
 ||||| | |||||
 Db 33 GCAAAATGAGCGCGCAGAGAGTCAGGTCA 6
 ||||| | |||||
RESULT 21
 AU149869 28 bp mRNA linear EST 30-MAR-1999
LOCUS tg52f07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
DEFINITION IMAGE:2112421 3' similar to TR:Q15424 Q15424 SCAFFOLD ATTACHMENT
 FACTOR ; contains element TAR1 repetitive element ; mRNA sequence.
ACCESSION AU149869
VERSION AU149869.1 GI:4265800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 28)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 2382 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
FEATURES Location/Qualifiers
 source
 1..28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2112421"
 /lab_host="DH10B"
 /clone_lib="Soares NFL T_GBC_S1"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung Nhl19W, testis NHT, and B-cell
 NCI CGAP GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."


```

/clone="TTbA063h15"
/dev stage="tailbud (stage 28-30)"
/lab host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5' of poly A+ RNA from tailbud.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
Query Match 40.6%; Score 13.4; DB 7; Length 50;
Best Local Similarity 73.9%; Pred. No. 5.4e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGGCAAGGCGTCT 23
Db 4 GCGAGGTGAGTGACATGGCGGCT 26

RESULT 26
A1123900/c
LOCUS
DEFINITION
q78g908.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:1692926 3' similar to TR:Q14976 Q14976 PHOSPHOPROTEIN. ;,
mRNA sequence.
ACCESSION
A1123900
VERSION
A1123900.1 GI:3539666
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 34)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1692926"
/sex="unknown"
/dev stage="19 weeks"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHH19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TTTTACCATCTGAAGTGGAGCGCGCCATCTTTTTTTTTTTT 3'],
double-stranded cDNA was sized selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library was constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

ORIGIN
Query Match 40.0%; Score 13.2; DB 1; Length 34;
Best Local Similarity 69.2%; Pred. No. 6.4e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 CACATGAGTGGCAAGGCGTCTGTGTA 28

/clone="TTbA063h15"
/dev stage="tailbud (stage 28-30)"
/lab host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5' of poly A+ RNA from tailbud.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
Query Match 40.6%; Score 13.4; DB 1; Length 50;
Best Local Similarity 73.9%; Pred. No. 5.4e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CATGAGTGGCAGCGCTCTGCTG 27
Db 1 CATGCGTGGATAGTCGCTCTCTG 23

RESULT 25
CR411978
LOCUS
DEFINITION
CR411978 XGC-tailbud Xenopus tropicalis cDNA clone TTbA063h15 5',
mRNA sequence.
ACCESSION
CR411978
VERSION
CR411978.1 GI:48680225
KEYWORDS
EST.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 50)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE_ID: TTbA063h15.plkSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: SP6.
Location/Qualifiers
1. 50
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"

FEATURES
source

```

|||||

34 CCATGAGTGACTATGTGGCTAGTCA 9

RESULT 27
CF322238
LOCUS
DEFINITION
HD-13-M08.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD-13-M08, mRNA sequence.

ACCESSION
CF322238
VERSION
CF322238.1
KEYWORDS
GI:33693999
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 34)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..34
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39347"
/clone="HD-13-M08"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO, Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 40.0%; Score 13.2; DB 6; Length 34;
Best Local Similarity 69.2%; Pred. No. 6.4e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY
6 ATGAGTGGCAAGCGTCTGGTGATAC 31
|||||

Db
3 AGGAGTAGAAAGCTGTCTAACGATAC 28
|||||

RESULT 28
AZ950884
LOCUS
DEFINITION
2M0215F08F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0215F08 F, genomic survey sequence.

ACCESSION
AZ950884
VERSION
AZ950884.1
KEYWORDS
GI:13822111
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0215 row: F column: 08
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
1..34
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0215F08"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 40.0%; Score 13.2; DB 8; Length 34;
Best Local Similarity 69.2%; Pred. No. 6.4e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY
7 TGAGTGGCAAGCGTCTGGTGATACC 32
|||||

Db
7 TGGGTGGGTAGGGGAGTGCCCATACC 32
|||||

RESULT 29
AZ952864/c
LOCUS
DEFINITION
2M0217B24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0217B24 R, genomic survey sequence.

ACCESSION
AZ952864
VERSION
AZ952864.1
KEYWORDS
GI:13824091
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 46)
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 unknown library type
 Insert Length: 494 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .46
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:198935"
 /tissue_type="poorly differentiated adenocarcinoma with
 signet ring cell features"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Gas4"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

ORIGIN
 Query Match 40.0%; Score 13.2; DB 1; Length 46;
 Best Local Similarity 83.3%; Pred. No. 6.5e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 11 TGGCAAGCGCTCTGGTGA 28
 ||||| ||| |||||
 Db 22 TGGCAAGCGCGGGTGA 39

RESULT 32
 BH903159/c
 LOCUS
 DEFINITION
 SALK_102169.22.15.x Arabidopsis thaliana DNA linear GSS 04-SEP-2002
 Arabidopsis thaliana genomic clone SALK_102169.22.15.x, genomic
 survey sequence.

ACCESSION BH903159 49 bp
 VERSION BH903159.1 GI:22714308
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 49)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 AT3g21080.
 Class: TDNA tagged.
 Location/Qualifiers
 1. .49
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"

FEATURES
 source


```

CAS08717, mRNA sequence.
ACCESSION AU102478
VERSION AU102478.1 GI:13551998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Suzuki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      40.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY      8 GAGTGGCAAGCGCTCGTGATACCG 33
      ||| ||| ||| ||| ||| ||| |||
DB     34 GAGCGCAATCGGGCGGTGACGCG 9

RESULT 36
AZ611718
LOCUS AZ611718
DEFINITION IM0438B18F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC1M0438B18 F, genomic survey sequence.
ACCESSION AZ611718
VERSION AZ611718.1 GI:11733908
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
TITLE Contact: Robert B. Weiss
JOURNAL University of Utah Genome Center
COMMENT University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0438 row: B column: 18
Seq primer: CCGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source           1..23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0438B18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUC1M library"
                     /note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

```


electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 39.4%; Score 13; DB 8; Length 23;
Best Local Similarity 76.2%; Pred. No. 7.7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 13 GCAAGCGTCTGGTGATACCG 33
|||||
DB 2 GCNAGGGTTGGTGCTAGCG 22

RESULT 37
AZ828724/c

LOCUS AZ828724 28 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0105224R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105224 R, genomic survey sequence.

ACCESSION AZ828724.1 GI:12998632
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

CONTACT: Robert B. Weiss

COMMENT

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0105 row: E column: 24

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 28.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M010524"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 39.4%; Score 13; DB 8; Length 28;
Best Local Similarity 76.2%; Pred. No. 7.7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CATGAGTGGCAAGCGCTCTGG 25
|||||
DB 27 CAGGAGGGCAGGGGTAGGG 7

RESULT 38

H79914

LOCUS H79914 44 bp mRNA linear EST 09-NOV-1995
DEFINITION yul0f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
IMAGE:233407 5', similar to gb:X69532_rnal INTER-ALPHA-TRYPsin
INHIBITOR COMPLEX COMPONENT III (HUMAN);, mRNA sequence.

ACCESSION H79914.1 GI:1058003
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 44)

REFERENCE

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoso,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE

Genome Res. 6 (9), 807-828 (1996)

JOURNAL

97044478

MEDLINE

8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 2600

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 2600 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..44

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="CDB:3786584"

/db_xref="taxon:9606"

/clone="IMAGE:233407"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal liver spleen 1NFLS"

/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)

with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 468.195 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-6

Perfect score: 26
Sequence: 1 gcgaagcgctagccatgcggtta 26

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	26	6	AR054575 Sequence
2	26	100.0	26	6	AR094137 Sequence
3	26	100.0	26	6	BD181367 A method
4	26	100.0	26	6	AX147021 Sequence
5	26	100.0	26	6	AX523947 Sequence
6	26	100.0	26	6	AX524845 Sequence
7	26	100.0	30	6	AR428911 Sequence
8	26	100.0	30	6	AR488114 Sequence
9	26	100.0	30	6	AX472307 Sequence
10	26	100.0	30	6	AX696019 Sequence
11	26	100.0	30	6	AX720383 Sequence
12	26	100.0	30	6	AX720387 Sequence
13	26	100.0	30	6	AX814298 Sequence
14	26	100.0	30	6	AX814301 Sequence
15	25	96.2	28	6	AR411537 Sequence
16	25	96.2	28	6	BD000263 Oligonucleotide
17	25	96.2	37	6	CQ830529 Sequence
18	24	92.3	24	6	A68287 Sequence 8
19	24	92.3	24	6	AR054578 Sequence

20	24	92.3	24	6	BD183046	BD183046 Nucleic acid
21	24	92.3	24	6	BD183877	BD183877 Method of
22	24	92.3	24	6	BD194954	BD194954 Method of
23	24	92.3	24	6	BD195155	BD195155 Ribonucleic
24	24	92.3	24	6	I22146	I22146 Sequence 5
25	24	92.3	24	6	I26949	I26949 Sequence 17
26	24	92.3	24	6	I40301	I40301 Sequence 9
27	24	92.3	24	6	I59678	I59678 Sequence 9
28	24	92.3	24	6	I68634	I68634 Sequence 7
29	24	92.3	24	6	AR211384	AR211384 Sequence
30	24	92.3	24	6	AX003941	AX003941 Sequence
31	24	92.3	24	6	AX021563	AX021563 Sequence
32	24	92.3	24	6	AX021622	AX021622 Sequence
33	24	92.3	24	6	AX147011	AX147011 Sequence
34	24	92.3	24	6	AX250664	AX250664 Sequence
35	24	92.3	24	6	AX428908	AX428908 Sequence
36	24	92.3	24	6	AX428981	AX428981 Sequence
37	24	92.3	24	6	BD138662	BD138662 Specific
38	24	92.3	26	6	I22147	I22147 Sequence 6
39	23	88.5	24	6	AX250672	AX250672 Sequence
40	22.8	87.7	50	6	AX397945	AX397945 Sequence
41	22.8	87.7	50	6	AX397956	AX397956 Sequence
42	22	84.6	36	6	BD171241	BD171241 Method of
43	21	80.8	21	6	AR131532	AR131532 Sequence
44	21	80.8	21	6	AR144109	AR144109 Sequence
45	21	80.8	21	6	BD175037	BD175037 Method of
46	21	80.8	21	6	AR199466	AR199466 Sequence
47	21	80.8	21	6	AR200937	AR200937 Sequence
48	21	80.8	21	6	AR488699	AR488699 Sequence
49	21	80.8	21	6	AR488923	AR488923 Sequence
50	21	80.8	21	6	AX250669	AX250669 Sequence
51	21	80.8	21	6	AX419688	AX419688 Sequence
52	21	80.8	21	6	AX710908	AX710908 Sequence
53	21	80.8	21	6	BD001049	BD001049 Method of
54	21	80.8	21	6	BD001478	BD001478 Method of
55	21	80.8	21	6	BD084950	BD084950 Target and
56	21	80.8	21	6	BD102537	BD102537 Method of
57	21	80.8	25	6	AX202932	AX202932 Sequence
58	20	76.9	20	6	AR167016	AR167016 Sequence
59	20	76.9	20	6	AR210671	AR210671 Sequence
60	20	76.9	20	6	AX803706	AX803706 Sequence
61	20	76.9	20	6	BD017182	BD017182 Method of
62	20	76.9	20	6	BD095631	BD095631 Genotype
63	20	76.9	21	6	AR068468	AR068468 Sequence
64	20	76.9	21	6	AR105980	AR105980 Sequence
65	20	76.9	21	6	AR107975	AR107975 Sequence
66	20	76.9	37	6	E06353	E06353 Primer. 9/1
67	20	76.9	37	6	E06549	E06549 Primer. 9/1
68	20	76.9	40	6	E17187	E17187 Partial seq
69	20	76.9	46	6	E17191	E17191 Partial seq
70	19	73.1	19	6	A98439	A98439 Sequence 23
71	19	73.1	19	6	BD142135	BD142135 A method
72	19	73.1	21	6	E39278	E39278 Labeled pri
73	19	73.1	21	6	AX022541	AX022541 Sequence
74	19	73.1	24	6	BD171240	BD171240 Method of
75	19	73.1	30	6	AR119843	AR119843 Sequence 4
76	19	73.1	30	6	I22145	I22145 Sequence 4
77	19	73.1	33	6	AR004390	AR004390 Sequence
78	19	73.1	33	6	AR064952	AR064952 Sequence
79	19	73.1	33	6	AR097182	AR097182 Sequence
80	19	73.1	33	6	AR130680	AR130680 Sequence
81	19	73.1	33	6	AR172029	AR172029 Sequence
82	19	73.1	33	6	BD189146	BD189146 HCV Genom
83	19	73.1	33	6	BD189293	BD189293 HCV Genom
84	19	73.1	33	6	BD189440	BD189440 HCV Genom
85	19	73.1	33	6	I82865	I82865 Sequence 44
86	18	69.2	21	6	AX802838	AX802838 Sequence
87	18	69.2	21	6	AR166993	AR166993 Sequence
88	18	69.2	21	6	AR210648	AR210648 Sequence
89	18	69.2	25	6	E09661	E09661 Primer for
90	18	69.2	25	6	I93329	I93329 Sequence 3
91	18	69.2	25	6	BD105581	BD105581 Process f
92	18	69.2	28	6	AR094966	AR094966 Sequence

93	18	69.2	28	6	AR094993	AR094993 Sequence	c 166	14	53.8	30	6	AR078329	AR078329 Sequence
94	18	69.2	41	6	AX802843	AX802843 Sequence	c 167	14	53.8	30	6	I34301	I34301 Sequence
95	17	65.4	18	6	AX397926	AX397926 Sequence	c 168	14	53.8	30	6	AR337308	AR337308 Sequence
96	17	65.4	20	6	AR106338	AR106338 Sequence	c 169	14	53.8	23	6	AR171739	AR171739 Sequence
97	17	65.4	20	6	AR106355	AR106355 Sequence	c 170	13.8	53.1	23	6	A36553	A36553 Sequence
98	17	65.4	20	6	E58846	E58846 Method for	c 171	13.8	53.1	27	6	I11507	I11507 Sequence
99	17	65.4	20	6	BD004846	BD004846 Method fo	c 172	13.8	53.1	27	6	I26933	I26933 Sequence
100	17	65.4	27	6	A98434	A98434 Sequence 18	c 173	13.8	53.1	27	6	I40097	I40097 Sequence
101	17	65.4	32	6	BD141962	BD141962 Gene dete	c 174	13.8	53.1	27	6	I50072	I50072 Sequence
102	16	61.5	16	6	AR234362	AR234362 Sequence	c 175	13.8	53.1	28	6	I12136	I12136 Sequence
103	16	61.5	26	6	A39031	A39031 Sequence 3	c 176	13.8	53.1	28	6	I41306	I41306 Sequence
104	16	61.5	26	6	AR063365	AR063365 Sequence	c 177	13.8	53.1	30	6	A38380	A38380 Sequence
105	16	61.5	26	6	AR123556	AR123556 Sequence	c 178	13.8	53.1	30	6	I74383	I74383 Sequence
106	16	61.5	26	6	BD178497	BD178497 Method of	c 179	13.8	53.1	36	6	I24862	I24862 Sequence
107	16	61.5	26	6	BD182890	BD182890 Detection	c 180	13.8	53.1	36	6	I40229	I40229 Sequence
108	16	61.5	26	6	AR267297	AR267297 Sequence	c 181	13.8	53.1	36	6	I72683	I72683 Sequence
109	16	61.5	26	6	AR305707	AR305707 Sequence	c 182	13.8	53.1	37	6	AX316122	AX316122 Sequence
110	16	61.5	26	6	AX023093	AX023093 Sequence	c 183	13.8	53.1	37	6	I12111	I12111 Sequence
111	16	61.5	26	6	AX398130	AX398130 Sequence	c 184	13.8	53.1	48	6	I41281	I41281 Sequence
112	16	61.5	26	6	AX417299	AX417299 Sequence	c 185	13.8	53.1	50	6	AX199516	AX199516 Sequence
113	16	61.5	26	6	AX717178	AX717178 Sequence	c 186	13.6	52.3	30	6	BD261533	BD261533 Assays fo
114	16	61.5	32	6	BD419164	BD419164 Gene dete	c 187	13.6	52.3	38	6	AX456890	AX456890 Sequence
115	16	61.5	37	6	AX686112	AX686112 Sequence	c 188	13.6	52.3	39	6	A71961	A71961 Sequence
116	16	61.5	40	6	E06352	E06352 Primer. 9/1	c 189	13.6	52.3	39	6	AR147149	AR147149 Sequence
117	16	61.5	40	6	E06548	E06548 Primer. 9/1	c 190	13.6	52.3	39	6	AR236310	AR236310 Sequence
118	15.8	60.8	38	6	AR287165	AR287165 Sequence	c 191	13.6	52.3	41	6	AX107440	AX107440 Sequence
119	15.8	60.8	38	6	BD069830	BD069830 Transgeni	c 192	13.6	52.3	41	6	AX107451	AX107451 Sequence
120	15.8	60.8	48	6	I12113	I12113 Sequence 18	c 193	13.6	52.3	41	6	AX107461	AX107461 Sequence
121	15.8	60.8	48	6	AX021613	AX021613 Sequence	c 194	13.6	52.3	41	6	AX021614	AX021614 Sequence
122	15.6	60.0	50	6	CQ759764	CQ759764 Enzymatic	c 195	13.4	51.5	22	6	BD262493	BD262493 Informati
123	15.4	59.2	15	6	BD206412	BD206412 Enzymatic	c 196	13.4	51.5	26	6	AX037916	AX037916 Sequence
124	15	57.7	15	6	BD206413	BD206413 Enzymatic	c 197	13.4	51.5	29	6	AX766391	AX766391 Sequence
125	15	57.7	15	6	BD208261	BD208261 Enzymatic	c 198	13.4	51.5	29	6	AX766395	AX766395 Sequence
126	15	57.7	15	6	BD208262	BD208262 Enzymatic	c 199	13.4	51.5	29	6	AX766399	AX766399 Sequence
127	15	57.7	15	6	AR011616	AR011616 Sequence	c 200	13.4	51.5	38	6	AX754948	AX754948 Sequence
128	15	57.7	20	6	AR027775	AR027775 Sequence	c 201	13.4	51.5	40	6	BD013760	BD013760 Molecule
129	15	57.7	20	6	AR037909	AR037909 Sequence	c 202	13.4	51.5	44	6	BD013007	BD013007 Sequence
130	15	57.7	20	6	AR037561	AR037561 Sequence	c 203	13.4	51.5	44	6	AR022050	AR022050 Sequence
131	15	57.7	20	6	AR066317	AR066317 Sequence	c 204	13.2	50.8	33	6	I92840	I92840 Sequence
132	15	57.7	20	6	E04272	E04272 DNA encodin	c 205	13.2	50.8	36	6	AR350032	AR350032 Sequence
133	15	57.7	20	6	E07609	E07609 PCR primer	c 206	13.2	50.8	39	6	AX600090	AX600090 Sequence
134	15	57.7	20	6	E08280	E08280 PCR primer	c 207	13.2	50.8	40	6	AR166973	AR166973 Sequence
135	15	57.7	20	6	E09425	E09425 Synthetic n	c 208	13.2	50.8	40	6	AR178159	AR178159 Sequence
136	15	57.7	20	6	E10531	E10531 Y probe whi	c 209	13.2	50.8	40	6	BD016678	BD016678 Method fo
137	15	57.7	20	6	E16395	E16395 PCR primer	c 210	13.2	50.8	44	6	AR094367	AR094367 Sequence
138	15	57.7	20	6	I12602	I12602 Sequence 12	c 211	13.2	50.8	44	6	AR098581	AR098581 Sequence
139	15	57.7	20	6	I25195	I25195 Sequence 9	c 212	13.2	50.8	47	6	BD105576	BD105576 Process f
140	15	57.7	20	6	AX250623	AX250623 Sequence	c 213	13.2	50.8	22	6	AX555047	AX555047 Sequence
141	15	57.7	20	6	BD012756	BD012756 Method fo	c 214	13	50.0	23	6	AX555066	AX555066 Sequence
142	15	57.7	20	6	AR406057	AR406057 Sequence	c 215	13	50.0	23	6	AX555678	AX555678 Sequence
143	15	57.7	25	6	E06774	E06774 Primer to d	c 216	13	50.0	27	6	AR167897	AR167897 Sequence
144	15	57.7	25	6	E11710	E11710 PCR primer	c 217	13	50.0	27	6	BD231848	BD231848 Method fo
145	15	57.7	25	6	E11710	E11710 PCR primer	c 218	13	50.0	27	6	BD231970	BD231970 Modified
146	15	57.7	30	6	AX781256	AX781256 Sequence	c 219	13	50.0	27	6	AX019768	AX019768 Sequence
147	15	57.7	30	6	AX781266	AX781266 Sequence	c 220	13	50.0	27	6	AX019818	AX019818 Sequence
148	15	57.7	30	6	AX781280	AX781280 Sequence	c 221	13	50.0	27	6	AX036349	AX036349 Sequence
149	15	57.7	39	6	AX537335	AX537335 Sequence	c 222	13	50.0	28	6	A25936	A25936 Synthetic o
150	15	57.7	39	6	AX537335	AX537335 Sequence	c 223	13	50.0	30	6	BD175851	BD175851 Glucamina
151	14.6	56.2	27	6	AX024182	AX024182 Sequence	c 224	13	50.0	31	6	I24794	I24794 Sequence
152	14.6	56.2	28	6	AX829263	AX829263 Sequence	c 225	13	50.0	31	6	AR302480	AR302480 Sequence
153	14.6	56.2	32	6	BD171299	BD171299 Seven-pas	c 226	13	50.0	31	6	AR364105	AR364105 Sequence
154	14.4	55.4	24	6	I03568	I03568 Sequence 5	c 227	13	50.0	31	6	BD001952	BD001952 Transform
155	14.4	54.6	28	6	AR381016	AR381016 Sequence	c 228	13	50.0	31	6	BD266625	BD266625 Regulatio
156	14.2	54.6	28	6	BD137440	BD137440 Polymeras	c 229	13	50.0	35	6	AX047306	AX047306 Sequence
157	14.2	54.6	40	6	C0760665	C0760665 Sequence	c 230	13	50.0	36	6	AX740373	AX740373 Sequence
158	14.2	54.6	46	6	AR257024	AR257024 Sequence	c 231	13	50.0	40	6	AR053624	AR053624 Sequence
159	14	53.8	19	6	AX590323	AX590323 Sequence	c 232	13	50.0	40	6	CQ831801	CQ831801 Sequence
160	14	53.8	20	6	AR167017	AR167017 Sequence	c 233	13	50.0	40	6	AR258559	AR258559 Sequence
161	14	53.8	21	6	AX210672	AX210672 Sequence	c 234	13	50.0	42	6	I68791	I68791 Sequence
162	14	53.8	21	6	AX004407	AX004407 Sequence	c 235	13	50.0	42	6	AR253389	AR253389 Sequence
163	14	53.8	21	6	BD077113	BD077113 Hepatitis	c 236	13	50.0	42	6	AX696431	AX696431 Sequence
164	14	53.8	28	6	AR094965	AR094965 Sequence	c 237	13	50.0	42	6		
165	14	53.8	28	6	AR094992	AR094992 Sequence	c 238	13	50.0	42	6		

C 239	13	50.0	44	6	A25937	A25937 Synthetic o	C 312	12.4	47.7	41	6	AR109128	AR109128 Sequence
C 240	13	50.0	50	6	CQ005631	CQ005631 Sequence	C 313	12.4	47.7	41	6	AR200783	AR200783 Sequence
C 241	12.8	49.2	20	6	BD228435	BD228435 IL-17 hom	314	12.4	47.7	41	6	AR301117	AR301117 Sequence
C 242	12.8	49.2	20	6	AR359660	AR359660 Sequence	C 315	12.4	47.7	42	6	AR104423	AR104423 Sequence
C 243	12.8	49.2	30	6	AX455679	AX455679 Sequence	C 316	12.4	47.7	42	6	BD062183	BD062183 Bacterici
C 244	12.8	49.2	30	6	AX455680	AX455680 Sequence	C 317	12.4	47.7	42	6	AR437342	AR437342 Sequence
C 245	12.8	49.2	31	6	AX249345	AX249345 Sequence	C 318	12.4	47.7	45	6	AX367161	AX367161 Sequence
C 246	12.8	49.2	34	6	AR088320	AR088320 Sequence	319	12.4	47.7	47	6	AX378339	AX378339 Sequence
C 247	12.8	49.2	36	6	CQ803276	CQ803276 Sequence	320	12.4	47.7	48	6	AX052950	AX052950 Sequence
C 248	12.8	49.2	36	6	BD007242	BD007242 Novel flt	C 321	12.4	47.7	50	6	CQ003965	CQ003965 Sequence
C 249	12.8	49.2	36	6	BD022516	BD022516 Multi-fun	C 322	12.4	47.7	50	6	E08489	E08489 Primer. 9/1
C 250	12.8	49.2	37	6	AR194610	AR194610 Sequence	323	12.4	47.7	50	6	E08490	E08490 Primer. 9/1
C 251	12.8	49.2	37	6	AR156410	AR156410 Sequence	C 324	12.4	47.7	50	6	AR410253	AR410253 Sequence
C 252	12.8	49.2	38	6	BD263030	BD263030 Trans-Spe	C 325	12.4	47.7	50	6	AX523294	AX523294 Sequence
C 253	12.8	49.2	39	6	AX600083	AX600083 Sequence	C 326	12.4	47.7	50	12	SYN33M13L	SYN33M13L
C 254	12.6	48.5	24	6	AX289383	AX289383 Sequence	327	12.2	46.9	20	6	AR137500	AR137500 Sequence
C 255	12.6	48.5	29	6	AX683921	AX683921 Sequence	C 328	12.2	46.9	20	6	E29027	E29027 Novel colle
C 256	12.6	48.5	30	6	AR125701	AR125701 Sequence	329	12.2	46.9	20	6	E29029	E29029 Novel colle
C 257	12.6	48.5	30	6	I47113	I47113 Sequence 43	330	12.2	46.9	20	6	I31997	I31997 Sequence 8
C 258	12.6	48.5	30	6	AX611395	AX611395 Sequence	331	12.2	46.9	20	6	I32681	I32681 Sequence 8
C 259	12.6	48.5	37	6	AR028904	AR028904 Sequence	332	12.2	46.9	20	6	AX294016	AX294016 Sequence
C 260	12.6	48.5	37	6	AR070309	AR070309 Sequence	C 333	12.2	46.9	21	6	AX096296	AX096296 Sequence
C 261	12.6	48.5	37	6	E10378	E10378 Oligonucleo	334	12.2	46.9	24	6	AR350029	AR350029 Sequence
C 262	12.6	48.5	37	6	AR211464	AR211464 Sequence	C 335	12.2	46.9	25	6	BD235493	BD235493 Desaturas
C 263	12.6	48.5	38	6	AX498608	AX498608 Sequence	336	12.2	46.9	25	6	AX115408	AX115408 Sequence
C 264	12.6	48.5	38	6	AX537941	AX537941 Sequence	C 337	12.2	46.9	27	6	AR381020	AR381020 Sequence
C 265	12.6	48.5	41	6	BD217566	BD217566 Glucoamyl	C 338	12.2	46.9	27	6	BD137444	BD137444 Polymeras
C 266	12.6	48.5	41	6	AR198446	AR198446 Sequence	C 339	12.2	46.9	28	6	AX4168	AX4168 Sequence 11
C 267	12.6	48.5	49	6	E27256	E27256 4(R)-Hydrox	340	12.2	46.9	29	6	AX328144	AX328144 Sequence
C 268	12.4	47.7	14	6	AX021616	AX021616 Sequence	C 341	12.2	46.9	30	6	AR219302	AR219302 Sequence
C 269	12.4	47.7	20	6	AX297040	AX297040 Sequence	C 342	12.2	46.9	30	6	AX316118	AX316118 Sequence
C 270	12.4	47.7	24	6	A23024	A23024 oligonucleo	343	12.2	46.9	32	6	AX094808	AX094808 Sequence
C 271	12.4	47.7	24	6	I23842	I23842 Sequence 6	C 344	12.2	46.9	33	6	AR062181	AR062181 Sequence
C 272	12.4	47.7	24	6	AX292407	AX292407 Sequence	C 345	12.2	46.9	33	6	AR135159	AR135159 Sequence
C 273	12.4	47.7	25	6	A44199	A44199 Sequence 4	C 346	12.2	46.9	33	6	AX356198	AX356198 Sequence
C 274	12.4	47.7	25	6	AR020949	AR020949 Sequence	347	12.2	46.9	35	6	BD178794	BD178794 Gene pane
C 275	12.4	47.7	25	6	E15944	E15944 Primer. 7/1	348	12.2	46.9	35	6	CQ784048	CQ784048 Sequence
C 276	12.4	47.7	25	6	AR428019	AR428019 Sequence	349	12.2	46.9	35	6	AX716607	AX716607 Sequence
C 277	12.4	47.7	25	6	BD057994	BD057994 Nucleic a	350	12.2	46.9	35	6	AX750424	AX750424 Sequence
C 278	12.4	47.7	27	6	I14900	I14900 Sequence 29	351	12.2	46.9	35	6	AX837771	AX837771 Sequence
C 279	12.4	47.7	27	6	AX023915	AX023915 Sequence	352	12.2	46.9	35	6	BD127972	BD127972 Primer fo
C 280	12.4	47.7	27	6	AX537795	AX537795 Sequence	C 353	12.2	46.9	35	11	BX664502	BX664502 Arabidops
C 281	12.4	47.7	28	6	AR173071	AR173071 Sequence	354	12.2	46.9	36	6	BD179472	BD179472 Gene expr
C 282	12.4	47.7	28	6	AR173072	AR173072 Sequence	355	12.2	46.9	36	6	BD188811	BD188811 Gene exp
C 283	12.4	47.7	28	6	AR400791	AR400791 Sequence	356	12.2	46.9	36	6	CQ768249	CQ768249 Sequence
C 284	12.4	47.7	30	6	AR018082	AR018082 Sequence	357	12.2	46.9	36	6	AX551333	AX551333 Sequence
C 285	12.4	47.7	30	6	AR051922	AR051922 Sequence	C 358	12.2	46.9	36	6	AX552033	AX552033 Sequence
C 286	12.4	47.7	30	6	AR166532	AR166532 Sequence	C 359	12.2	46.9	37	6	AR473388	AR473388 Sequence
C 287	12.4	47.7	30	6	AR166533	AR166533 Sequence	C 360	12.2	46.9	37	6	BD138024	BD138024 Expressio
C 288	12.4	47.7	30	6	E03441	E03441 a primer to	C 361	12.2	46.9	38	6	CQ768250	CQ768250 Sequence
C 289	12.4	47.7	30	6	I14133	I14133 Sequence 7	C 362	12.2	46.9	38	6	AR349361	AR349361 Sequence
C 290	12.4	47.7	31	6	BD264523	BD264523 Compounds	C 363	12.2	46.9	38	6	AX551334	AX551334 Sequence
C 291	12.4	47.7	31	6	AR229334	AR229334 Sequence	C 364	12.2	46.9	38	6	AX552034	AX552034 Sequence
C 292	12.4	47.7	31	6	AR321952	AR321952 Sequence	C 365	12.2	46.9	39	6	CQ784049	CQ784049 Sequence
C 293	12.4	47.7	31	6	AX155961	AX155961 Sequence	C 366	12.2	46.9	39	6	AX716608	AX716608 Sequence
C 294	12.4	47.7	31	6	AX361811	AX361811 Sequence	C 367	12.2	46.9	39	6	AX750425	AX750425 Sequence
C 295	12.4	47.7	31	6	AX597830	AX597830 Sequence	C 368	12.2	46.9	39	6	AX754930	AX754930 Sequence
C 296	12.4	47.7	31	6	AX800166	AX800166 Sequence	C 369	12.2	46.9	39	6	AX837772	AX837772 Sequence
C 297	12.4	47.7	32	6	I58622	I58622 Sequence 8	C 370	12.2	46.9	39	6	BD127973	BD127973 Primer fo
C 298	12.4	47.7	32	6	I63520	I63520 Sequence 8	C 371	12.2	46.9	42	6	AX754928	AX754928 Sequence
C 299	12.4	47.7	33	6	A23023	A23023 oligonucleo	372	12.2	46.9	42	9	HSA224213	HSA224213 Homo sapi
C 300	12.4	47.7	33	6	AR171737	AR171737 Sequence	C 373	12.2	46.9	44	6	AR094370	AR094370 Sequence
C 301	12.4	47.7	33	6	CQ788404	CQ788404 Sequence	C 374	12.2	46.9	44	6	AR098584	AR098584 Sequence
C 302	12.4	47.7	33	6	CQ793255	CQ793255 Sequence	C 375	12.2	46.9	47	6	AR289956	AR289956 Sequence
C 303	12.4	47.7	33	6	CQ793524	CQ793524 Sequence	C 376	12.2	46.9	48	6	AR014580	AR014580 Sequence
C 304	12.4	47.7	33	6	I23841	I23841 Sequence 5	C 377	12.2	46.9	48	6	CQ775533	CQ775533 Sequence
C 305	12.4	47.7	34	6	AR301122	AR301122 Sequence	C 378	12.2	46.9	48	6	AR212171	AR212171 Sequence
C 306	12.4	47.7	35	6	A09905	A09905 Probe. 1/19	C 379	12.2	46.9	48	6	AR235382	AR235382 Sequence
C 307	12.4	47.7	38	6	AR075136	AR075136 Sequence	C 380	12.2	46.9	48	6	BD101372	BD101372 Chimeric
C 308	12.4	47.7	38	6	I40784	I40784 Sequence 11	C 381	12.2	46.9	48	6	BD135148	BD135148 Chitin-bi
C 309	12.4	47.7	39	6	CQ824334	CQ824334 Sequence	C 382	12.2	46.9	50	6	CQ003286	CQ003286 Sequence
C 310	12.4	47.7	40	6	CQ827143	CQ827143 Sequence	383	12	46.2	16	6	AR285631	AR285631 Sequence
C 311	12.4	47.7	40	6	E22422	E22422 Method for	384	12	46.2	16	6	AR397622	AR397622 Sequence

385	12	46.2	17	6	CQ622720	Sequence	458	12	46.2	30	6	AX244134	Sequence
386	12	46.2	17	6	CQ622721	Sequence	C 459	12	46.2	30	6	AX244135	Sequence
387	12	46.2	17	6	CQ622722	Sequence	C 460	12	46.2	30	6	BD058042	Nucleic a
388	12	46.2	17	6	CQ622723	Sequence	461	12	46.2	32	6	BD070090	Modified
389	12	46.2	17	6	CQ622724	Sequence	C 462	12	46.2	33	6	AR106268	Sequence
390	12	46.2	17	6	CQ622725	Sequence	463	12	46.2	33	6	AX958724	Sequence
391	12	46.2	17	6	AR463783	Sequence	C 464	12	46.2	33	6	BD008836	Sequence
392	12	46.2	17	6	AR463784	Sequence	C 465	12	46.2	34	6	AX467640	Sequence
393	12	46.2	17	6	AR463785	Sequence	466	12	46.2	35	6	AR050782	Sequence
394	12	46.2	17	6	AR463786	Sequence	467	12	46.2	35	6	E35050	Novel nucle
395	12	46.2	17	6	AR463787	Sequence	468	12	46.2	36	6	A20625	IN-Phase fu
396	12	46.2	17	6	AR463788	Sequence	469	12	46.2	36	6	E26546	DTSD1 gene
397	12	46.2	18	6	I12114	Sequence 19	C 470	12	46.2	37	6	BD268930	Anti-vira
398	12	46.2	18	6	I41284	Sequence 19	C 471	12	46.2	37	6	AR302583	Sequence
399	12	46.2	18	6	AX059438	Sequence 2	C 472	12	46.2	37	6	AX019151	Sequence
400	12	46.2	20	6	A52657	Sequence 2	C 473	12	46.2	37	6	AX035482	Sequence
401	12	46.2	20	6	AR167015	Sequence	C 474	12	46.2	37	6	AX056855	Sequence
402	12	46.2	20	6	BD185858	Sequence	475	12	46.2	37	6	AX127699	Sequence
403	12	46.2	20	6	AR210670	Sequence	C 476	12	46.2	37	6	BD130487	Antiviral
404	12	46.2	21	6	AX959816	Sequence	C 477	12	46.2	38	6	A71965	Sequence 27
405	12	46.2	22	6	I76916	Sequence 24	C 478	12	46.2	38	6	AR147153	Sequence
406	12	46.2	23	6	CQ815557	Sequence	C 479	12	46.2	38	6	AR236314	Sequence
407	12	46.2	23	6	AR400955	Sequence	C 480	12	46.2	38	6	BD009841	Avian pol
408	12	46.2	23	6	AX074114	Sequence	C 481	12	46.2	39	6	AR111241	Sequence
409	12	46.2	23	6	A42939	Sequence 9	C 482	12	46.2	39	6	BD086914	Nucleic a
410	12	46.2	24	6	CQ815555	Sequence	C 483	12	46.2	40	6	BD185268	Method fo
411	12	46.2	24	6	AR400953	Sequence	484	12	46.2	40	6	BD185271	Method fo
412	12	46.2	24	6	AX074112	Sequence	C 485	12	46.2	40	6	AX107452	Sequence
413	12	46.2	24	6	AX710123	Sequence	C 486	12	46.2	40	10	MARHV2	Woodchuck D
414	12	46.2	25	6	AR082286	Sequence	487	12	46.2	41	6	A98352	Sequence 26
415	12	46.2	25	6	AR120828	Sequence	C 488	12	46.2	41	6	CQ841202	Sequence
416	12	46.2	25	6	CQ627612	Sequence	489	12	46.2	41	6	AX107218	Sequence
417	12	46.2	25	6	CQ627613	Sequence	490	12	46.2	41	6	AX107448	Sequence
418	12	46.2	25	6	CQ627614	Sequence	491	12	46.2	41	6	AX515136	Sequence
419	12	46.2	25	6	CQ627615	Sequence	492	12	46.2	41	6	AX521344	Sequence
420	12	46.2	25	6	CQ627616	Sequence	493	12	46.2	42	6	AX107220	Sequence
421	12	46.2	25	6	CQ627617	Sequence	494	12	46.2	42	6	AX107449	Sequence
422	12	46.2	25	6	CQ627618	Sequence	495	12	46.2	43	6	I21480	Sequence 27
423	12	46.2	25	6	CQ627619	Sequence	C 496	12	46.2	43	6	AX664845	Sequence
424	12	46.2	25	6	CQ627620	Sequence	C 497	12	46.2	43	6	I08940	Sequence 3
425	12	46.2	25	6	CQ627621	Sequence	498	12	46.2	43	6	A98356	Sequence 30
426	12	46.2	25	6	CQ627622	Sequence	499	12	46.2	44	6	A98358	Sequence 32
427	12	46.2	25	6	CQ627623	Sequence	C 500	12	46.2	48	6	AR078404	Sequence
428	12	46.2	25	6	CQ627624	Sequence	501	12	46.2	48	6	BD217296	Mammalian
429	12	46.2	25	6	CQ627625	Sequence	502	12	46.2	48	6	AJ525150	Arabidops
430	12	46.2	25	6	CQ627625	Sequence	C 503	12	46.2	48	6	AXH525150	Sequence
431	12	46.2	25	6	I78332	Sequence 14	C 504	12	46.2	49	6	CQ815558	Sequence
432	12	46.2	25	6	AR468675	Sequence	C 505	12	46.2	49	6	AX400956	Sequence
433	12	46.2	25	6	AR468676	Sequence	C 506	12	46.2	50	6	CQ005630	Sequence
434	12	46.2	25	6	AR468677	Sequence	507	12	46.2	50	6	CQ008788	Sequence
435	12	46.2	25	6	AR468678	Sequence	C 508	12	46.2	50	6	CQ008807	Sequence
436	12	46.2	25	6	AR468679	Sequence	C 509	12	46.2	50	6	CQ008808	Sequence
437	12	46.2	25	6	AR468680	Sequence	C 510	11.8	45.4	18	9	S81156	T cell anti
438	12	46.2	25	6	AR468681	Sequence	511	11.8	45.4	20	6	AR109061	Sequence
439	12	46.2	25	6	AR468682	Sequence	512	11.8	45.4	20	6	BD196071	Antisense
440	12	46.2	25	6	AR468683	Sequence	513	11.8	45.4	20	6	AR200716	Sequence
441	12	46.2	25	6	AR468684	Sequence	C 514	11.8	45.4	20	6	AR311568	Sequence
442	12	46.2	25	6	AR468685	Sequence	515	11.8	45.4	20	6	AR313073	Sequence
443	12	46.2	25	6	AR468686	Sequence	516	11.8	45.4	20	6	AR382862	Sequence
444	12	46.2	25	6	AR468687	Sequence	C 517	11.8	45.4	21	6	BD013407	Method fo
445	12	46.2	25	6	AR468688	Sequence	518	11.8	45.4	22	6	A86925	Sequence 16
446	12	46.2	25	6	A21139	Oligonucleo	519	11.8	45.4	22	6	AR048337	Sequence
447	12	46.2	27	6	CQ774577	Sequence	520	11.8	45.4	22	6	AR079228	Sequence
448	12	46.2	27	6	E35051	Novel nucle	521	11.8	45.4	22	6	AR224003	Sequence
449	12	46.2	27	6	AX259721	Sequence	522	11.8	45.4	22	6	AR309659	Sequence
450	12	46.2	27	6	HUMRP20A	Sequence	523	11.8	45.4	22	6	AX376674	Sequence
451	12	46.2	29	6	BD44422	Mutants o	524	11.8	45.4	24	6	BD234631	Thymidine
452	12	46.2	30	6	BD244423	Mutants o	525	11.8	45.4	24	6	AR230227	Sequence
453	12	46.2	30	6	BD244423	Mutants o	526	11.8	45.4	25	6	CQ627159	Sequence
454	12	46.2	30	6	AX428067	Sequence	527	11.8	45.4	25	6	CQ627160	Sequence
455	12	46.2	30	6	AX027139	Sequence	528	11.8	45.4	25	6	CQ627161	Sequence
456	12	46.2	30	6	AX027140	Sequence	C 529	11.8	45.4	25	6	AR428019	Sequence
457	12	46.2	30	6	AX027140	Sequence	530	11.8	45.4	25	6	AR468222	Sequence

531	11.8	45.4	25	6	AR468223	Sequence	AR468223	Sequence	11.8	45.4	604	42	6	AR222675	Sequence
532	11.8	45.4	25	6	AR468224	Sequence	AR468224	Sequence	11.8	45.4	605	42	6	AR399762	Sequence
533	11.8	45.4	25	6	BD057994	Nucleic a	BD057994	Nucleic a	11.8	45.4	606	42	6	AR474780	Sequence
534	11.8	45.4	26	6	AR072051	Sequence	AR072051	Sequence	11.8	45.4	607	42	6	AX448991	Sequence
535	11.8	45.4	26	6	AR165219	Sequence	AR165219	Sequence	11.8	45.4	608	42	6	AX555552	Sequence
536	11.8	45.4	26	6	BD244653	Low tempe	BD244653	Low tempe	11.8	45.4	609	42	6	BD070956	Novel hum
537	11.8	45.4	26	6	AR254653	Sequence	AR254653	Sequence	11.8	45.4	610	43	6	AR034922	Sequence
538	11.8	45.4	26	6	AR343261	Sequence	AR343261	Sequence	11.8	45.4	611	44	6	CQ760661	Sequence
539	11.8	45.4	26	6	AR455528	Sequence	AR455528	Sequence	11.8	45.4	612	44	6	AX427216	Sequence
540	11.8	45.4	26	6	AR224994	Sequence	AR224994	Sequence	11.8	45.4	613	46	6	AR175600	Sequence
541	11.8	45.4	27	6	AL7048	oligonucleo	AL7048	oligonucleo	11.8	45.4	614	47	6	AR289222	Sequence
542	11.8	45.4	27	6	AL7448	oligonucleo	AL7448	oligonucleo	11.8	45.4	615	47	6	AR291247	Sequence
543	11.8	45.4	27	6	AR014423	Sequence	AR014423	Sequence	11.8	45.4	616	47	6	AR291871	Sequence
544	11.8	45.4	27	6	AR137130	Sequence	AR137130	Sequence	11.8	45.4	617	48	6	AX777183	Sequence
545	11.8	45.4	27	6	AR140406	Sequence	AR140406	Sequence	11.8	45.4	618	48	6	AX927790	Sequence
546	11.8	45.4	27	6	IL1866	Sequence 32	IL1866	Sequence 32	11.8	45.4	619	48	8	AJ718213	Nicotiana
547	11.8	45.4	27	6	AR277649	Sequence	AR277649	Sequence	11.8	45.4	620	49	6	AR011811	Sequence
548	11.8	45.4	27	6	BD131033	Plant-ori	BD131033	Plant-ori	11.8	45.4	621	49	6	AR129029	Sequence
549	11.8	45.4	28	6	AX591059	Sequence	AX591059	Sequence	11.8	45.4	622	49	6	BD433380	Nucleic a
550	11.8	45.4	28	6	AX712098	Sequence	AX712098	Sequence	11.8	45.4	623	49	6	I77134	Sequence 6
551	11.8	45.4	29	6	AX075128	Sequence	AX075128	Sequence	11.8	45.4	624	49	6	AR239789	Sequence
552	11.8	45.4	29	6	AX098923	Sequence	AX098923	Sequence	11.8	45.4	625	49	6	AX279591	Sequence
553	11.8	45.4	29	6	AX099343	Sequence	AX099343	Sequence	11.8	45.4	626	50	6	CQ004071	Sequence
554	11.8	45.4	29	6	AX275252	Sequence	AX275252	Sequence	11.8	45.4	627	50	6	CQ798735	Sequence
555	11.8	45.4	29	6	AX598462	Sequence	AX598462	Sequence	11.8	45.4	628	50	6	AR356569	Sequence
556	11.8	45.4	30	6	I79319	Sequence 22	I79319	Sequence 22	11.8	45.4	629	50	6	AR381687	Sequence
557	11.8	45.4	31	6	AR084215	Sequence	AR084215	Sequence	11.8	45.4	630	50	6	AR381689	Sequence
558	11.8	45.4	31	6	AR171738	Sequence	AR171738	Sequence	11.8	45.4	631	50	6	AX395198	Sequence
559	11.8	45.4	31	6	I90358	Sequence 2	I90358	Sequence 2	11.8	45.4	632	50	6	AX395201	Sequence
560	11.8	45.4	31	6	BD002681	Gene comp	BD002681	Gene comp	11.8	45.4	633	50	6	BD070868	Insect ex
561	11.8	45.4	32	6	BD211474	Adenovira	BD211474	Adenovira	11.6	44.6	634	18	6	BD274782	CANCER CE
562	11.8	45.4	32	6	AR430574	Sequence	AR430574	Sequence	11.6	44.6	635	18	6	AR205248	Sequence
563	11.8	45.4	32	6	AX073434	Sequence	AX073434	Sequence	11.6	44.6	636	19	6	AX138863	Sequence
564	11.8	45.4	33	6	AR368978	Sequence	AR368978	Sequence	11.6	44.6	637	20	6	AX138863	Sequence
565	11.8	45.4	33	6	AR409609	Sequence	AR409609	Sequence	11.6	44.6	638	20	6	AX293770	Sequence
566	11.8	45.4	33	6	AX081230	Sequence	AX081230	Sequence	11.6	44.6	639	20	6	BD015558	Novel pol
567	11.8	45.4	33	6	AX675239	Sequence	AX675239	Sequence	11.6	44.6	640	21	6	E38282	Modified se
568	11.8	45.4	33	6	BD011010	Hiv probe	BD011010	Hiv probe	11.6	44.6	641	22	6	AX343843	Sequence
569	11.8	45.4	35	6	AX39869	Sequence 3	AX39869	Sequence 3	11.6	44.6	642	23	6	AR363348	Sequence
570	11.8	45.4	35	6	A69029	Sequence 17	A69029	Sequence 17	11.6	44.6	643	24	6	AX289137	Sequence
571	11.8	45.4	35	6	AR171740	Sequence	AR171740	Sequence	11.6	44.6	644	24	6	AX444840	Sequence
572	11.8	45.4	35	6	BD211475	Adenovira	BD211475	Adenovira	11.6	44.6	645	24	6	AX937076	Sequence
573	11.8	45.4	35	6	AR193479	Sequence	AR193479	Sequence	11.6	44.6	646	25	6	AX951934	Sequence
574	11.8	45.4	35	6	AX073435	Sequence	AX073435	Sequence	11.6	44.6	647	25	6	AR007404	Sequence
575	11.8	45.4	35	6	BD006106	Feline po	BD006106	Feline po	11.6	44.6	648	25	6	AR007407	Sequence
576	11.8	45.4	36	6	AR119928	Sequence	AR119928	Sequence	11.6	44.6	649	25	6	BD177988	Acylated
577	11.8	45.4	36	6	CQ803276	Sequence	CQ803276	Sequence	11.6	44.6	650	25	6	BD177991	Acylated
578	11.8	45.4	36	6	BD006745	Novel pol	BD006745	Novel pol	11.6	44.6	651	25	6	AX487732	Sequence
579	11.8	45.4	36	6	BD078872	Tumor pro	BD078872	Tumor pro	11.6	44.6	652	26	6	A83432	Sequence 18
580	11.8	45.4	38	6	AR106214	Sequence	AR106214	Sequence	11.6	44.6	653	26	6	CQ778371	Sequence
581	11.8	45.4	38	6	AR178180	Sequence	AR178180	Sequence	11.6	44.6	654	27	6	AR105799	Sequence
582	11.8	45.4	38	6	BD235325	Enzyme fo	BD235325	Enzyme fo	11.6	44.6	655	27	6	AR280223	Sequence
583	11.8	45.4	38	6	AR336455	Sequence	AR336455	Sequence	11.6	44.6	656	27	6	AX081590	Sequence
584	11.8	45.4	38	6	AR473662	Sequence	AR473662	Sequence	11.6	44.6	657	27	6	AX374771	Sequence
585	11.8	45.4	38	6	AX219576	Sequence	AX219576	Sequence	11.6	44.6	658	28	6	A05814	Oligonucleo
586	11.8	45.4	39	6	AR361446	Sequence	AR361446	Sequence	11.6	44.6	659	28	6	I07809	Sequence 5
587	11.8	45.4	39	6	AR361467	Sequence	AR361467	Sequence	11.6	44.6	660	28	6	AX023918	Sequence
588	11.8	45.4	39	6	AX058342	Sequence	AX058342	Sequence	11.6	44.6	661	29	6	AR363828	Sequence
589	11.8	45.4	39	6	AX058364	Sequence	AX058364	Sequence	11.6	44.6	662	30	6	AR118762	Sequence
590	11.8	45.4	39	6	AX062302	Sequence	AX062302	Sequence	11.6	44.6	663	30	6	BD262240	Informati
591	11.8	45.4	40	6	AR146102	Sequence	AR146102	Sequence	11.6	44.6	664	30	6	I06394	Sequence 14
592	11.8	45.4	40	6	BD226390	Neisseria	BD226390	Neisseria	11.6	44.6	665	30	6	AR308733	Sequence
593	11.8	45.4	40	6	CQ771869	Sequence	CQ771869	Sequence	11.6	44.6	666	30	6	AX037663	Sequence
594	11.8	45.4	40	6	AR228736	Sequence	AR228736	Sequence	11.6	44.6	667	30	6	AX298214	Sequence
595	11.8	45.4	40	6	AR476110	Sequence	AR476110	Sequence	11.6	44.6	668	30	6	AX460252	Sequence
596	11.8	45.4	42	6	AR044709	Sequence	AR044709	Sequence	11.6	44.6	669	31	6	A05813	Oligonucleo
597	11.8	45.4	42	6	AR052356	Sequence	AR052356	Sequence	11.6	44.6	670	32	6	AX452011	Sequence
598	11.8	45.4	42	6	AR055154	Sequence	AR055154	Sequence	11.6	44.6	671	32	6	AX538800	Sequence
599	11.8	45.4	42	6	AR089670	Sequence	AR089670	Sequence	11.6	44.6	672	32	6	BD022405	Multi-fun
600	11.8	45.4	42	6	AR158025	Sequence	AR158025	Sequence	11.6	44.6	673	33	6	AX280474	Sequence
601	11.8	45.4	42	6	I13542	Sequence 27	I13542	Sequence 27	11.6	44.6	674	35	6	AR212155	Sequence
602	11.8	45.4	42	6	I15801	Sequence 27	I15801	Sequence 27	11.6	44.6	675	35	6	BD135132	Chitin bi
603	11.8	45.4	42	6	I92505	Sequence 27	I92505	Sequence 27	11.6	44.6	676	36	6	A68640	Sequence 8

C 677	11.6	44.6	36	6	AR048679	Sequence	750	11.4	43.8	25	6	AR468220	Sequence
C 678	11.6	44.6	36	6	AR214446	Sequence	751	11.4	43.8	25	6	AR468221	Sequence
C 679	11.6	44.6	36	6	AR12296	Sequence	C 752	11.4	43.8	25	6	AX119661	Sequence
C 680	11.6	44.6	36	6	AR492783	Sequence	C 753	11.4	43.8	25	6	AX268940	Sequence
C 681	11.6	44.6	36	6	BD070096	Modified	C 754	11.4	43.8	25	6	AX305191	Sequence
C 682	11.6	44.6	37	6	AS9306	Sequence 6	C 755	11.4	43.8	25	6	AX447595	Sequence
C 683	11.6	44.6	37	6	AX063383	Sequence	756	11.4	43.8	25	6	AX688910	Sequence
C 684	11.6	44.6	38	6	AR305250	Sequence	757	11.4	43.8	25	6	AX688911	Sequence
C 685	11.6	44.6	38	6	AR309354	Sequence	758	11.4	43.8	25	6	AX688912	Sequence
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C 687	11.6	44.6	39	6	AR122257	Sequence	760	11.4	43.8	25	6	AX688914	Sequence
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C 689	11.6	44.6	39	6	AR301046	Sequence	C 762	11.4	43.8	25	6	BD075788	G protein
C 690	11.6	44.6	39	6	AX600082	Sequence	C 763	11.4	43.8	25	6	BD106039	Novel LDL
C 691	11.6	44.6	41	6	AR600087	Sequence	764	11.4	43.8	25	6	AR087901	Sequence
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C 693	11.6	44.6	41	6	AR141189	Sequence	766	11.4	43.8	25	6	I80119	Sequence 8
C 694	11.6	44.6	41	6	AR154917	Sequence	767	11.4	43.8	25	6	I80145	Sequence 34
C 695	11.6	44.6	42	6	AR139460	Sequence	768	11.4	43.8	25	6	AX300582	Sequence
C 696	11.6	44.6	42	6	E22566	Process for	C 769	11.4	43.8	25	6	AR112688	Sequence
C 697	11.6	44.6	42	6	E25724	Method for	770	11.4	43.8	25	6	E00584	DNA encodin
C 698	11.6	44.6	42	6	AX202530	Sequence	771	11.4	43.8	25	6	I07895	Sequence 3
C 699	11.6	44.6	42	6	BD092982	A primer	772	11.4	43.8	25	6	AR252343	Sequence
C 700	11.6	44.6	43	6	A73753	Sequence 2	773	11.4	43.8	25	6	AR473616	Sequence
C 701	11.6	44.6	43	6	AR059885	Sequence	C 774	11.4	43.8	25	6	AX544271	Sequence
C 702	11.6	44.6	43	6	AR059885	Sequence	775	11.4	43.8	25	6	A49272	Sequence 2
C 703	11.6	44.6	44	6	AR146157	Sequence	776	11.4	43.8	25	6	AR122136	Sequence
C 704	11.6	44.6	44	6	AR146157	Sequence	C 777	11.4	43.8	25	6	AR206959	Sequence
C 705	11.6	44.6	44	6	AX026431	Sequence	778	11.4	43.8	25	6	BD107720	Tissue pl
C 706	11.6	44.6	44	6	AX026431	Sequence	C 779	11.4	43.8	25	6	CQ788604	Sequence
C 707	11.6	44.6	44	6	AX057956	Sequence	C 780	11.4	43.8	25	6	AX060666	Sequence
C 708	11.6	44.6	44	6	AR242018	Sequence	781	11.4	43.8	25	6	BD184121	Method an
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ALIGNMENTS

RESULT 1
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LOCUS Sequence 1 from patent US 5837442.
DEFINITION AR054575
ACCESSION AR054575
VERSION AR054575.1 GI:5980152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Tsang,S.Yen.
TITLE Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL Patent: US 5837442-A 1 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..26
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Best Local Similarity 100.0%; Pred. No. 0.091;
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RESULT 2
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LOCUS Sequence 3 from patent US 6001611.
DEFINITION AR094137
ACCESSION AR094137
VERSION AR094137.1 GI:10020882
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Will,S.Gordon.
TITLE Modified nucleic acid amplification primers
JOURNAL Patent: US 6001611-A 3 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..26
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS A method for determination of a nucleic acid using a control.
DEFINITION BD181367
ACCESSION BD181367
VERSION JP 2002335981-A/6.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 6 26-NOV-2002;
COMMENT F HOFFMANN LA ROCHE AG
OS Artificial Sequence
PN JP 2002335981-A/6
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/53,G01N33/566,G01N33/58,
C12N15/00
CC Description of Artificial Sequence: ST280 HCV-specific Primer-
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FH Key Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
AX147021 26 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 15 from Patent WO0137291.
DEFINITION AX147021
ACCESSION AX147021
VERSION AX147021.1 GI:14346292
KEYWORDS

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SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Weindel,K., Riedling,M. and Geiger,A.
TITLE        Magnetic glass particles, method for their preparation and uses
JOURNAL      Patent: WO 0137291-A 15 25-MAY-2001;
              Roche Diagnostics GmbH (DE)
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RESULT 5
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DEFINITION     Sequence 6 from Patent EP1236804.
ACCESSION      AX523947
VERSION        AX523947.1 GI:25168878
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE       1
AUTHORS         Jaeger,S.
TITLE          A method for determination of a nucleic acid using a control
JOURNAL        Patent: EP 1236804-A 6 04-SEP-2002;
              Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES       source
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Query Match      100.0%; Score 26; DB 6; Length 26;
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RESULT 6
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DEFINITION     Sequence 6 from Patent EP1236805.
ACCESSION      AX524845
VERSION        AX524845.1 GI:25169939
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE       1
AUTHORS         Jaeger,S.

SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Weindel,K., Riedling,M. and Geiger,A.
TITLE        Magnetic glass particles, method for their preparation and uses
JOURNAL      Patent: WO 0137291-A 15 25-MAY-2001;
              Roche Diagnostics GmbH (DE)
FEATURES     source
              1..26
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic oligonucleotide primer (HCV forward)"
modified_base 26
              /note="derivatization with a p-(t-butyl)benzyl-residue"
              /mod_base=OTHER

ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 7
AR428911
LOCUS          AR428911                30 bp      DNA          linear          PAT 18-DEC-2003
DEFINITION     Sequence 1 from patent US 6642204.
ACCESSION      AR428911
VERSION        AR428911.1 GI:40188742
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE       1 (bases 1 to 30)
AUTHORS         Llinas-Brunet,M. and Gorys,V.J.
TITLE          Hepatitis C inhibitor tri-peptides
JOURNAL        Patent: US 6642204-A 1 04-NOV-2003;
              Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES       source
              1..30
              /organism="unknown"
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ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 8
AR488114
LOCUS          AR488114                30 bp      DNA          linear          PAT 15-MAY-2004
DEFINITION     Sequence 17 from patent US 6706874.
ACCESSION      AR488114
VERSION        AR488114.1 GI:47253862
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE       1 (bases 1 to 30)
AUTHORS         Kukolj,G. and Pause,A.
TITLE          Self-replicating RNA molecule from hepatitis C virus
JOURNAL        Patent: US 6706874-A 17 16-MAR-2004;
              Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES       source
              1..30
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 9
AR488114
LOCUS          AR488114                30 bp      DNA          linear          PAT 15-MAY-2004
DEFINITION     Sequence 17 from patent US 6706874.
ACCESSION      AR488114
VERSION        AR488114.1 GI:47253862
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE       1 (bases 1 to 30)
AUTHORS         Kukolj,G. and Pause,A.
TITLE          Self-replicating RNA molecule from hepatitis C virus
JOURNAL        Patent: US 6706874-A 17 16-MAR-2004;
              Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES       source
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              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

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QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
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Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 9
AX472307
LOCUS AX472307 30 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 17 from Patent WO02052015.
ACCESSION AX472307
VERSION AX472307.1 GI:22207326
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Beaulieu, P.L., Fazal, G., Kukolj, G., Jolicoeur, E., Gillard, J.,
TITLE Viral polymerase inhibitors
JOURNAL Poupart, M.A. and Rancourt, J.
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source 1..30
note="Forward Primer"
ORIGIN
Query Match 100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 10
AX696019
LOCUS AX696019 30 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2 from Patent WO03007945.
ACCESSION AX696019
VERSION AX696019.1 GI:29419181
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Beaulieu, P.L., Fazal, G., Goulet, S., Kukolj, G., Poirier, M. and
TITLE Viral polymerase inhibitors
JOURNAL Tsantrizos, Y.S.
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source 1..30
note="Forward Primer"
ORIGIN
Query Match 100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 11
AX720383
LOCUS AX720383 30 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 2 from Patent WO03010140.
ACCESSION AX720383
VERSION AX720383.1 GI:29892202
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Beaulieu, P.L., Fazal, G., Kukolj, G., Jolicoeur, E., Gillard, J.,
TITLE Viral polymerase inhibitors
JOURNAL Poupart, M.A. and Rancourt, J.
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source 1..30
note="Forward Primer"
ORIGIN
Query Match 100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 12
AX720387
LOCUS AX720387 30 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 2 from Patent WO03010141.
ACCESSION AX720387
VERSION AX720387.1 GI:29892207
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Beaulieu, P.L., Fazal, G., Goulet, S., Kukolj, G., Poirier, M.,
TITLE Viral polymerase inhibitors
JOURNAL Tsantrizos, Y.S., Jolicoeur, E., Gillard, J., Poupart, M.A. and
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source 1..30
note="Forward Primer"
ORIGIN
Query Match 100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 13
AX814298
LOCUS AX814298 30 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 1 from Patent WO03064455.
ACCESSION AX814298
VERSION AX814298.1 GI:39103539
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

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artificial sequences.
1
REFERENCE
AUTHORS      Llinas-Brunet,M. and Gorys,V.J.
TITLE        Macrocyclic peptides active against the hepatitis c virus
JOURNAL      Patent: WO 03064455-A 1 07-AUG-2003;
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source      Location/Qualifiers
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Forward primer"

ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
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Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 14
AX814301
LOCUS          AX814301          30 bp      DNA          linear          PAT 05-DEC-2003
DEFINITION     Sequence 1 from Patent WO03064456.
ACCESSION      AX814301
VERSION        AX814301.1 GI:39103542
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.

REFERENCE
AUTHORS      Llinas-Brunet,M. and Gorys,V.J.
TITLE        Tripeptides having a hydroxyproline ether of a substituted
              quinoline for the inhibition of ns3 (hepatitis c)
JOURNAL      Patent: WO 03064456-A 1 07-AUG-2003;
              Boehringer Ingelheim International GmbH (DE)
FEATURES
source      Location/Qualifiers
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Forward primer"

ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 15
AR411537
LOCUS          AR411537          28 bp      DNA          linear          PAT 18-DEC-2003
DEFINITION     Sequence 1 from patent US 6638714.
ACCESSION      AR411537
VERSION        AR411537.1 GI:40163881
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.

REFERENCE
AUTHORS      Llinas,J.M. and Gorman,K.M.
TITLE        Oligonucleotide primers for efficient detection of hepatitis C
              virus (HCV) and methods of use thereof
JOURNAL      Patent: US 6638714-A 1 28-OCT-2003;
              Location/Qualifiers
FEATURES
source      1. .28

artificial sequences.
1
REFERENCE
AUTHORS      Llinas-Brunet,M. and Gorman,K.M.
TITLE        Oligonucleotide primers for efficient detection of hepatitis C
              virus (HCV) and methods of use thereof
JOURNAL      Patent: JP 2000279200-A 1 10-OCT-2000;
              ORTHO CLINICAL DIAGNOSTICS INC
COMMENT       OS Artificial Sequence
              PN JP 2000279200-A/1
              PD 10-OCT-2000
              PF 03-FEB-2000 JP 2000032656
              PR 03-FEB-1999 US 60/118497
              PI JEFFREY M LYNNEN,KEVIN M GORMAN
              PC C12Q1/68;C12N15/09/(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
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FEATURES
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Query Match      96.2%; Score 25; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
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Db 1 CAGAAAGCGTCTAGCCATGGCGTTA 25

RESULT 16
BD000263
LOCUS          BD000263          28 bp      DNA          linear          PAT 31-JAN-2002
DEFINITION     Oligonucleotide primers for efficient detection of hepatitis C
              virus (HCV) and methods of use thereof.
ACCESSION      BD000263
VERSION        BD000263.1 GI:18623342
KEYWORDS       JP 2000279200-A/1.
SOURCE         synthetic construct
ORGANISM       synthetic construct
              artificial sequences.
              1 (bases 1 to 28)
              Lynen,J.M. and Gorman,K.M.
              Oligonucleotide primers for efficient detection of hepatitis C
              virus (HCV) and methods of use thereof
              Patent: JP 2000279200-A 1 10-OCT-2000;
              ORTHO CLINICAL DIAGNOSTICS INC
              OS Artificial Sequence
              PN JP 2000279200-A/1
              PD 10-OCT-2000
              PF 03-FEB-2000 JP 2000032656
              PR 03-FEB-1999 US 60/118497
              PI JEFFREY M LYNNEN,KEVIN M GORMAN
              PC C12Q1/68;C12N15/09/(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
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              CC
              FH Key
              FT source
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FEATURES
source      Location/Qualifiers
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ORIGIN
Query Match      96.2%; Score 25; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 1 CAGAAAGCGTCTAGCCATGGCGTTA 25

RESULT 17
CQ830529
LOCUS          CQ830529          37 bp      DNA          linear          PAT 12-JUL-2004
DEFINITION     Sequence 3 from Patent WO2004055210.
ACCESSION      CQ830529
VERSION        CQ830529.1 GI:50250862
KEYWORDS       synthetic construct
SOURCE         synthetic construct
              artificial sequences.
              1
              Balakireva,L.
              Molecules inhibiting hepatitis c virus protein synthesis and method
              for screening same
              Patent: WO 2004055210-A 3 01-JUL-2004;

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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QY	1	GCAGAAAGCGTCTAGCCATGGCGT	24																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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EBERHARD RUSSMANN, THOMAS MAIER, RAINER SCHMUCK, JOHNNY STABEELS, PI
UWE WEHNES
PC C12Q1/37, C12N9/54, C12N15/09, C12N15/09, C12Q1/68//C12N9/54, PC
C12R1/07),
PC C12N15/00, C12N15/00
CC Method for analyzing non-protein component
using protease from
CC bacillus
CC strain Location/Qualifiers
FH Key 1..24
FT source /organism='Hepatitis virus (hepatitis C FT
virus)'
FT Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

FEATURES
source
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 22
BD194954
LOCUS 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of specifically and highly sensitively detecting nucleic
acid.
ACCESSION BD194954
VERSION BD194954.1 GI:33004707
KEYWORDS JP 2002509694-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler, C., Harverhuizen, G., Bartl, K. and Orumu, H.
TITLE Method of specifically and highly sensitively detecting nucleic
acid
JOURNAL Patent: JP 2002509694-A 1 02-APR-2002;
COMMENT ROCHE DIAGNOSTICS GMBH
OS Unidentified
PN JP 2002509694-A/1
PD 02-APR-2002
PF 03-NOV-1998 JP 2000519104
PR 04-NOV-1997 DE 197 48 690.8, 28-MAR-1998 DE 198 14 001.0 PR
02-APR-1998 DE 198 14 828.3
PI CHRISTOPHE KESSLER, GERU TO HARVERHUIZEN, KNUD BARTL, HENRICK PI
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PC C12Q1/68//C12N15/09, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Method of specifically and highly sensitively detecting CC
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DEFINITION Ribonuclease resistant RNA preparation and utilization.
ACCESSION BD195155
VERSION BD195155.1 GI:33004915
KEYWORDS JP 2002514905-A/7.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dubois, D.B., Winkler, M.M., Pasloske, B.L. and Brown, D.
TITLE Ribonuclease resistant RNA preparation and utilization
JOURNAL Patent: JP 2002514905-A 7 21-MAY-2002;
COMMENT AMBION INC, CENETRON DIAGNOSTICS LLC
OS Unidentified
PN JP 2002514905-A/7
PD 21-MAY-2002
PF 02-JUL-1997 JP 1998504527
PR 03-JUL-1996 US 08/675153, 03-JUL-1996 US 60/021145 PR
24-JUN-1997 US 08/881571
PI DWIGHT B DUBOIS, MATTHEW M WINKLER, BRITTAN L PASLOSKE, DAVID PI
BROWN
PC C12N15/40, C12N15/48, C12N15/51, C12N15/10, C12N15/88, C12N7/04, PC
C12Q1/68,
PC C12Q1/70, C12P19/34
CC Strandedness: Single;
CC Topology: Linear;
CC Ribonuclease resistant RNA preparation and utilization FH
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DEFINITION Sequence 5 from patent US 5527669.
ACCESSION I22146
VERSION I22146.1 GI:1602500
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Resnick, R.M. and Young, K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel
variants
JOURNAL Patent: US 5527669-A 5 18-JUN-1996;
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LOCUS 24 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 17 from patent US 5561058.
ACCESSION 126949
VERSION 126949.1 GI:1606819
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gelfand,D.H., Myers,T.W. and Sigua,C.L.
TITLE Methods for coupled high temperatures reverse transcription and polymerase chain reactions
JOURNAL Patent: US 5561058-A 17 01-OCT-1996;
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DEFINITION Sequence 9 from patent US 5620852.
ACCESSION 140301
VERSION 140301.1 GI:2082593
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lin,L., Cimino,G. and Zhu,Y.S.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5620852-A 9 15-APR-1997;
FEATURES Location/Qualifiers
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LOCUS 24 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 9 from patent US 5654179.

ACCESSION I59678
VERSION I59678.1 GI:2478310
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lin,L.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5654179-A 9 05-AUG-1997;
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ACCESSION 168634
VERSION 168634.1 GI:2830756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS DuBois,D.B., Winkler,M.M. and Pasloske,B.L.
TITLE Ribonuclease resistant viral RNA standards
JOURNAL Patent: US 5677124-A 7 14-OCT-1997;
FEATURES Location/Qualifiers
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DEFINITION Sequence 7 from patent US 6399307.
ACCESSION AR211384
VERSION AR211384.1 GI:21514692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Pasloske,B.L., DuBois,D.B., Brown,D.M. and Winkler,M.M.
TITLE Methods of quantifying viral load in an animal with a ribonuclease resistant RNA preparation
JOURNAL Patent: US 6399307-A 7 04-JUN-2002;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

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6

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 26)
AUTHORS Resnick, R.M. and Young, K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel variants

JOURNAL
PATENT: US 5527669-A 6 18-JUN-1996;
FEATURES Location/Qualifiers
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ACCESSION AX250672
VERSION AX250672.1 GI:15984416
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Kneteman, N.M., Tyrrell, L.D. and Mercer, D.F.
TITLE Chimeric animal model susceptible to human hepatitis C virus infection

JOURNAL
PATENT: WO 0167854-A 5 20-SEP-2001;
Kneteman, Norman M. (CA) ; Tyrrell, Lorne D. (CA) ; Mercer, David F. (CA)

FEATURES Location/Qualifiers
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DEFINITION Sequence 23 from Patent WO0220054.
ACCESSION AX397945
VERSION AX397945.1 GI:21260802
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS Thomas, H.C., Taylor-Robinson, S.D., Karayiannis, P. and Forton, D.M.
TITLE Methods of treatment and diagnosis of HCV infection in CNS based on magnetic resonance spectroscopy

JOURNAL Patent: WO 0220054-A 23 14-MAR-2002;
IMPERIAL COLLEGE OF SCIENCE, TECHNOLOGY AND MEDICINE (GB)
FEATURES Location/Qualifiers
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 1000 summaries

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77	19	73.1	19	10	ADF52213	ADF52213 Hepatitis
78	19	73.1	19	10	ADF52205	ADF52205 Hepatitis
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85	19	73.1	19	10	ADF52221	ADF52221 Hepatitis
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87	19	73.1	19	10	ADF51509	ADF51509 Hepatitis
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92	19	73.1	27	4	AAZ23734	AAZ23734 plus sens
93	19	73.1	27	10	ADD67934	ADD67934 Hepatitis
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C 103	19	73.1	40	9	ACF04205	Hepatitis	
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C 108	18	69.2	19	10	ADF52217	Hepatitis	
C 109	18	69.2	19	10	ADF52211	Hepatitis	
C 110	18	69.2	20	8	ABT15972	HCV varia	
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C 112	18	69.2	25	2	AAQ98273	Hepatitis	
C 113	18	69.2	25	4	ABAQ3380	Bovine vi	
C 114	18	69.2	28	2	AAQ05214	Hepatitis	
C 115	18	69.2	28	2	AAQ05241	Hepatitis	
C 116	18	69.2	28	3	AAZ57750	Hepatitis	
C 117	18	69.2	28	3	AAZ57781	Hepatitis	
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C 119	18	69.2	32	12	ADQ05659	HCV DNA f	
C 120	17	65.4	17	8	ACD65857	HCV minus	
C 121	17	65.4	17	8	ACD65858	HCV minus	
C 122	17	65.4	17	8	ACD56818	HCV DNazY	
C 123	17	65.4	17	8	ACD56819	HCV DNazY	
C 124	17	65.4	17	8	ACD65856	HCV minus	
C 125	17	65.4	17	8	ACD56820	HCV DNazY	
C 126	17	65.4	17	10	AD118588	RT-PCR pr	
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C 131	17	65.4	17	12	AD187295	HCV DNazY	
C 132	17	65.4	17	12	AD187294	HCV DNazY	
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C 143	17	65.4	32	6	ABL50817	INT-1-A p	
C 144	17	65.4	47	12	ADP87770	Extended	
C 145	16	61.5	16	2	AAQ90599	Hepatitis	
C 146	16	61.5	16	3	AAQ13416	Hepatitis	
C 147	16	61.5	16	8	ABX74335	Hepatitis	
C 148	16	61.5	17	8	ACD65855	HCV minus	
C 149	16	61.5	17	8	ACD56817	HCV DNazY	
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C 153	16	61.5	19	10	ADF52212	Hepatitis	
C 154	16	61.5	19	10	ADF51537	Hepatitis	
C 155	16	61.5	19	10	ADF51516	Hepatitis	
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C 158	16	61.5	22	4	AAH44911	HCV speci	
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c 169	15.4	59.2	35	9	ABT444831
170	15	57.7	15	3	AAZ618134
171	15	57.7	15	3	AAZ633683
172	15	57.7	15	3	AAZ633684
173	15	57.7	15	3	AAZ618135
174	15	57.7	15	6	ABX002240
175	15	57.7	15	6	ABX003376
176	15	57.7	15	6	ABX011798
177	15	57.7	15	6	ABX011799
178	15	57.7	15	6	ABX033377
179	15	57.7	15	6	ABX01800
180	15	57.7	15	6	ABX00221
181	15	57.7	15	8	ACD65927
182	15	57.7	15	8	ACD65915
183	15	57.7	15	8	ACD66042
184	15	57.7	15	12	AD187514
185	15	57.7	15	12	AD187526
186	15	57.7	15	12	AD187576
187	15	57.7	18	12	ADJ53723
188	15	57.7	19	10	ADFS15366
c 189	15	57.7	19	10	ADFS2214
c 190	15	57.7	19	10	ADFS2232
191	15	57.7	19	10	ADFS1518
192	15	57.7	20	2	AAQ15379
193	15	57.7	20	2	AAQ29640
194	15	57.7	20	2	AAQ24454
195	15	57.7	20	2	AAQ31479
196	15	57.7	20	2	AAQ31586
197	15	57.7	20	2	AAQ43115
198	15	57.7	20	2	AAQ43859
199	15	57.7	20	2	AAQ63747
200	15	57.7	20	2	AAQ45239
201	15	57.7	20	2	AAQ70443
202	15	57.7	20	2	AAQ48474
203	15	57.7	20	2	AAQ75229
204	15	57.7	20	2	AAT01496
205	15	57.7	20	2	AAT45058
206	15	57.7	20	2	AAV35203
207	15	57.7	20	4	AAF82029
208	15	57.7	20	4	AAD19015
209	15	57.7	20	8	AAD51032
210	15	57.7	20	8	ABV76991
211	15	57.7	20	10	ADF45372
212	15	57.7	20	12	AD043432
c 213	15	57.7	20	12	AD080852
214	15	57.7	24	3	AAA98958
215	15	57.7	24	8	AAJ56618
216	15	57.7	24	8	AAJ56611
217	15	57.7	25	2	AAQ44487
218	15	57.7	26	2	AAT42786
c 219	15	57.7	26	12	ADP87772
c 220	15	57.7	30	10	ADK65980
c 221	15	57.7	32	8	AAD48334
222	15	57.7	39	6	ABL55831
223	15	57.7	39	6	ABS65320
c 224	14.6	56.2	27	3	AAA15381
225	14.6	56.2	28	8	ABZ22635
c 226	14.6	56.2	30	10	ADE48266
227	14.6	56.2	32	2	AAK86688
228	14.6	56.2	40	12	ADK41343
c 229	14.2	54.6	46	10	ADP70708
c 230	14.2	54.6	46	10	ADI01239
231	14	53.8	17	8	ACD56821
232	14	53.8	17	12	ADI82777
233	14	53.8	19	8	ABZ57828
c 234	14	53.8	19	10	ADFS2201
235	14	53.8	19	10	ADFS1508
236	14	53.8	19	10	ADFS1533
c 237	14	53.8	20	2	ADFS2222
c 238	14	53.8	20	2	AAQ65020
c 239	14	53.8	20	2	AAQ58396
240	14	53.8	21	2	AAK37228

Adh22646 RT-PCR prim
Adh4481 PCR prime
Aa261834 HCV 5' no
Aa263683 Substrate
Aa263684 Substrate
Aa261835 HCV 5' no
Aa260220 Hepatitis
Abx03376 Hepatitis
Abx01798 Hepatitis
Abx01377 Hepatitis
Abx03377 Hepatitis
Abx01800 Hepatitis
Abx00221 Hepatitis
Acd55927 Anti-HCV
Acd55915 Anti-HCV
Acd66042 Anti-HCV
Ad187514 Anti-HCV
Ad187526 Anti-HCV
Ad187562 Anti-HCV
Ad153723 HCV spec
Ad151536 Hepatitis
Ad52214 Hepatitis
Ad52232 Hepatitis
Ad515118 Hepatitis
Aa253739 PCR prime
Aa252964 PCR prime
Aa244454 NANB hepa
Aa241479 NANB hepa
Aa241586 Hepatitis
Aa243115 HCV 5'NCR
Aa243859 NANB hepa
Aa263747 NANBH de
Aa245239 HCV prime
Aa270443 Primer/pr
Aa294874 HCV gene.
Aa2947229 Sense pri
Aa014598 Hepatitis
Aa014506 CN14 cdNA
Aa252023 Hepatitis
Aa252029 Hepatitis
Aa219015 Hepatitis
Aa215032 Hepatitis
Aa276991 Sense PCR
Ad45372 Forward pr
Ad453432 HCV RT-PCR
Aa280852 PCR prime
Aa289958 Hepatitis
Aa156618 Oligonuc
Aa156611 Oligonuc
Aa244487 HCV virus
Aa242786 Human mye
Ad287772 Extended
Ad265980 MBP-prot
Aa284826 Primer of
Aa286688 PCR prime
Adk14349 Human chr
Adf70708 Forward
Ad012339 Human EP
Acd56821 HCV DNaz
Ad182771 HCV DNaz
Abz57828 Hepatitis
Adf52201 Hepatitis
Adf15505 Hepatitis
Adf15531 Hepatitis
Adf52227 Hepatitis
Aa265020 Antisense
Aa258396 Antisense
Aa237228 HCV sense

241	14	53.8	28	2	AT05240	Aat05240 Hepatitis	C 314	13	50.0	17	12	AD187292	Adi87292 HCV DNaz
242	14	53.8	28	2	AT05240	Aat05213 Hepatitis	C 315	13	50.0	19	10	ADF52246	Adf52246 Hepatitis
243	14	53.8	28	3	AZ57780	Aaz57780 Hepatitis	C 316	13	50.0	19	10	ADF51506	Adf51506 Hepatitis
244	14	53.8	28	3	AZ57749	Aaz57749 Hepatitis	C 317	13	50.0	19	10	ADF52202	Adf52202 Hepatitis
245	14	53.8	28	6	ABQ96713	Abq96713 Human dis	C 318	13	50.0	19	10	ADF51550	Adf51550 Hepatitis
246	14	53.8	28	10	ADD12206	Add12206 Human DVL	C 319	13	50.0	21	12	ADQ25845	Adq25845 Chimaeric
247	14	53.8	30	2	AG93151	Ag93151 Growth ho	C 320	13	50.0	22	4	ABA03375	Ab03375 Human gen
248	14	53.8	30	10	ADE48252	Ade48252 Primer of	C 321	13	50.0	23	6	ABK52661	Abk52661 Hepatitis
249	14	53.8	33	2	AAV14925	Aav14925 psbL and	C 322	13	50.0	24	6	ABL55376	AbL55376 Human ger
250	14	53.8	42	10	ACF04691	Acf04691 Human bre	C 323	13	50.0	24	6	ABQ78213	Abq78213 Sense PCR
251	13.8	53.1	23	2	AAQ54364	Aaq54364 Primer/pr	C 324	13	50.0	25	9	ACI41689	AcI41689 Human mic
252	13.8	53.1	25	10	ADC61212	Adc61212 Full-leng	C 325	13	50.0	27	2	AAx91048	Aax91048 Probe 4 u
253	13.8	53.1	25	12	ADP17385	Adp17385 Renal cel	C 326	13	50.0	27	2	AAx99917	Aax99917 Probe 3 r
254	13.8	53.1	25	12	ADP17386	Adp17386 Renal cel	C 327	13	50.0	28	3	AAx82590	Aax82590 Hammerhea
255	13.8	53.1	27	2	AAQ64664	Aaq64664 Tma polym	C 328	13	50.0	31	2	AAQ14164	Aaq14164 Pssu 301
256	13.8	53.1	27	2	AAQ79948	Aaq79948 Tth polym	C 329	13	50.0	31	2	AAQ65584	Aaq65584 Bacillus
257	13.8	53.1	27	2	AAQ79584	Aaq79584 Primer fo	C 330	13	50.0	31	6	ABx72719	Abx72719 Cryptococ
258	13.8	53.1	27	2	AAQ73351	Aaq73351 Primer A	C 331	13	50.0	32	2	AAQ35979	Aaq35979 Antisense
259	13.8	53.1	28	2	AAQ22074	Aaq22074 T. mariti	C 332	13	50.0	32	4	AAQ82031	Aaq82031 Hepatitis
260	13.8	53.1	31	8	ABZ63831	Abz63831 Human H-R	C 333	13	50.0	33	2	AAQ24771	Aaq24771 Human gla
261	13.8	53.1	31	11	ADL74180	Adl74180 Human PKR	C 334	13	50.0	34	3	AAZ87373	Aaz87373 Hepatitis
262	13.8	53.1	37	6	AAD24040	Aad24040 PRRSV mem	C 335	13	50.0	35	4	AAQ02192	Aaq02192 Actin2 in
263	13.8	53.1	50	4	AAQ32358	Aaq32358 E. coli A	C 336	13	50.0	36	10	ADQ03377	Adq03377 Human imm
264	13.8	53.1	50	4	AAQ32356	Aaq32356 E. coli A	C 337	13	50.0	39	6	ABN88681	Abn88681 E2F aptam
265	13.8	53.1	50	4	AAH89665	Aah89665 Human onc	C 338	13	50.0	40	2	AAQ69446	Aaq69446 Flaemid p
266	13.6	52.3	22	6	ABA90757	Ab090757 Lactococc	C 339	13	50.0	40	2	AAx88870	Aax88870 Circular
267	13.6	52.3	24	6	ABL54619	AbL54619 Human DNA	C 340	13	50.0	40	6	ABA98145	Ab098145 Oligonuc1
268	13.6	52.3	24	12	ADP47388	Adp47388 Intellige	C 341	13	50.0	42	10	ADQ03724	Adq03724 Oligonuc1
269	13.6	52.3	30	3	AAQ90909	Aaq90909 PCR prime	C 342	13	50.0	42	10	ADC02588	Adc02588 Ex vivo s
270	13.6	52.3	32	10	ACF04902	Acf04902 Cancer-as	C 343	13	50.0	42	12	AD158263	Ad158263 Human int
271	13.6	52.3	32	10	ACF04906	Acf04906 Cancer-as	C 344	13	50.0	47	4	AAI65788	Adi65788 Oligonuc1
272	13.6	52.3	38	6	ABK70636	Abk70636 Human G-p	C 345	13	50.0	47	4	ADL71350	Adl71350 Human pre
273	13.6	52.3	39	2	AAH49355	Aah49355 Primer CD	C 346	13	50.0	50	4	AAQ31063	Aaq31063 Human SNP
274	13.6	52.3	41	4	AAH50075	Aah50075 Bacterial	C 347	12.8	49.2	29	3	AAA62757	Aaa62757 Endogluca
275	13.6	52.3	41	4	AAH50085	Aah50085 Bacterial	C 348	12.8	49.2	30	6	AAQ39273	Aaq39273 Murine To
276	13.6	52.3	41	4	AAH50064	Aah50064 Bacterial	C 349	12.8	49.2	30	6	AAQ39272	Aaq39272 Murine To
277	13.4	51.5	26	5	AAI17139	Aai17139 Informati	C 350	12.8	49.2	30	10	ACF36729	Acf36729 Murine To
278	13.4	51.5	29	10	ADC24678	Adc24678 HIV gp41	C 351	12.8	49.2	30	10	ACF36728	Acf36728 Murine To
279	13.4	51.5	29	10	ADC24686	Adc24686 HIV gp41	C 352	12.8	49.2	31	8	ACD54943	Adc54943 HBV DNaz
280	13.4	51.5	29	10	ADC24682	Adc24682 HIV gp41	C 353	12.8	49.2	31	12	ADM63052	Adm63052 Hepatitis
281	13.4	51.5	34	3	AAQ53970	Aaq53970 Primer us	C 354	12.8	49.2	31	12	ADI90441	Adi90441 HCV DNaz
282	13.4	51.5	38	8	ACD23124	Acd23124 Human LDL	C 355	12.8	49.2	34	2	AAQ58020	Aaq58020 Sequence
283	13.4	51.5	40	5	AAH45393	Aah45393 Nucleotid	C 356	12.8	49.2	35	2	AAQ38863	Aaq38863 Primer fo
284	13.4	51.5	44	2	AAV53699	Aav53699 Synleotic	C 357	12.8	49.2	35	6	ABA91295	Ab091295 Yeast alp
285	13.2	50.8	19	10	ADF48167	Adf48167 Human Myb	C 358	12.8	49.2	35	12	ADG74164	Adg74164 Yeast alp
286	13.2	50.8	19	10	ADF48346	Adf48346 Human Myb	C 359	12.8	49.2	36	2	AAV55483	Aav55483 Plt-3 rec
287	13.2	50.8	20	10	ABZ86668	Abz86668 Human oli	C 360	12.8	49.2	36	2	AAV44545	Aav44545 Primer 39
288	13.2	50.8	20	11	ABD22898	Abd22898 Human myo	C 361	12.8	49.2	36	12	ADP20784	Adp20784 CD40ex-F1
289	13.2	50.8	20	12	ADP77502	Adp77502 Chimeric	C 362	12.8	49.2	37	8	AAQ56246	Aaq56246 Mouse L37
290	13.2	50.8	20	12	ADP77859	Adp77859 Chimeric	C 363	12.8	49.2	38	3	AAA48982	Aaa48982 Mutagenic
291	13.2	50.8	20	12	ADP77219	Adp77219 Chimeric	C 364	12.8	49.2	39	6	ABQ73321	Abq73321 TPO mimet
292	13.2	50.8	22	3	AAZ50168	Aaz50168 3'PCR pri	C 365	12.8	49.2	39	12	ADQ16658	Adq16658 Human Kap
293	13.2	50.8	24	6	ABZ25749	Abz25749 Human cel	C 366	12.8	49.2	41	6	ABQ75868	Abq75868 Human cvc
294	13.2	50.8	25	12	ADP14367	Adp14367 Renal cel	C 367	12.6	48.5	22	12	ADN27381	Adn27381 Plasminog
295	13.2	50.8	27	8	ABT43607	Abt43607 RS4 PCR p	C 368	12.6	48.5	24	6	AB184686	Ab184686 Capture o
296	13.2	50.8	36	9	ADB25887	Adb25887 B. stearo	C 369	12.6	48.5	24	6	AB184687	Ab184687 Capture o
297	13.2	50.8	39	2	AAV13448	Aav13448 Primer fo	C 370	12.6	48.5	25	9	ACI03940	AcI03940 Human mic
298	13.2	50.8	39	6	ABQ73328	Abq73328 TPO mimet	C 371	12.6	48.5	25	9	ACK11937	Ack11937 Human mic
299	13.2	50.8	39	12	ADQ16665	Adq16665 Human Kap	C 372	12.6	48.5	25	9	ACI04576	AcI04576 Human mic
300	13.2	50.8	40	2	AAV54717	Aav54717 Nucleotid	C 373	12.6	48.5	25	9	ACK11936	Ack11936 Human mic
301	13.2	50.8	40	5	AAI17388	Aai17388 Bovine MH	C 374	12.6	48.5	29	8	AAQ52073	Aaq52073 Escherich
302	13.2	50.8	44	12	ADH42836	Adh42836 Novel hum	C 375	12.6	48.5	29	10	ABZ75148	Abz75148 Murine in
303	13.2	50.8	47	12	ADM67674	Adm67674 Rice Bhd1	C 376	12.6	48.5	30	2	AAQ63067	Aaq63067 Random re
304	13	50.0	13	8	ABZ81784	Abz81784 HCV 5' UT	C 377	12.6	48.5	30	4	AAQ98345	Aaq98345 bFGF fami
305	13	50.0	13	8	ACD65985	Acd65985 Anti-HCV	C 378	12.6	48.5	30	4	AAQ70581	Aaq70581 SELEX exp
306	13	50.0	13	8	ACD65984	Acd65984 Anti-HCV	C 379	12.6	48.5	30	5	AAQ04789	Aaq04789 Synthetic
307	13	50.0	13	8	ACD65926	Acd65926 Anti-HCV	C 380	12.6	48.5	30	10	ACC00436	Acc00436 Human DNA
308	13	50.0	13	12	ADI87525	Adi87525 Anti-HCV	C 381	12.6	48.5	30	12	ADQ33710	Adq33710 PCR prime
309	13	50.0	13	12	ADI87553	Adi87553 Anti-HCV	C 382	12.6	48.5	34	2	AAQ71180	Aaq71180 Ribonucle
310	13	50.0	13	12	ADI87554	Adi87554 Anti-HCV	C 383	12.6	48.5	34	4	AAQ02841	Aaq02841 A. thalia
311	13	50.0	15	8	ACD65928	Acd65928 Anti-HCV	C 384	12.6	48.5	36	3	AAQ35626	Aaq35626 Permutatein
312	13	50.0	15	12	ADI87527	Adi87527 Anti-HCV	C 385	12.6	48.5	37	2	AAQ72197	Aaq72197 Rat PACAP
313	13	50.0	17	8	ACD65854	Acd65854 HCV minus	C 386	12.6	48.5	38	6	ABQ74563	Abq74563 Human Lp8

387	12.6	48.5	38	6	ABV73093	Abv73093 Human LP8	460	12.4	47.7	50	2	AAQ80313	AaQ80313 Primer PC
388	12.6	48.5	38	8	ACD53624	AcD53624 HBV zinzy	C 461	12.4	47.7	50	2	AAQ34293	AaQ34293 T.Variabi
389	12.6	48.5	38	12	ADM62075	AdM62075 Hepatitis	C 462	12.4	47.7	50	4	AAZ29397	AaZ29397 Human SNP
390	12.6	48.5	41	3	AAZ87885	AaZ87885 AMG varia	C 463	12.4	47.7	50	8	ABZ09804	AbZ09804 Human oli
391	12.6	48.5	49	2	AAI78434	AaI78434 JPI115557	C 464	12.4	47.7	50	8	AAZ50910	AaZ50910 Oligonucl
392	12.4	47.7	20	6	AB197082	Ab197082 Capture o	C 465	12.4	47.7	50	10	ABZ79257	AbZ79257 Tumour su
393	12.4	47.7	23	3	AAAG4531	AaAG4531 PCR prime	C 466	12.4	47.7	50	12	ADJ47510	AdJ47510 Pir-GILT
394	12.4	47.7	24	6	AB190735	Ab190735 Capture o	C 467	12.4	47.7	50	12	ADJ58616	AdJ58616 GILT 5 ol
395	12.4	47.7	24	6	AB190734	Ab190734 Capture o	C 468	12.2	46.9	18	6	ABK89927	AbK89927 Bovine vi
396	12.4	47.7	25	2	AAQ88306	AaQ88306 Yeast ret	C 469	12.2	46.9	18	12	ADP83278	AdP83278 Primer of
397	12.4	47.7	25	2	AAV64007	AaV64007 Mycobacte	C 470	12.2	46.9	20	2	AAQ54916	AaQ54916 katG-lacZ
398	12.4	47.7	25	2	AAV22972	AaV22972 PCR prime	C 471	12.2	46.9	20	2	AAZ88344	AaZ88344 Human col
399	12.4	47.7	25	2	AAV70646	AaV70646 PCR prime	C 472	12.2	46.9	20	2	AAZ88342	AaZ88342 Human col
400	12.4	47.7	25	2	AAZ81059	AaZ81059 PCR prime	C 473	12.2	46.9	20	3	AAA38181	AaA38181 Primer us
401	12.4	47.7	25	9	ACHS6460	AcHS6460 DNA targe	C 474	12.2	46.9	20	6	AB194058	Ab194058 Capture o
402	12.4	47.7	25	9	ACHS6460	AcHS6460 DNA targe	C 475	12.2	46.9	20	9	ADA74116	AdA74116 Equine la
403	12.4	47.7	25	12	ADM46688	AdM46688 4-acetox	C 476	12.2	46.9	20	10	ABZ92976	AbZ92976 Human oli
404	12.4	47.7	25	3	AAZ39597	AaZ39597 M. tuberc	C 477	12.2	46.9	20	10	ABZ91563	AbZ91563 Human oli
405	12.4	47.7	27	6	AAU50061	AaU50061 Murine al	C 478	12.2	46.9	20	11	ABD29206	AbD29206 AA105000-
406	12.4	47.7	28	2	AAQ85574	AaQ85574 B. subtil	C 479	12.2	46.9	20	11	ABD27793	AbD27793 AA102454-
407	12.4	47.7	28	2	AAQ85574	AaQ85574 B. subtil	C 480	12.2	46.9	20	12	ADP77963	AdP77963 ChimERIC
408	12.4	47.7	28	3	AAQ00987	AaQ00987 Primer #1	C 481	12.2	46.9	20	12	ADP76905	AdP76905 ChimERIC
409	12.4	47.7	28	10	ADH62365	AdH62365 CAPS mark	C 482	12.2	46.9	21	10	ADH34377	AdH34377 Mouse DEC
410	12.4	47.7	30	2	AAQ20963	AaQ20963 HTLV-1 pr	C 483	12.2	46.9	22	3	AAZ95442	AaZ95442 Cat flea
411	12.4	47.7	30	2	AAQ58132	AaQ58132 cbhl-ph 2	C 484	12.2	46.9	22	6	AAZ18076	AaZ18076 Human cla
412	12.4	47.7	30	2	AAQ98754	AaQ98754 Primer fo	C 485	12.2	46.9	24	9	ABD25884	AbD25884 DNA downs
413	12.4	47.7	30	2	AAZ26610	AaZ26610 PCR prime	C 486	12.2	46.9	24	9	AAZ35206	AaZ35206 Corn shru
414	12.4	47.7	30	2	AAZ26610	AaZ26610 PCR prime	C 487	12.2	46.9	25	3	AAZ35206	AaZ35206 Corn shru
415	12.4	47.7	30	10	ADH48262	AdH48262 Primer of	C 488	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
416	12.4	47.7	30	12	ADK98502	AdK98502 Osteoclas	C 489	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
417	12.4	47.7	30	12	ADK98503	AdK98503 Osteoclas	C 490	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
418	12.4	47.7	31	3	AAAG4772	AaAG4772 C. tracho	C 491	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
419	12.4	47.7	31	4	AAH56275	AaH56275 Chlamydia	C 492	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
420	12.4	47.7	31	6	ABL32504	AbL32504 Chlamydia	C 493	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
421	12.4	47.7	31	6	ACN32543	AcN32543 WNV minus	C 494	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
422	12.4	47.7	31	8	ACD58203	AcD58203 HCV DNAY	C 495	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
423	12.4	47.7	31	8	ACF04099	AcF04099 E coli Xa	C 496	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
424	12.4	47.7	31	10	ABT17604	AbT17604 Invader d	C 497	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
425	12.4	47.7	31	12	AD188228	Ad188228 HCV DNAY	C 498	12.2	46.9	25	9	AAH37735	AaH37735 SNP speci
426	12.4	47.7	32	2	AAQ93887	AaQ93887 Fas-delta	C 499	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
427	12.4	47.7	33	2	AAQ26369	AaQ26369 HGH end o	C 500	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
428	12.4	47.7	33	2	AAV14923	AaV14923 pBL and o	C 501	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
429	12.4	47.7	33	10	ADH48269	AdH48269 Primer of	C 502	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
430	12.4	47.7	34	2	AAAT73600	AaAT73600 Primer us	C 503	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
431	12.4	47.7	35	1	AAAN94216	AaAN94216 Sequence	C 504	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
432	12.4	47.7	35	2	AAQ56601	AaQ56601 Human gro	C 505	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
433	12.4	47.7	36	2	AAQ88333	AaQ88333 Maize alp	C 506	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
434	12.4	47.7	37	10	ADJ81800	AdJ81800 Primer fa	C 507	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
435	12.4	47.7	38	2	AAAT8586	AaAT8586 Secretory	C 508	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
436	12.4	47.7	38	11	ADL56467	AdL56467 Human PKR	C 509	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
437	12.4	47.7	39	2	AAAT59803	AaAT59803 Hepatitis	C 510	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
438	12.4	47.7	39	12	ADP18478	AdP18478 S pneumon	C 511	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
439	12.4	47.7	40	2	AAAL8398	AaAL8398 Primer MI	C 512	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
440	12.4	47.7	40	6	ABA99472	AbA99472 A. thalia	C 513	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
441	12.4	47.7	40	12	ADP43301	AdP43301 Human pit	C 514	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
442	12.4	47.7	41	6	ABV75544	AbV75544 Alcohol d	C 515	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
443	12.4	47.7	41	6	ABZ50760	AbZ50760 Human gly	C 516	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
444	12.4	47.7	41	6	ABZ44550	AbZ44550 Human gly	C 517	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
445	12.4	47.7	41	6	ABL96060	AbL96060 Brassica	C 518	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
446	12.4	47.7	42	2	AAO5717	AaO5717 BEI prote	C 519	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
447	12.4	47.7	42	9	ADBY5662	AdBY5662 PCR prime	C 520	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
448	12.4	47.7	42	12	AD180491	Ad180491 Human mut	C 521	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
449	12.4	47.7	43	9	ADBY5663	AdBY5663 PCR prime	C 522	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
450	12.4	47.7	43	9	ADBY5663	AdBY5663 PCR prime	C 523	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
451	12.4	47.7	44	9	ADBY5658	AdBY5658 PCR prime	C 524	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
452	12.4	47.7	45	6	ABA91338	AbA91338 Streptoco	C 525	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
453	12.4	47.7	45	6	ABA91338	AbA91338 Streptoco	C 526	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
454	12.4	47.7	45	6	ABA91338	AbA91338 Streptoco	C 527	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
455	12.4	47.7	46	6	ABK40880	AbK40880 Human obe	C 528	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
456	12.4	47.7	47	8	AAZ50914	AaZ50914 Oligonucl	C 529	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
457	12.4	47.7	47	12	ADFA7514	AdFA7514 Pir-GILT	C 530	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
458	12.4	47.7	47	12	ADJ58620	AdJ58620 GILT 9 ol	C 531	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci
459	12.4	47.7	48	5	AAAF16712	AaAF16712 dGMP-spec	C 532	12.2	46.9	25	10	AAH37735	AaH37735 SNP speci

C 533	12.2	46.9	44	8	ACAL1542	Acal14542	Prokaryot	606	12	46.2	25	9	ACH61325	ACH61325	DNA target
C 534	12.2	46.9	48	2	AAQ49569	Aaq49569	Corynebac	607	12	46.2	25	12	ADP87775	ADP87775	Hepatitits
C 535	12.2	46.9	48	2	AAQ94959	Aaq94959	dapA gene	C 608	12	46.2	27	2	AAQ10740	AAQ10740	Oligonucle
C 536	12.2	46.9	48	2	AAV35800	Aav35800	PCR primer	C 609	12	46.2	27	3	AZ44696	Az44696	Human bra
C 537	12.2	46.9	48	2	AAV99495	Aav99495	Corynebac	610	12	46.2	27	12	ADL22791	ADL22791	Wheat RAF
C 538	12.2	46.9	48	2	AAZ22624	Aaz22624	CBD_alpha	611	12	46.2	29	3	AZ99862	Az99862	Nucleocid
C 539	12.2	46.9	48	6	ADA42649	Ada42649	Human chi	C 612	12	46.2	29	8	ABZ59146	Abz59146	Human ak
C 540	12.2	46.9	48	8	ADA16019	Ada16019	Corynebac	613	12	46.2	30	2	AAT10255	Aat10255	Human lip
C 541	12.2	46.9	48	9	ACH03665	Ach03665	Corynebac	614	12	46.2	30	2	AAV64016	Aav64016	Mycobacte
C 542	12.2	46.9	48	10	AAH2878	Aad62878	Human chi	C 615	12	46.2	30	2	AAV81107	Aav81107	PCR prime
C 543	12.2	46.9	50	4	AAZ28718	Aal28718	Human SNP	C 616	12	46.2	30	3	AAA64835	Aag64835	PCR prime
C 544	12.2	46.9	50	6	AAZ05594	Abz05594	Human leu	C 617	12	46.2	30	3	AAA64836	Aag64836	PCR prime
C 545	12	46.2	13	8	ACD65986	Acd65986	Anti-HCV	C 618	12	46.2	30	5	AAAD16849	Aad16849	Mutagenic
C 546	12	46.2	13	12	ADN07555	Adi07555	Anti-HCV	619	12	46.2	30	5	AAAD16848	Aad16848	Mutagenic
C 547	12	46.2	17	6	ABN07470	Abn07470	Human GDM	620	12	46.2	31	9	ACF04106	Acf04106	RBS regio
C 548	12	46.2	17	6	ABN07472	Abn07472	Human GDM	621	12	46.2	32	2	AAV55001	Aav55001	Sense PCR
C 549	12	46.2	17	6	ABN07468	Abn07468	Human GDM	622	12	46.2	32	2	AAV58473	Aav58473	Primer fo
C 550	12	46.2	17	6	ABN07473	Abn07473	Human GDM	623	12	46.2	32	8	ABX79057	Abx79057	PCR prime
C 551	12	46.2	17	6	ABN07469	Abn07469	Human GDM	624	12	46.2	33	1	AAAN90583	Aan90583	DNA 57SLE
C 552	12	46.2	17	6	ABN07471	Abn07471	Human GDM	C 625	12	46.2	33	2	AAT95709	Aat95709	DNA from
C 553	12	46.2	17	8	ACD56822	Acd56822	HCV DNazzy	C 626	12	46.2	33	2	AAV04924	Aav04924	Primer LR
C 554	12	46.2	17	12	ADI82772	Adi82772	HCV DNazzy	C 627	12	46.2	33	2	AAV09865	Aav09865	Primer LR
C 555	12	46.2	18	2	AAQ22068	Aaq22068	Sequence	C 628	12	46.2	33	2	AAV15222	Aax15222	PCR prime
C 556	12	46.2	18	3	AAZ22655	Aaf22265	Arabidops	C 629	12	46.2	33	3	AAA90158	Aaa90158	PCR prime
C 557	12	46.2	19	10	ADF51547	Adf51547	Hepatitits	C 630	12	46.2	33	3	AAI72531	Aai72531	Nested PC
C 558	12	46.2	19	10	ADF51513	Adf51513	Hepatitits	631	12	46.2	33	6	ABQ73389	Abq73389	Human cut
C 559	12	46.2	19	10	ADF52209	Adf52209	Hepatitits	632	12	46.2	33	6	ABA95866	Abag95866	Human zin
C 560	12	46.2	19	10	ADF52243	Adf52243	Hepatitits	C 633	12	46.2	33	8	ABX11224	Abx11224	HIV-1 PCR
C 561	12	46.2	20	2	AAQ58394	Aag58394	Antisense	634	12	46.2	33	10	ADB61440	Adb61440	GPR40 DNA
C 562	12	46.2	20	2	AAQ58394	Aag58394	Antisense	635	12	46.2	33	12	ADG17542	Adg17542	Human GPR
C 563	12	46.2	20	2	AAQ58394	Aag58394	Antisense	636	12	46.2	33	12	ADO21539	Ado21539	Human GPR
C 564	12	46.2	20	6	ABS57333	Abd57333	PCR prime	C 637	12	46.2	34	6	AAQ40546	Aad40546	hGH signa
C 565	12	46.2	20	10	ABT23602	Abt23602	Stabilisi	638	12	46.2	35	2	AAQ99919	Aaq99919	HIV-1 mRN
C 566	12	46.2	20	10	ABZ86738	Abz86738	Human oli	639	12	46.2	35	3	AAZ44695	Aaz44695	Human bra
C 567	12	46.2	20	10	ABZ88229	Abz88229	Human oli	C 640	12	46.2	35	8	ABX08330	Abx08330	Forward R
C 568	12	46.2	20	10	ABZ92975	Abz92975	Human oli	C 641	12	46.2	35	9	ACD28444	Acd28444	HIV-1 gen
C 569	12	46.2	20	11	ABD29205	Abd29205	AA150500-	642	12	46.2	36	2	AAV78065	Aav78065	Rat DTDTST
C 570	12	46.2	20	11	ABD34459	Abd34459	AT652901-	C 643	12	46.2	37	3	AAZ08739	Aaz08739	HCNV/HIV-
C 571	12	46.2	20	11	ABD22968	Abd22968	Human myo	C 644	12	46.2	37	3	AAA94001	Aaa94001	Antiviral
C 572	12	46.2	21	2	AAV40611	Aav40611	Human TSC	C 645	12	46.2	37	4	AAAC86895	Aac86895	PCR prime
C 573	12	46.2	21	4	AAAF84798	Aaf84798	PCR prime	646	12	46.2	37	4	AAH20082	Aah20082	Asp 1 gen
C 574	12	46.2	21	12	ADE52353	Ade52353	Inhibitor	647	12	46.2	37	12	ADO59185	Ado59185	PCR prime
C 575	12	46.2	21	12	ADE52352	Ade52352	Inhibitor	C 648	12	46.2	38	2	AAV49359	Aav49359	Primer AB
C 576	12	46.2	22	2	AAAT45327	Aat45327	Mycoplasm	C 649	12	46.2	39	2	AAAX85413	Aax85413	RNA ligan
C 577	12	46.2	23	2	AAAT65095	Aat65095	Hepatitits	650	12	46.2	39	12	ADL64466	Adl64466	Human sin
C 578	12	46.2	23	3	AAAG64218	Aag64218	Primer fo	651	12	46.2	39	12	ADL64467	Adl64467	Human sin
C 579	12	46.2	23	5	AAAF56559	Aaf56559	HIV-1 det	652	12	46.2	40	4	AAH50076	Aah50076	Bacterial
C 580	12	46.2	23	9	ACF05116	Acf05116	Retrovira	C 553	12	46.2	40	10	ADC46975	Adc46975	Synthesis
C 581	12	46.2	24	2	AAQ75820	Aaq75820	Sense pri	654	12	46.2	40	10	ADC46977	Adc46977	Synthesis
C 582	12	46.2	24	3	AAAT51431	Aat51431	Primer Ab	C 555	12	46.2	40	10	ADC56755	Adc56755	Self asse
C 583	12	46.2	24	3	AAZ45815	Aaz45815	PCR prime	656	12	46.2	40	10	ADC56758	Adc56758	Self asse
C 584	12	46.2	24	3	AAZ45809	Aaz45809	PCR prime	657	12	46.2	41	2	AAV44490	Aav44490	tRNA-Lys3
C 585	12	46.2	24	5	AAAF56557	Aaf56557	HIV-1 det	658	12	46.2	41	4	AAH49842	Aah49842	Bacterial
C 586	12	46.2	24	10	ADE36828	Ade36828	Rhesus ro	659	12	46.2	41	4	AAH50072	Aah50072	Bacterial
C 587	12	46.2	24	10	ABX13008	Abx13008	Oxidative	C 660	12	46.2	41	12	ADH06159	Adh06159	Gene poly
C 588	12	46.2	25	2	AAQ81978	Aaq81978	Human sol	C 661	12	46.2	41	12	ADH05486	Adh05486	Gene poly
C 589	12	46.2	25	6	ABN12363	Abn12363	Human GDM	C 662	12	46.2	41	12	ADH91273	Adh91273	1-beta-me
C 590	12	46.2	25	6	ABN12368	Abn12368	Human GDM	C 663	12	46.2	41	12	ADH91946	Adh91946	1-beta-me
C 591	12	46.2	25	6	ABN12365	Abn12365	Human GDM	C 664	12	46.2	42	4	AAH50073	Aah50073	Bacterial
C 592	12	46.2	25	6	ABN12366	Abn12366	Human GDM	665	12	46.2	42	4	AAH49844	Aah49844	Bacterial
C 593	12	46.2	25	6	ABN12360	Abn12360	Human GDM	C 666	12	46.2	43	2	AAQ38111	Aaq38111	Mycobacte
C 594	12	46.2	25	6	ABN12367	Abn12367	Human GDM	C 667	12	46.2	43	6	ABK96447	Abk96447	PCR prime
C 595	12	46.2	25	6	ABN12373	Abn12373	Human GDM	C 668	12	46.2	43	10	AAAS3316	Aas3316	Bovine ma
C 596	12	46.2	25	6	ABN12372	Abn12372	Human GDM	C 669	12	46.2	47	3	AAZ67089	Aaz67089	Human map
C 597	12	46.2	25	6	ABN12371	Abn12371	Human GDM	C 670	12	46.2	48	2	AAZ28179	Aaz28179	Murine al
C 598	12	46.2	25	6	ABN12362	Abn12362	Human GDM	671	12	46.2	48	3	AAZ56997	Aaz56997	Forward a
C 599	12	46.2	25	6	ABN12369	Abn12369	Human GDM	C 672	12	46.2	48	3	AAZ99162	Aaz99162	Murine pe
C 600	12	46.2	25	6	ABN12364	Abn12364	Human GDM	C 673	12	46.2	49	5	AAZ56560	Aaz56560	HIV-1 det
C 601	12	46.2	25	6	ABN12370	Abn12370	Human GDM	C 674	12	46.2	50	4	AAAL31062	Aal31062	Human SNP
C 602	12	46.2	25	6	ABN12361	Abn12361	Human GDM	675	12	46.2	50	4	AAAL34220	Aal34220	Human SNP
C 603	12	46.2	25	9	ACK149162	Aci49162	Human mic	C 676	12	46.2	50	4	AAAL34240	Aal34240	Human SNP
C 604	12	46.2	25	9	ACK15513	Ack15513	Human mic	C 677	12	46.2	50	4	AAAL34239	Aal34239	Human SNP
C 605	12	46.2	25	9	ACH53993	Ach53993	DNA target	678	11.8	45.4	17	6	ACN01221	Acn01221	WNV Hamme

c 679	11.8	45.4	17	6	ACN12457	ACN12457 WNV minus	c 752	11.8	45.4	36	5	AAC90748	Aac90748 Human sec
c 680	11.8	45.4	17	6	ACN04523	ACN04523 WNV Zinz	c 753	11.8	45.4	36	8	AAD55014	Aad55014 VEGF alte
c 681	11.8	45.4	17	6	ACN09924	ACN09924 WNV minus	c 754	11.8	45.4	36	12	ADP20784	Adp20784 CD40ex-F1
c 682	11.8	45.4	20	2	AAX38389	Aax38389 E. coli K	c 755	11.8	45.4	37	10	ADP89504	Adp89504 PCR prime
c 683	11.8	45.4	20	2	AAX92804	Aax92804 PCR prime	c 756	11.8	45.4	38	2	AAQ58536	Aaq58536 LFA-3 sen
c 684	11.8	45.4	20	2	AAX94284	Aax94284 PCR prime	c 757	11.8	45.4	38	2	AAQ36524	Aaq36524 PCR prime
c 685	11.8	45.4	20	2	ABL95993	Abi95993 Brassica	c 758	11.8	45.4	38	2	AAZ98262	Aaz98262 Z. ramige
c 686	11.8	45.4	20	12	ADP78056	Adp78056 Chimeric	c 759	11.8	45.4	38	3	AAA63922	Aaa63922 PCR prime
c 687	11.8	45.4	20	12	ADP78163	Adp78163 Chimeric	c 760	11.8	45.4	38	4	ABK05018	Abk05018 Human NOG
c 688	11.8	45.4	21	9	ADH58224	Adh58224 Cytokine	c 761	11.8	45.4	38	6	ABK92848	Abk92848 Transmemb
c 689	11.8	45.4	21	12	ADH50962	Adh50962 Endotheli	c 762	11.8	45.4	38	11	ADL54071	Adl54071 Human IKK
c 690	11.8	45.4	22	2	AAV75365	Aav75365 cDNA synt	c 763	11.8	45.4	38	11	ADF47532	Adf47532 IGF-II ta
c 691	11.8	45.4	22	2	AAV59947	Aav59947 PCR prime	c 764	11.8	45.4	38	12	ADO26075	Ado26075 Arabidops
c 692	11.8	45.4	22	6	ABK10153	Abk10153 Douglas f	c 765	11.8	45.4	39	5	AAC85342	Aac85342 cDNA prim
c 693	11.8	45.4	22	10	ADC39505	Adc39505 FmbIP pro	c 766	11.8	45.4	39	5	AAC85321	Aac85321 Primer Sa
c 694	11.8	45.4	23	3	AAA40595	Aaa40595 Human Arp	c 767	11.8	45.4	39	5	AAC85321	Aac85321 Primer Sa
c 695	11.8	45.4	24	4	AHH44338	Aah44338 Human par	c 768	11.8	45.4	39	5	AAV63974	Aav63974 Human tan
c 696	11.8	45.4	24	6	ABL52682	Abi52682 Insulin-1	c 769	11.8	45.4	39	6	ABS61220	Abs61220 Human pol
c 697	11.8	45.4	24	6	ABX04799	Abx04799 Guanylate	c 770	11.8	45.4	40	2	AAV49999	Aav49999 PCR prime
c 698	11.8	45.4	24	9	ACT05089	Act05089 Bovine th	c 771	11.8	45.4	40	2	AAV55934	Aav55934 Primer us
c 699	11.8	45.4	25	2	AAV64007	Aav64007 Mycobacte	c 772	11.8	45.4	40	2	AAV57583	Aav57583 Primer us
c 700	11.8	45.4	25	2	AAV64007	Aav64007 Mycobacte	c 773	11.8	45.4	40	2	AAZ95996	Aaz95996 Polynucle
c 701	11.8	45.4	25	6	ABN11908	Abn11908 Human GDM	c 774	11.8	45.4	40	3	AZ338920	Az338920 Neisseria
c 702	11.8	45.4	25	6	ABN11909	Abn11909 Human GDM	c 775	11.8	45.4	42	2	AAQ91729	Aaq91729 Alpha-d 3
c 703	11.8	45.4	25	6	ABN11907	Abn11907 Human GDM	c 776	11.8	45.4	42	2	AAQ91729	Aaq91729 Alpha-d 3
c 704	11.8	45.4	25	9	ACT197410	Act197410 Human mic	c 777	11.8	45.4	42	2	AAV65896	Aav65896 IT3-8 inv
c 705	11.8	45.4	25	9	ACK16141	Ack16141 Human mic	c 778	11.8	45.4	42	2	AAV31554	Aav31554 Beta2 int
c 706	11.8	45.4	25	9	ACK103835	Act103835 Human mic	c 779	11.8	45.4	42	2	AAV35250	Aav35250 Human bet
c 707	11.8	45.4	25	9	ACK15012	Ack15012 Human mic	c 780	11.8	45.4	42	2	AAV63796	Aav63796 Human alp
c 708	11.8	45.4	25	9	ACK126150	Ack126150 Human mic	c 781	11.8	45.4	42	2	AAV08460	Aav08460 Primer fo
c 709	11.8	45.4	25	9	ACH59996	Ach59996 DNA targ	c 782	11.8	45.4	42	3	AAA60028	Aaa60028 Human alp
c 710	11.8	45.4	26	2	AAT16230	Aat16230 Primer #6	c 783	11.8	45.4	42	6	AAV75505	Aav75505 Prospero
c 711	11.8	45.4	26	3	AAZ50993	Aaz50993 PCR prime	c 784	11.8	45.4	42	6	ABK82418	Abk82418 Human bet
c 712	11.8	45.4	26	4	AAV15663	Aav15663 PCR prime	c 785	11.8	45.4	42	6	ADP52965	Adp52965 FEN-1 rel
c 713	11.8	45.4	26	8	ACD17031	Act17031 Sample pr	c 786	11.8	45.4	42	6	ADP52965	Adp52965 FEN-1 rel
c 714	11.8	45.4	26	8	ADA89432	Ada89432 Rice hype	c 787	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 715	11.8	45.4	26	9	ADA89432	Ada89432 Rice hype	c 788	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 716	11.8	45.4	27	2	AAT32410	Aat32410 Interfero	c 789	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 717	11.8	45.4	27	2	AAX80818	Aax80818 Plant lum	c 790	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 718	11.8	45.4	27	3	AAZ36882	Aaz36882 PCR prime	c 791	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 719	11.8	45.4	28	8	ABZ79464	Abz79464 MGR1a re	c 792	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 720	11.8	45.4	28	8	AAZ79464	Aaz79464 MGR1a re	c 793	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 721	11.8	45.4	29	2	AAQ81250	Aaq81250 Ribozyme	c 794	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 722	11.8	45.4	29	2	AAQ59802	Aaq59802 Hepatitis	c 795	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 723	11.8	45.4	29	2	AAQ76036	Aaq76036 TK-(tetO)	c 796	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 724	11.8	45.4	29	4	AAQ01429	Aaq01429 Unknown p	c 797	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 725	11.8	45.4	29	5	AAV57566	Aav57566 Calcium p	c 798	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 726	11.8	45.4	29	6	AAV17545	Aav17545 Human ace	c 799	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 727	11.8	45.4	30	10	ADP48270	Adp48270 Primer of	c 800	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 728	11.8	45.4	30	12	ADJ63957	Adj63957 Plant lip	c 801	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 729	11.8	45.4	31	2	AAV14924	Aav14924 pBL and	c 802	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 730	11.8	45.4	31	3	AAV78977	Aav78977 Human gen	c 803	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 731	11.8	45.4	31	6	ACN33015	Actn33015 WNV minus	c 804	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 732	11.8	45.4	31	6	ACN32800	Actn32800 WNV minus	c 805	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 733	11.8	45.4	32	3	AAZ47085	Aaz47085 Mouse alb	c 806	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 734	11.8	45.4	32	3	AAZ47085	Aaz47085 Mouse alb	c 807	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 735	11.8	45.4	32	4	AAV31194	Aav31194 Oligonuc	c 808	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 736	11.8	45.4	32	6	ABN84385	Abn84385 Mouse alb	c 809	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 737	11.8	45.4	33	2	AAQ46728	Aaq46728 HIV ampli	c 810	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 738	11.8	45.4	33	3	AAQ89504	Aaq89504 Human imm	c 811	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 739	11.8	45.4	33	3	AAA08646	Aaa08646 Primer GV	c 812	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 740	11.8	45.4	33	4	ACN85512	Actn85512 Primer #9	c 813	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 741	11.8	45.4	33	6	ABO75561	Abq75561 Xenopus l	c 814	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 742	11.8	45.4	33	11	ADW77930	Adw77930 Acetylglu	c 815	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 743	11.8	45.4	34	4	AAV81340	Aav81340 Rubisco S	c 816	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 744	11.8	45.4	34	9	ADA44835	Ada44835 PCR prime	c 817	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 745	11.8	45.4	35	2	AAV1719	Aav1719 Primer fo	c 818	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 746	11.8	45.4	35	2	AAV14926	Aav14926 pBL and	c 819	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 747	11.8	45.4	35	3	AAV49277	Aav49277 Primer AB	c 820	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 748	11.8	45.4	35	3	AAZ47086	Aaz47086 Primer Su	c 821	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 749	11.8	45.4	35	3	AAV31195	Aav31195 Oligonuc	c 822	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 750	11.8	45.4	36	2	AAV02899	Aav02899 Alpha gal	c 823	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime
c 751	11.8	45.4	36	2	AAV21835	Aav21835 Primer EB	c 824	11.8	45.4	43	2	AAV31306	Aav31306 PCR prime

C 825	11.6	44.6	22	12	ADIS3310	Adi53310 CXCR4 RT-	C 898	11.6	44.6	39	2	AAQ090912	AaQ90912 hMLH1 gen
C 826	11.6	44.6	23	12	ADI60025	Adi60025 siRNA -ve	C 899	11.6	44.6	39	3	AAA50248	AaA50248 Maize hea
C 827	11.6	44.6	24	3	AAZ57985	Aaz57985 T cell re	C 900	11.6	44.6	39	4	AAAF32320	AaF32320 E. coli A
C 828	11.6	44.6	24	6	ABQ06527	Abq06527 Oligonucle	C 901	11.6	44.6	39	4	AAH26481	AaH26481 Maize hea
C 829	11.6	44.6	24	6	ABQ06486	Abq06486 Oligonucle	C 902	11.6	44.6	39	6	ABQ73325	AbQ73325 TPO minet
C 830	11.6	44.6	24	6	ABQ01288	Abq01288 Oligonucle	C 903	11.6	44.6	39	6	ABQ73320	AbQ73320 TPO minet
C 831	11.6	44.6	24	6	ABQ184194	Abq184194 Capture o	C 904	11.6	44.6	39	8	AAAD50761	AaD50761 Arabidops
C 832	11.6	44.6	24	6	AB184195	Ab184195 Capture o	C 905	11.6	44.6	39	9	ACA62043	AcA62043 Maize mit
C 833	11.6	44.6	24	6	ABL42444	AbL42444 Tyrosinas	C 906	11.6	44.6	39	10	ABV75300	AbV75300 AANT1 cod
C 834	11.6	44.6	24	10	ADE86775	Ade86775 Pax5-lacz	C 907	11.6	44.6	39	12	ADQ16662	AdQ16662 Human Kap
C 835	11.6	44.6	25	2	AAQ86410	AaQ86410 Human ins	C 908	11.6	44.6	39	12	ADQ16657	AdQ16657 Human Kap
C 836	11.6	44.6	25	2	AAQ86401	AaQ86401 Human ins	C 909	11.6	44.6	40	5	AA91413	Aa91413 R. renifo
C 837	11.6	44.6	25	6	ABZ30813	AbZ30813 Candida a	C 910	11.6	44.6	40	5	AA91386	Aa91386 R. renifo
C 838	11.6	44.6	25	9	ACK10759	AcK10759 Human mic	C 911	11.6	44.6	40	9	ACD32772	AcD32772 Backtrans
C 839	11.6	44.6	25	9	ACT00461	AcI00461 Human mic	C 912	11.6	44.6	40	9	ACD32772	AcD32772 Backtrans
C 840	11.6	44.6	25	9	ACK22159	AcK22159 Human mic	C 913	11.6	44.6	40	9	ACD32799	AcD32799 Backtrans
C 841	11.6	44.6	25	9	ACH54512	AcH54512 DNA target	C 914	11.6	44.6	40	10	ADD24544	AdD24544 DNA polym
C 842	11.6	44.6	26	2	AAV65088	AaV65088 Human ZPB	C 915	11.6	44.6	40	10	ADG79087	AdG79087 Schizophr
C 843	11.6	44.6	26	12	ADJ76805	Adj76805 FETUB rev	C 916	11.6	44.6	40	10	ABZ72394	AbZ72394 Tomato sp
C 844	11.6	44.6	27	2	AAT18018	Aat18018 Chemokine	C 917	11.6	44.6	41	2	AAAX5892	AaX5892 Primer us
C 845	11.6	44.6	27	3	AA898797	Aa898797 Mutagenic	C 918	11.6	44.6	41	4	AAAC87946	AaC87946 Oligonucle
C 846	11.6	44.6	27	4	AA812797	Aa812797 Mutagenic	C 919	11.6	44.6	41	4	AAAC87935	AaC87935 B43 scFv
C 847	11.6	44.6	27	4	AAF91469	Aaf91469 N. mening	C 920	11.6	44.6	41	8	ACD23093	AcD23093 Human LPL
C 848	11.6	44.6	27	4	AAF91499	Aaf91499 N. mening	C 921	11.6	44.6	42	2	AAAX27116	AaX27116 Primer p5
C 849	11.6	44.6	27	6	ABL40620	AbL40620 P. putida	C 922	11.6	44.6	42	2	AAAX84825	AaX84825 PCR prime
C 850	11.6	44.6	27	6	ABK37882	AbK37882 Promoter	C 923	11.6	44.6	42	4	AAAC92427	AaC92427 PRSEKLA
C 851	11.6	44.6	27	6	ABK37849	AbK37849 pCMK(+) c	C 924	11.6	44.6	42	4	AAAF55358	AaF55358 PCR prime
C 852	11.6	44.6	28	3	AAZ55351	AaZ55351 Neisseria	C 925	11.6	44.6	42	4	AAH23279	AaH23279 3x2F ZGS
C 853	11.6	44.6	28	3	AAA39600	Aa39600 M. tuberc	C 926	11.6	44.6	44	10	ADD41404	AdD41404 Recombina
C 854	11.6	44.6	28	10	ADJ33191	Adj33191 Primer se	C 927	11.6	44.6	45	4	AAH70659	AaH70659 Human cer
C 855	11.6	44.6	30	3	AAA30758	Aa30758 Human G p	C 928	11.6	44.6	47	3	AAA48364	Aa48364 Fungal xy
C 856	11.6	44.6	30	5	AAAF16886	Aaf16886 Informati	C 929	11.6	44.6	47	3	AAA48338	Aa48338 Thermomyc
C 857	11.6	44.6	30	6	ABK97364	AbK97364 Stratum c	C 930	11.6	44.6	47	3	AAZ67840	AaZ67840 Human map
C 858	11.6	44.6	30	6	ABL58394	AbL58394 RSV F env	C 931	11.6	44.6	47	3	AAZ66849	AaZ66849 Human map
C 859	11.6	44.6	30	10	ADC22767	AdC22767 Human G p	C 932	11.6	44.6	47	9	AAAC86569	AaC86569 Primer us
C 860	11.6	44.6	30	10	ADH14240	AdH14240 Human GPR	C 933	11.6	44.6	48	4	AAH23286	AaH23286 3x2F ZGL
C 861	11.6	44.6	31	2	AAQ52229	AaQ52229 Neuroblas	C 934	11.6	44.6	48	8	ABX79981	AbX79981 EST polym
C 862	11.6	44.6	31	3	AAZ50968	Aaz50968 E. haloch	C 935	11.6	44.6	48	12	ADG15848	AdG15848 Insect de
C 863	11.6	44.6	31	4	AAI30936	Aai30936 Human sin	C 936	11.6	44.6	48	12	ADG15848	AdG15848 Insect de
C 864	11.6	44.6	31	6	ACN32043	AcN32043 WNV minus	C 937	11.6	44.6	49	8	ABZ09198	AbZ09198 Human oli
C 865	11.6	44.6	31	8	ACD43766	AcD43766 Human Gen	C 938	11.6	44.6	49	10	ABZ78651	AbZ78651 Tumour su
C 866	11.6	44.6	31	8	ACD56868	AcD56868 HCV DNaz	C 939	11.6	44.6	50	2	AAQ80312	AaQ80312 Primer PC
C 867	11.6	44.6	31	8	ACD54785	AcD54785 HBV DNaz	C 940	11.6	44.6	50	3	AAZ48338	AaZ48338 Primer sp
C 868	11.6	44.6	31	12	ADM62947	Adm62947 Hepatitis	C 941	11.6	44.6	50	4	AAI73659	Aai73659 Human sil
C 869	11.6	44.6	31	12	ADI87323	Adi87323 HCV DNaz	C 942	11.6	44.6	50	4	AAI76811	Aai76811 Human sil
C 870	11.6	44.6	32	2	AAAT65548	Aat65548 Oligonucle	C 943	11.6	44.6	50	4	AAI76809	Aai76809 Human sil
C 871	11.6	44.6	32	2	AAAT60363	Aat60363 Oligonucle	C 944	11.6	44.6	50	6	ABZ05181	AbZ05181 Human leu
C 872	11.6	44.6	32	2	AAV55454	Aav55454 Interleuk	C 945	11.6	44.6	50	6	ABZ03212	AbZ03212 Human leu
C 873	11.6	44.6	32	6	AAAD44047	Aad44047 Rubisco-R	C 946	11.6	44.6	50	6	ABZ03262	AbZ03262 Human leu
C 874	11.6	44.6	32	6	ABR00192	AbR00192 Probe Rub	C 947	11.6	44.6	50	12	ADJ87546	AdJ87546 Human cyt
C 875	11.6	44.6	33	5	AB197645	Ab197645 Endogenou	C 948	11.4	43.8	17	6	ABL31695	AbL31695 Human HLA
C 876	11.6	44.6	33	6	ABA05764	AbA05764 Telomeric	C 949	11.4	43.8	18	3	AAA67000	AaA67000 Human leu
C 877	11.6	44.6	33	6	ABA99050	AbA99050 Human myb	C 950	11.4	43.8	20	4	AAH26389	AaH26389 Chloromph
C 878	11.6	44.6	33	10	ADC47066	AdC47066 Polypepti	C 951	11.4	43.8	20	5	AAAF54653	AaF54653 Human HLA
C 879	11.6	44.6	33	10	ADD29143	AdD29143 Diphospho	C 952	11.4	43.8	20	6	AB194688	Ab194688 Capture o
C 880	11.6	44.6	33	12	ADQ59181	AdQ59181 PCR prime	C 953	11.4	43.8	20	10	ADC26395	AdC26395 NOV prote
C 881	11.6	44.6	35	2	AAZ20958	Aaz20958 Primer SE	C 954	11.4	43.8	20	10	ADD42530	AdD42530 Human inf
C 882	11.6	44.6	35	6	ADAD2633	AdA2633 PCR prime	C 955	11.4	43.8	20	10	ADD42531	AdD42531 Human inf
C 883	11.6	44.6	35	8	ACN10046	AcN10046 Necrosis	C 956	11.4	43.8	21	11	ADH52817	AdH52817 PCR prime
C 884	11.6	44.6	35	10	AAAD62862	Aad62862 Secreted	C 957	11.4	43.8	21	11	ADM07049	AdM07049 Aspergill
C 885	11.6	44.6	36	2	AAV59926	Aav59926 Sense pri	C 958	11.4	43.8	21	12	ADQ80724	AdQ80724 Porcine I
C 886	11.6	44.6	36	2	AAV58458	Aav58458 Primer OM	C 959	11.4	43.8	22	4	Aaf59046	Aaf59046 Vector pu
C 887	11.6	44.6	36	2	AAV10641	Aav10641 A. thalia	C 960	11.4	43.8	22	6	AB555549	Ab555549 Human bet
C 888	11.6	44.6	36	2	AAAX03350	Aax03350 Forward P	C 961	11.4	43.8	22	8	ACC70183	AcC70183 Probe spe
C 889	11.6	44.6	36	3	AAA35749	Aa35749 Permutain	C 962	11.4	43.8	22	9	ACH00156	AcH00156 Human Bet
C 890	11.6	44.6	36	3	AAA35771	Aa35771 Permutain	C 963	11.4	43.8	22	9	ACH00156	AcH00156 Human Bet
C 891	11.6	44.6	37	8	ABX79063	AbX79063 Human ret	C 964	11.4	43.8	23	6	ABL55482	AbL55482 Helicobac
C 892	11.6	44.6	37	8	AAAT60960	Aat60960 Nicotiana	C 965	11.4	43.8	23	11	ADL59853	AdL59853 Bacterial
C 893	11.6	44.6	37	2	AAH79805	AaH79805 PCR prime	C 966	11.4	43.8	23	11	ADL59853	AdL59853 Bacterial
C 894	11.6	44.6	37	5	ABL58057	AbL58057 Human Apo	C 967	11.4	43.8	24	3	AAZ99428	AaZ99428 Primer so
C 895	11.6	44.6	37	9	ACC83857	Acc83857 Allele-sp	C 968	11.4	43.8	24	6	AAAD40216	AaD40216 Soy24mer
C 896	11.6	44.6	38	2	AAQ92449	AaQ92449 CD3 epsil	C 969	11.4	43.8	24	6	ABQ04096	AbQ04096 Oligonucle
C 897	11.6	44.6	38	2	AAV85709	Aav85709 LRP5 exon	C 970	11.4	43.8	24	6	ABQ10424	AbQ10424 Oligonucle

CC Amplification of HCV nucleic acid using this primer is up to 100 times
CC more efficient than amplification with prior art primers
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 2
AAV59058
ID AAV59058 standard; DNA; 26 BP.
XX
AC AAV59058;
XX
DT 07-JAN-1999 (first entry)
XX
DE Primer ST280A for HCV fragment.
XX
KW PCR primer; HCV; nucleic acid amplification; ss.
XX
OS Synthetic.
OS Human herpesvirus 5.
XX
PH Key modified_base 26 Location/Qualifiers
FT FT /*tag= a
FT FT /note= "optionally benzylated, methylated, or
FT FT nitrobenzylated"

XX EP866071-A2.
XX
XX 23-SEP-1998.
XX
XX 12-MAR-1998; 98EP-00104461.
XX
XX 20-MAR-1997; 97US-0041127P.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Will SG, Young KKY;
XX
XX WPI; 1998-482929/42.
XX
XX Oligo-nucleotide(s) containing N-substituted nucleotide - useful as
XX PT primers for nucleic acid amplification.
XX
XX Example 6; Page 16; 38pp; English.
XX
XX This sequence represents a primer for a fragment of HCV, and is an
XX example of an oligonucleotide of the invention. The oligonucleotides of
XX the invention are of the formula 5'-S1-Nu-3' or 5'-S1-Nu-S2-3', where S1
XX is a sequence of 5-50 nucleotides; S2 is a sequence of 1-3 nucleotides;
XX and Nu is a nucleotide with a purine or pyrimidine base having an
XX exocyclic amino group substituted by CHR1R2; R1, R2 are H, 1-10C alkyl,
XX alkoxy, optionally substituted phenyl, phenoxy or optionally substituted
XX naphthyl. The oligonucleotides are useful as primers for nucleic acid
XX amplification, preferably by polymerase chain reaction. Use of the
XX modified primers reduces non-specific amplification, especially primer
XX dimer formation, with a concomitant increase in the yield of the intended
XX target
XX
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1
AAT67193
ID AAT67193 standard; DNA; 26 BP.
XX
AC AAT67193;
XX
XX 13-FEB-1998 (first entry)
XX
XX Hepatitis C virus (HCV) RNA amplification primer ST280A.
XX
XX Hepatitis C virus; HCV; ST280A; reverse transcription PCR; RT-PCR;
XX KW PCR primer; ss.
XX
XX Synthetic.
XX
XX EP776981-A2.
XX
XX 04-JUN-1997.
XX
XX 21-NOV-1996; 96EP-00118704.
XX
XX 29-NOV-1995; 95US-0007739P.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Tsang SY;
XX
XX WPI; 1997-291296/27.
XX
XX Oligonucleotide primers for hepatitis C virus RNA amplification - by
XX PT polymerase chain reaction.
XX
XX Claim 1; Page 11; 16pp; English.
XX
XX This upstream primer ST280A is used in the amplification of the Hepatitis
XX C virus (HCV) RNA by reverse transcription PCR. This is used to amplify a
XX 250 base pair product from the 5' untranslated region of the HCV genome.
XX This can be used to detect HCV in a sample with increased sensitivity.

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QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 3
AAH25413
ID AAH25413 standard; DNA; 26 BP.
XX AC
XX AAH25413;
XX
DT 22-AUG-2001 (first entry)
XX
XX Forward PCR primer used to amplify a HCV DNA fragment.
DE
XX Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
XX Hepatitis C virus.
OS
XX Key Location/Qualifiers
FH modified_base 26
FT /*tag= a
FT /note= "derivatisation with a p-(t-butyl)benzyl-residue"
FT
XX WO200137291-A1.
FN
XX 25-MAY-2001.
PD
XX 17-NOV-2000; 2000WO-EP011459.
PF
XX
XX 17-NOV-1999; 99EP-00122853.
PR
XX 12-MAY-2000; 2000EP-00110165.
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
XX Weindel K, Riedling M, Geiger A;
PI
XX WPI; 2001-381247/40.
DR
XX Novel composition of magnetic glass particles for purification of DNA or
PT RNA in automated processes.
PT
XX Example 7; Page 98; 105pp; English.
XX
XX The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between 5
CC -500 nm. The composition is useful for the purification of nucleic acids.
CC The composition can be used to process large quantities of nucleic acid
CC samples, because it does not involve the particles being centrifuged or
CC the fluids being drawn through glass fiber filters. PCR primers AAH25413-
CC 14 were used to amplify HCV DNA fragments. The amplified fragment can be
CC purified using the method of the invention
XX
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ
    Query Match 100.0%; Score 26; DB 4; Length 26;
    Best Local Similarity 100.0%; Pred. No. 0.0052;
    Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 4
ADC84692
ID ADC84692 standard; DNA; 26 BP.
XX AC
XX ADC84692;
XX
DT 01-JAN-2004 (first entry)
XX
XX PCR primer, #1, used to amplify HCV 5' UTR cDNA.
DE

```

```

XX RNA purification; undegraded RNA; RNA binding solution;
KW RNA-complexing salt; chaotropic substance; non-silica solid support;
KW RNA lysing solution; amphiphilic reagent; PCR; ss; primer; 5' UTR;
KW untranslated region.
XX
XX Hepatitis C virus.
OS
XX US2003073830-A1.
XX
XX 17-APR-2003.
PD
XX 12-OCT-2001; 2001US-00974798.
PF
XX 12-OCT-2001; 2001US-00974798.
PR
XX (HEAT/) HEATH E M.
PA (WAGE/) WAGES J M.
XX
XX Heath EM, Wages JM;
PI WPI; 2003-786889/74.
DR
XX Purifying substantially pure and undegraded RNA from biological material
PT involves use of high pH- and strong chaotropic substance-free RNA binding
PT solution that allows RNA to preferentially bind to a solid support.
XX
XX Example 10; Page 11; 14pp; English.
XX
XX The invention discloses a method for purifying substantially pure and
CC undegraded RNA from biological material (B). The method comprises mixing
CC (B) with RNA binding solution (I) that has RNA-complexing salt and is
CC free of strong chaotropic substance, to form a mixture which is contacted
CC with to a non-silica solid support (SS) such that nucleic acids
CC comprising substantially undegraded RNA in mixture preferentially bind to
CC SS, washing SS and eluting bound substantially undegraded RNA from SS.
CC The method may also comprise mixing (B), with an RNA lysing solution (II)
CC buffered at a pH of greater than about 7, and comprising an amphiphilic
CC reagent, and RNA-complexing salt, and is free of a strong chaotropic
CC substance, lysing (B) with (II) to form a lysate comprising nucleic acids
CC comprising substantially undegraded RNA and non-nucleic acid biological
CC matter, contacting the lysate to an immobilised non-silica SS such that
CC the nucleic acids comprising substantially undegraded RNA in the lysate
CC preferentially bind to SS, washing SS and eluting bound substantially
CC undegraded RNA. The methods are useful for purifying substantially pure
CC and undegraded RNA (e.g. total RNA chosen from mRNA, tRNA, rRNA and viral
CC RNA, or its combinations) from biological material containing RNA. The
CC method is useful for purifying RNA from crude and partially purified
CC mixtures of nucleic acids, from (B) such as eukaryotic, prokaryotic,
CC microbial, bacterial or plant cells, mycoplasma, protozoa, bacteria,
CC fungi, viruses, yeasts, rickettsia or their homogenates. The method is
CC also useful for purifying RNA from (B) such as whole blood, bone marrow,
CC blood spots, blood serum, blood plasma, buffy coat preparations, saliva,
CC cerebrospinal fluid, solid animal tissues, faeces, urine, tears, sweat or
CC from environmental samples taken from air, water sediment or soil. The
CC purified RNA is useful in analytical and diagnostic methods such as
CC reverse transcriptase-PCR and micro array analyses. The method purifies
CC RNA from a variety of biological materials without the use of hazardous
CC substances such as phenol and chloroform or hazardous chaotropic
CC substances such as guanidinium salts, urea, etc. The method allows the
CC elution of RNA in low salt reagents thus eliminating tedious desalting
CC steps. The method is versatile and effective. The sequence presented is a
CC PCR primer which was used to amplify Hepatitis C virus (HCV) 5'
CC untranslated region (UTR) to demonstrate the integrity of the purified
CC mRNA.
XX
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ
    Query Match 100.0%; Score 26; DB 10; Length 26;
    Best Local Similarity 100.0%; Pred. No. 0.0052;
    Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

```

Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 5
AAD43287
ID AAD43287 standard; DNA; 27 BP.

XX AAD43287;
AC

XX 14-NOV-2002 (first entry)
DT

XX HCV DNA amplifying PCR primer, ST280.
DE

XX Amplification; target nucleic acid; PCR; primer; ss.
KW

XX Hepatitis C virus.
OS

XX Key Location/Qualifiers
FH stem_loop 1..16

FT misc_binding 1..5

FT misc_binding 11..16

FT bound_moiety= "Nucleotides 16-11"

FT bound_moiety= "Nucleotides 5-1"

XX EPI236805-A1.
PN

XX 04-SEP-2002.
PD

XX 27-FEB-2002; 2002EP-00004483.
PF

XX 02-MAR-2001; 2001EP-00105172.
PR

XX (HOFF) ROCHE DIAGNOSTICS GMBH.
PA

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA

XX Jaeger S;
PI

XX WPI; 2002-610695/66.
DR

XX Amplification of a target nucleic acid region using a specific control
sequence.

XX Example 2; Fig 3; 28pp; English.
PS

CC The invention relates to a method for amplification of a target nucleic
acid region in a sample using a specific control sequence. The invention
is also directed to a method of determination of a target nucleic acid
using a special control nucleic acid. Nucleic acids of the invention are
used as a control in a hybridisation reaction for amplifying target nucleic acids and
as a control in a hybridisation reaction for determination of target
nucleic acids. The present sequence is HCV DNA (Hepatitis C virus) type I
DNA amplifying PCR primer. This primer is used to illustrate the methods
of the invention. Note: This sequence is stated to be same as that shown
as SEQ ID NO:6 in sequence listing. However this sequence has additional
A at its 3' end

XX Sequence 27 BP; 8 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 26; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 6
AAD43739

ID AAD43739 standard; DNA; 27 BP.

XX AAD43739;
AC

XX 07-AUG-2003 (revised)
DT

XX 14-NOV-2002 (first entry)
DT

XX HCV DNA amplifying PCR primer, ST280.
DE

XX Amplification; target nucleic acid; control nucleic acid; PCR; primer;
ss.

XX Hepatitis C virus.
OS

XX Key Location/Qualifiers
FH stem_loop 1..16

FT misc_binding 1..5

FT misc_binding 11..16

FT bound_moiety= "Nucleotides 16-11"

FT bound_moiety= "Nucleotides 5-1"

XX EPI236804-A1.
PN

XX 04-SEP-2002.
PD

XX 02-MAR-2001; 2001EP-00105172.
PF

XX 02-MAR-2001; 2001EP-00105172.
PR

XX (HOFF) ROCHE DIAGNOSTICS GMBH.
PA

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA

XX Jaeger S;
PI

XX WPI; 2002-610694/66.
DR

XX Amplification of a target nucleic acid region using control sequences.
PS

XX Example 2; Fig 3; 29pp; English.
PS

CC The invention relates to a method for amplification of a target nucleic
acid region. The method is useful for amplification of a nucleic acid
molecule using control nucleic acid sequences. The control nucleic acid
sequences are at least in part parallel-complementary to the sequence of
the target nucleic acid. The present sequence is HCV DNA amplifying PCR
primer. Note: This sequence is stated to be same as that shown as SEQ ID
NO:6 in sequence listing. However this sequence has additional A at its
3' end. (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 27 BP; 8 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 26; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 7
ABK88588

ID ABK88588 standard; DNA; 30 BP.

XX ABK88588;
AC

XX 21-OCT-2002 (first entry)
DT

XX Hepatitis C virus (HCV) forward RT-PCR primer.
DE

XX

KW Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor;
 KW cell culture replication; reverse transcriptase PCR; RT-PCR; primer; ss.
 XX
 OS Hepatitis C virus.
 XX
 FN WO200252015-A2.
 XX
 PD 04-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-CA001843.
 XX
 PR 22-DEC-2000; 2000US-0257857P.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM CANADA LTD.
 XX
 PI Kukolj G, Pause A;
 XX
 DR WPI; 2002-575382/61.
 XX
 PT New self-replicating RNA molecules from Hepatitis C virus (HCV), which
 PT possess enhanced transduction or replication efficiency, useful for
 PT evaluating potential inhibitors of HCV replication.
 XX
 PS Example 9; Page 24; 140pp; English.
 XX
 CC The invention describes a self-replicating hepatitis C virus (HCV)
 CC polynucleotide molecule comprising a 5'-non translated region (NTR),
 CC where guanine at position 1 is substituted for adenine, a HCV polyprotein
 CC region coding for a HCV polyprotein; and a 3'-NTR region. The self-
 CC replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating
 CC potential inhibitors of HCV replication. The HCV RNA molecule is also
 CC useful for efficiently establishing cell culture replication. The self-
 CC replicating polynucleotide molecule contains a 5'-NTR, where G at
 CC position 1 is substituted for A, and therefore provides an alternative to
 CC existing systems comprising a self-replicating HCV RNA molecule that, in
 CC conjunction with mutations in the HCV non-structural region, such as the
 CC G(2042)C/R mutations, transduces and/or replicates with greater
 CC efficiency. This sequence represents a reverse transcriptase PCR primer
 CC used to amplify HCV RNA during testing of replicon RNA levels in cell
 CC lines
 XX
 SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 26; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
 Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
 RESULT 8
 ACC48582
 ID ACC48582 standard; DNA; 30 BP.
 XX
 AC ACC48582;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Hepatitis C virus 5' untranslated region forward PCR primer.
 XX
 KW HCV; RNA polymerase; enzyme; inhibitor; virucide; hepatotropic;
 KW antiinflammatory; heterocycle; PCR; primer; ss.
 XX
 OS Hepatitis c virus.
 XX
 FN WO2003010140-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 18-JUL-2002; 2002WO-CA001127.
 XX

PR 25-JUL-2001; 2001US-0307674P.
 PR 07-DEC-2001; 2001US-0338061P.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM CANADA LTD.
 XX
 PI Beaulieu PL, Fazal G, Kukolj G, Jolicoeur E, Gillard J;
 PI Poupart M, Rancourt J;
 XX
 DR WPI; 2003-342387/32.
 XX
 PT New heterocyclic compounds are viral polymerase inhibitors, useful for
 PT treating hepatitis C virus.
 XX
 PS Example 25; Page 74; 112pp; English.
 XX
 CC The invention provides novel heterocyclic compounds that have inhibitory
 CC activity against the RNA-dependent RNA polymerase NSSB (see ABR41892) of
 CC hepatitis C virus (HCV). The present sequence is a forward primer for the
 CC 5' untranslated region of HCV. This forward primer, the reverse primer
 CC given in ACC48583 and the fluorescent probe given in ACC48584 were used
 CC for real-time RT-PCR in a cell-based HCV RNA replication assay. RT-PCR
 CC data allowed the HCV RNA copy number in each well of a cell culture plate
 CC to be determined, and this was used as a measure of the amount of
 CC replicating HCV RNA in the presence of various concentrations of
 CC different HCV RNA polymerase inhibitors. The cell-based HCV RNA
 CC replication assay showed that selected compounds had IC50 values of less
 CC than 500 nM to over 1 uM. These compounds can be used in the treatment or
 CC prevention of HCV infection
 XX
 SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 26; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
 Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
 RESULT 9
 AAD51019
 ID AAD51019 standard; DNA; 30 BP.
 XX
 AC AAD51019;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Hepatitis C virus (HCV) E2 cDNA specific probe.
 XX
 KW Transmembrane protein; extracellular domain; rous sarcoma virus; RSV;
 KW intracellular internalisation signal; vaccine; therapy; viral infection;
 KW hepatitis C virus; HCV; human immunodeficiency virus; herpes B virus;
 KW HBV; HIV; gene therapy; virucide; probe; ss.
 XX
 OS Hepatitis C virus.
 XX
 FN WO200294874-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 24-MAY-2002; 2002WO-CA000762.
 XX
 PR 24-MAY-2001; 2001GB-00012652.
 XX
 PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
 XX
 PI Tan YH, Tan YJ, Lim SP, Lim SG, Hong WJ, Goh PY;
 XX
 DR WPI; 2003-120788/11.
 XX
 PT Chimeric transmembrane protein for manufacturing a medicament for
 PT treating or preventing viral infection, comprises an extracellular domain

PT capable of binding a virus and an intracellular internalization signal.

XX Example 1; Col 23; 33pp; English.

PS The invention relates to a chimeric transmembrane protein comprising an

CC extracellular domain capable of binding a virus and an intracellular

CC internalisation signal. The protein is useful for identifying an

CC antiviral agent or a vaccine, which is used for manufacturing a

CC medicament for treating or preventing viral infection. The viral

CC infections are hepatitis C virus (HCV), human immunodeficiency virus

CC (HIV), herpes B virus (HBV), rous sarcoma virus (RSV), influenza virus,

CC herpes simplex virus, rabies virus, coxsackie virus, or rhinovirus. The

CC invention is also used in gene therapy. The present sequence is a probe

CC specific for HCV E2 cDNA. This sequence is used in the exemplification of

CC the invention

XX

SQ Sequence 30 BP; 8 A; 6 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

DB 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 10

ACC43164

ID ACC43164 standard; DNA; 30 BP.

AC ACC43164;

XX 17-JUN-2003 (first entry)

DT PCR primer used to amplify a 256 bp region of the 5' UTR of HCV.

DE HCV; viral polymerase inhibitor; HCV replication; HCV infection; PCR;

KW primer; ss.

XX Hepatitis C virus.

OS WO2003010141-A2.

XX

PN 06-FEB-2003.

PD 18-JUL-2002; 2002WO-CA001128.

PF 25-JUL-2001; 2001US-0307674P.

PR 07-DEC-2001; 2001US-0338061P.

XX (BOEH) BOEHRINGER INGELHEIM CANADA LTD.

PA Beaulieu PL, Fazal G, Goulet S, Kukolj G, Poirier M;

XX Tsantrizos YS, Jolicoeur E, Gillard J, Poupard M, Rancourt J;

PI WPI; 2003-300442/29.

DR New viral polymerase inhibitors, useful in the treatment of hepatitis C

XX virus.

XX Example 48; Page 146; 336pp; English.

PS PCR primers ACC43164-65 and probe ACC43166 were used to amplify and

CC detect, respectively, a 256 bp fragment of the 5' untranslated region (5'

CC UTR) of Hepatitis C virus (HCV). The primers and probe were used to

CC determine the effect on HCV replication of compounds of the invention.

CC The specification describes viral polymerase inhibitor compounds, and

CC their isomers, enantiomers, diastereomers or tautomers. The compounds are

CC of a formula given in the specification. Viral polymerase inhibitor

CC compounds of the invention are inhibitors of HCV replication, and are

CC used in the treatment or prevention of HCV infection

XX

SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 11

ACF36230

ID ACF36230 standard; DNA; 30 BP.

XX ACF36230;

XX 04-DEC-2003 (first entry)

DT HCV 5' IRES quantifying forward primer.

DE HCV; hepatotropic; antiinflammatory; virucide. NS3 protease; RT-PCR;

KW RNA replication; IRES; primer; ss.

XX Hepatitis C virus.

OS WO2003064455-A2.

XX 07-AUG-2003.

PD 24-JAN-2003; 2003WO-CA000089.

PF 30-JAN-2002; 2002CA-02369711.

PR (BOEH) BOEHRINGER INGELHEIM CANADA LTD.

PA Llinas-Brunet M, Gorys VJ;

XX WPI; 2003-663463/62.

DR New heterocyclic tripeptides are Hepatitis C Virus (HCV) NS3 protease

PT inhibitors, used in treatment of hepatitis C viral infection and

PT producing fewer side effects.

XX Example 10; Page 34; 21pp; English.

PS The invention relates to heterocyclic tripeptides of specified formula.

CC The compounds inhibit the activity of Hepatitis C virus (HCV) NS3

CC protease activity and also inhibit HCV RNA replication. The compounds

CC show good pharmacokinetic properties and can be used in the manufacture

CC of a medicament for the treatment or prevention of HCV infection in

CC mammals. The present sequence represents a primer used for amplifying a

CC 5' UTR fragment of HCV, used in a RT-PCR quantification of HCV 5' IRES

CC sequence

XX

SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 12

ACF36227

ID ACF36227 standard; DNA; 30 BP.

XX ACF36227;

XX 04-DEC-2003 (first entry)

DT


```

XX HCV 5' IRES quantifying forward primer.
XX HCV; hepatotropic; antiinflammatory; virucide. NS3 protease; RT-PCR;
XX RNA replication; IRES; primer; ss.
XX Hepatitis C virus.
OS WO2003064416-A1.
XX
XX PD 07-AUG-2003.
XX
XX PF 24-JAN-2003; 2003WO-CA000091.
XX
XX PR 01-FEB-2002; 2002CA-02369970.
XX
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
XX PI Llinas-Brunet M, Bailey MD, Ghire E;
XX
XX DR WPI; 2003-663458/62.
XX
XX PT New heterocyclic tripeptides useful for the treatment of hepatitis C
XX viral infection.
XX
XX PS Example 10; Page 32; 21pp; English.
XX
XX CC The invention relates to heterocyclic tripeptides of specified formula.
XX The compounds inhibit the activity of Hepatitis C virus (HCV) NS3
XX protease activity and also inhibit HCV RNA replication. The compounds
XX show good pharmacokinetic properties and can be used in the manufacture
XX of a medicament for the treatment or prevention of HCV infection in
XX mammals. The present sequence represents a primer used for amplifying a
XX 5' UTR fragment of HCV, used in in a RT-PCR quantification of HCV 5' IRES
XX sequence
XX
XX SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 26; DB 10; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.0054;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
XX |||||||||||||||||||||||||||
XX Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
XX
XX RESULT 13
XX ACF36280
XX ID ACF36280 standard; DNA; 30 BP.
XX
XX AC ACF36280;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE HCV 5' IRES quantifying forward primer.
XX
XX KW HCV; hepatotropic; antiinflammatory; virucide; NS3 protease; RT-PCR;
XX RNA replication; IRES; primer; ss.
XX
XX OS Hepatitis C virus.
XX
XX PN WO2003064456-A1.
XX
XX PD 07-AUG-2003.
XX
XX PF 24-JAN-2003; 2003WO-CA000090.
XX
XX PR 01-FEB-2002; 2002CA-02370396.
XX
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
XX PI Llinas-Brunet M, Gorys VJ;

```

```

XX WPI; 2003-671487/63.
XX
XX PT New tripeptides (having substituted quinoline with hydroxyproline ether
XX side chain) derivatives are Hepatitis C virus (HCV) NS3 protease activity
XX inhibitors useful in treatment of hepatitis C viral infection with fewer
XX side effects.
XX
XX PS Example 11; Page 43; 28pp; English.
XX
XX CC The invention relates to tripeptides (having substituted quinoline with
XX hydroxyproline ether side chain) derivatives of specified formula. The
XX compounds inhibit the activity of Hepatitis C virus (HCV) NS3 protease
XX activity and also inhibit HCV RNA replication. The compounds show good
XX pharmacokinetic properties and can be used in the manufacture of a
XX medicament for the treatment or prevention of HCV infection in mammals.
XX The present sequence represents a primer used for amplifying a 5' UTR
XX fragment of HCV, used in in a RT-PCR quantification of HCV 5' IRES
XX sequence
XX
XX SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 26; DB 10; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.0054;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
XX |||||||||||||||||||||||||||
XX Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
XX
XX RESULT 14
XX ABZ76307
XX ID ABZ76307 standard; DNA; 30 BP.
XX
XX AC ABZ76307;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX DE HCV RNA 5' IRES quantifying forward primer.
XX
XX KW NS5B; benzimidazole; viral polymerase; virucide; hepatotropic; IRES;
XX antiinflammatory; RT-PCR; primer; ss.
XX
XX OS Hepatitis C virus.
XX
XX PN WO2003007945-A1.
XX
XX PD 30-JAN-2003.
XX
XX PF 18-JUL-2002; 2002WO-CA001129.
XX
XX PR 20-JUL-2001; 2001US-0306669P.
XX
XX PR 07-DEC-2001; 2001US-0338324P.
XX
XX PA (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
XX
XX PI Beaulieu PL, Fazal G, Goulet S, Kukolj G, Poirier M;
XX Tsantrizos YS;
XX
XX DR WPI; 2003-289764/28.
XX
XX PT New 5-substituted benzimidazole derivatives, useful for treating
XX hepatitis C virus infection by inhibiting viral polymerase, and their
XX intermediates are new.
XX
XX PS Example 24; Page 161; 166pp; English.
XX
XX CC The invention relates to isomers, diastereoisomers, enantiomers and
XX tautomers of 5-substituted benzimidazole compounds of specified formula.
XX The compounds are viral polymerase inhibitors, especially they are potent
XX inhibitors of HCV NS5B polymerase. The compounds are used to treat or
XX prevent infection by hepatitis C virus. The present sequence represents a

```

CC primer used in real-time RT-PCR quantification of the 5' IRES (internal
CC ribosome entry sequence) of HCV RNA
XX
SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 26; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
RESULT 15
ADP20412
ID ADP20412 standard; DNA; 37 BP.
XX
XX
AC ADP20412;
XX 09-SEP-2004 (first entry)
DT
DE Hepatitis C virus IRES region II consensus sequence, SEQ ID 3.
XX
XX Virucide; Cytostatic; p110 subunit;
KW eukaryotic translation initiation factor eIF3; region II;
KW internal ribosome entry site; IRES; aminoglycoside;
KW hepatitis C infection; swine fever; bovine diarrhoea; viral infection;
KW cancer; ds.
XX
OS Hepatitis C virus.
XX
XX FR2848572-A1.
XX
XX 18-JUN-2004.
XX 12-DEC-2002; 2002FR-00015718.
XX 12-DEC-2002; 2002FR-00015718.
PR
XX (UYFO-) UNIV FOURIER JOSEPH.
XX Balakireva L;
XX
XX WPI; 2004-452919/43.
XX
XX In vitro screening for antiviral agents, from ability to inhibit complex
XX formation between the p110 subunit of translation initiation factor eIF3
XX and region II of the viral internal ribosome binding site.
XX
XX Claim 3; SEQ ID NO 3; 45pp; French.
XX
XX The present invention relates to an in vitro method of screening for
XX compounds (A) that inhibit the formation of a complex between the p110
XX subunit (ADP20413) of the eukaryotic translation initiation factor eIF3
XX and region II of the internal ribosome entry site (IRES; ADP20411) of
XX hepatitis C virus (HCV). Preferably the p110 recognition motif (ADP20414)
XX and the region II consensus sequence (ADP20412), or fragment of it
XX containing at least 8 consecutive nucleotides, are used. (A) is
XX especially an aminoglycoside, specifically tobramycin or an
XX oligonucleotide antisense to consensus sequence ADP20412, or parts of it.
XX (A) are used for treating infection by hepatitis C, swine fever and
XX bovine diarrhoea viruses, also for treating viral or non-viral diseases
XX which involve proteins synthesis of which is initiated from an IRES, e.g.
XX cancer.
XX
SQ Sequence 37 BP; 8 A; 10 C; 9 G; 10 T; 0 U; 0 Other;
Query Match 96.2%; Score 25; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGTT 25

DB 13 GCAGAAAGCGTCTAGCCATGGCGTT 37
RESULT 16
AAQ37573
ID AAQ37573 standard; DNA; 24 BP.
XX
XX AC AAQ37573;
XX
XX 25-MAR-2003 (revised)
DT 23-JUN-1993 (first entry)
DE HCV conserved region upstream primer/probe KY80, position 56-79.
XX
XX Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW regulation; US; Japan; C9; ss.
XX
OS Synthetic.
XX
XX EP529493-A2.
XX
XX 03-MAR-1993.
XX
XX 19-AUG-1992; 92EP-00114115.
XX
XX 27-AUG-1991; 91US-00751305.
PR
XX 21-JUL-1992; 92US-00918844.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Resnick RM, Young KKY;
XX
XX WPI; 1993-068572/09.
XX
XX Compens. comprising oligo:nucleotide probe-primer - used for detecting
XX hepatitis C virus strains Japan, US and C9.
XX
XX Claim 4; Page 7; 43pp; English.
XX
XX The sequences given in AAQ37569-96 are oligonucleotides which can be used
XX as primers or probes which hybridise to the conserved region at the 5' -
XX end of the hepatitis C virus (HCV) genome. HCV is a small RNA virus
XX containing a small, positive sense, molecule of RNA about 10,000
XX nucleotides in length. the genome contains a single, long, open reading
XX frame believed to translated in to a single, large polyprotein and
XX subsequently processed. The open reading frame begins at nucleotide 343
XX (using the numbering system from the prototype virus) following an
XX untranslated region (UTR) the 5'UTR sequence is relatively conserved and
XX may be important in viral replication and regulation. The 5' end of the
XX coding region is also conserved. These primer/probes can be used to
XX identify different HCV isolates such as US, Japan and C9 (see also
XX AAQ37597-601). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGTT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGTT 24
RESULT 17
AAQ79964
ID AAQ79964 standard; DNA; 24 BP.
XX
XX AC AAQ79964;
XX

DT 25-MAR-2003 (revised)
 DT 01-AUG-1995 (first entry)
 XX
 DE Primer KY90 for HCV RNA.
 XX
 KW Primer; PCR; polymerase chain reaction; amplification; RNA detection;
 KW reverse transcription; hepatitis C virus; HCV; ss.
 XX
 OS Synthetic.
 XX
 PN EP632134-A2.
 XX
 XX
 PD 04-JAN-1995.
 XX
 XX 20-JUN-1994; 94EP-00109468.
 PF
 XX 01-JUL-1993; 93US-00086483.
 PR
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX Gelfand DH, Myers TW, Sigua CL;
 PI
 XX WPI; 1995-037815/06.
 DR
 XX Improved amplification method for target RNA - using buffering agent
 PT which buffers both pH and divalent cation concn.
 PT
 XX Example 6; Page 22; 37pp; English.
 PS
 XX The primers given in AAQ79963-64 were used to amplify HCV templates for
 CC use in a novel method of RNA amplification involving high-temp. reverse
 CC transcription and PCR. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 RESULT 18
 AAT93541
 ID AAT93541 standard; DNA; 24 BP.
 XX
 AC AAT93541;
 XX
 DT 19-FEB-1998 (first entry)
 XX
 XX Sense primer KY80 for amplification of HCV RNA.
 DE
 XX Armoured RNA; bacteriophage M2; RT-PCR; ribonuclease; recombinant;
 KW Human immunodeficiency virus; HIV; Hepatitis C Virus; HCV; viral RNA;
 KW detection; quantification standard; maturase protein; coat protein;
 KW PCR primer; OS RNA; reverse transcriptase-PCR; ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus; Virus.
 XX
 PN US5677124-A.
 XX
 PD 14-OCT-1997.
 XX
 XX 03-JUL-1996; 96US-00675153.
 PF
 XX 03-JUL-1996; 96US-00675153.
 PR
 XX (AMEI-) AMEION INC.
 PA (CENE-) CENETRON DIAGNOSTICS LLC.
 XX

PI Pasloske BL, Dubois DB, Winkler MM;
 XX WPI; 1997-511866/47.
 DR
 XX Recombinant RNA segment encapsidated in bacteriophage viral coat protein
 PT - RNA detection and/or quantification standard.
 PT
 XX Example 5; Col 22; 23pp; English.
 PS
 XX This sense primer is used in the RT-PCR amplification of HCV RNA to
 CC create a quantitative HCV "armoured RNA" standard. An "armoured RNA" is a
 CC recombinant RNA segment encapsidated in bacteriophage viral coat protein.
 CC The recombinant RNA segment comprises an operator coding sequence, a
 CC viral maturase protein binding site, and a non-bacteriophage sequence.
 CC The recombinant RNA in its packaged form is highly resistant to
 CC ribonucleases, insuring that the RNA standard is not compromised by
 CC inadvertent ribonuclease contamination. The armoured RNA standards are
 CC ideal as RNA standards for the quantification of RNA viruses such as HIV
 CC and HCV from human body fluids such as blood and cerebrospinal fluid
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 RESULT 19
 AAT87096
 ID AAT87096 standard; DNA; 24 BP.
 XX
 AC AAT87096;
 XX
 XX 25-MAR-2003 (revised)
 DT 07-JAN-1998 (first entry)
 DT
 XX HCV gene PCR primer KY80.
 DE
 XX RNA; plasma; hepatitis C virus; HCV; primer; PCR;
 KW polymerase chain reaction; ss.
 KW
 XX Synthetic.
 OS
 XX US5654179-A.
 PN
 XX 05-AUG-1997.
 PD
 XX 03-OCT-1994; 94US-00317220.
 PF
 XX 14-NOV-1990; 90US-00614921.
 PR 19-JUN-1992; 92US-00901545.
 PR 08-APR-1993; 93US-00044649.
 XX
 PA (HYDS) HRI RES INC.
 XX
 XX Lin L;
 PI
 XX WPI; 1997-401849/37.
 DR
 XX Preparation of RNA samples from plasma - by alcohol precipitation after
 PT lysis with guanidinium thiocyanate.
 PT
 XX Disclosure; Col 47; 60pp; English.
 PS
 XX Primer KY80 (AAT87096) and primer KY78 (AAT87095) were used for the PCR
 CC amplification of a 305 bp hepatitis C virus gene product (see AAT87088).
 CC A claimed method for preparing RNA samples comprises: (a) mixing plasma
 CC with an aqueous buffer solution containing guanidinium thiocyanate and
 CC beta-mercaptoethanol; (b) heating the mixture; (c) adding an equal volume

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CC of an alcohol to precipitate RNA; and (d) recovering the RNA. The method
 CC can be used to prepare RNA samples for subsequent amplification,
 CC especially for detecting pathogens, e.g. hepatitis C virus or HIV.
 CC Compared with the known 'Isoquick' and 'RNazol' methods, the method
 CC uses fewer tubes (just one), requires fewer steps, takes less time and
 CC produces no toxic waste. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 20
 AAT64887
 ID AAT64887 standard; DNA; 24 BP.
 XX
 AC AAT64887;
 XX
 AC
 XX 25-MAR-2003 (revised)
 DT 12-MAR-1998 (first entry)
 XX
 DE Hepatitis C virus (HCV) oligonucleotide KY80.
 XX
 DE Hepatitis C virus; reverse transcription; probe; PCR primer; detection;
 KW ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 EP787807-A2.
 XX
 PD 06-AUG-1997.
 XX
 PF 19-AUG-1992; 97EP-00106534.
 XX
 PR 27-AUG-1991; 91US-00751305.
 PR 21-JUL-1992; 92US-00918844.
 PR 19-AUG-1992; 92EP-00114115.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 PI Resnick RM, Young KKY;
 XX
 XX WPI; 1997-387489/36.
 DR
 XX
 XX Oligo:nucleotide probes and primers for detecting hepatitis C virus
 PT nucleic acid - from many different strains without loss of specificity,
 PT allow single step reverse transcription and amplification.
 XX
 XX Claim 2 and 5; Page 7; 35pp; English.
 PS
 XX
 XX This oligonucleotide KY80 can be used as a probe for detecting hepatitis
 CC C virus (HCV) nucleic acid from a Japanese or US prototype strain. This
 CC oligonucleotide can also be used as a primer for amplifying HCV nucleic
 CC acid. This primer is capable of amplifying HCV C9 prototype strains also.
 CC The sequence of this oligonucleotide is contained in a specific region of
 CC the HCV genomic nucleic acid. The probe or the primer is preferably labelled.
 CC The probe is used to detect HCV nucleic acid, preferably after this has
 CC been amplified using the new primer in reverse transcription polymerase
 CC chain reaction (RT-PCR), for both diagnostic and epidemiological
 CC applications. The primer is effective for both reverse transcription and
 CC PCR, eliminating the need to open the reaction tube during the procedure.
 CC Amplification is effective (no need for a second round of PCR with nested
 CC primers) and provides high sensitivity. The probe is directed to
 CC conserved regions and so can detect many different strains without loss
 CC of specificity. (Updated on 25-MAR-2003 to correct PF field.) (Updated on
 CC 25-MAR-2003 to correct PR field.)

XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 21
 AAV15320
 ID AAV15320 standard; DNA; 24 BP.
 XX
 AC AAV15320;
 XX
 AC
 XX 25-MAR-2003 (revised)
 DT 28-MAY-1998 (first entry)
 XX
 DE Hepatitis C virus PCR primer PKY80.
 XX
 XX Hepatitis C virus; HCV; PCR primer; detection; reverse transcription;
 KW enzyme immunoassay; viral RNA; ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 PN WO9746716-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 03-JUN-1997; 97WO-IT000128.
 XX
 PR 07-JUN-1996; 96IT-RM000404.
 XX
 PA (WESA) WABCO BV.
 XX
 PI Bosio P, Strumia C, Clemenza F;
 XX
 WPI; 1998-042222/04.
 DR
 XX
 PT Detection of hepatitis C virus - by reverse transcription, single-step
 PT PCR and detection by DNA enzyme immunoassay.
 XX
 XX Disclosure; Page 4; 26pp; English.
 PS
 XX
 XX The present sequence represents a PCR primer involved in the method of
 CC the present invention for detecting hepatitis C virus (HCV). The method
 CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
 CC resulting cDNA by a single polymerase chain reaction in a reaction
 CC mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme unit
 CC ; and (c) detecting the amplification product by DEIA (DNA enzyme
 CC immunoassay) using an oligonucleotide probe. The sensitivity of this
 CC method is at least equal to that achievable by more complicated assays
 CC using nested PCR. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 22
 AAV18849
 ID AAV18849 standard; DNA; 24 BP.
 XX

AC AAV18849;
 DT 11-JUN-1998 (first entry)
 DE Primer KY80 for HCV DNA.
 KW PCR primer; HCV; nucleic acid standard; Armored RNA; ss.
 XX
 OS Synthetic.
 OS Hepatitis virus.
 PN WO9800547-A1.
 XX
 PD 08-JAN-1998.
 XX
 PF 02-JUL-1997; 97WO-US012551.
 PR 03-JUL-1996; 96US-0021145P.
 PR 03-JUL-1996; 96US-00675153.
 PR 24-JUN-1997; 97US-00881571.
 XX
 PA (AMBI-) AMBION INC.
 PA (CENE-) CENETRON DIAGNOSTICS LLC.
 XX
 PI Dubois DB, Winkler MM, Pasloske BL;
 XX
 DR WPI; 1998-086972/08.
 XX
 PT Ribonuclease resistant RNA molecules and their production - useful as
 PT standards in quantitative PCR for pathogens, e.g. HIV-1, HIV-2 and HCV.
 XX
 PS Example 5; Page 41; 134pp; English.
 XX
 CC The present sequence is a primer for hepatitis C virus (HCV) DNA, which
 CC was used in the preparation of a nucleic acid standard, comprising a
 CC nuclease resistant nucleic acid segment encoding a standard nucleic acid,
 CC i.e. RNA. The ribonuclease resistant RNA standard, designated Armored RNA
 CC (RTM) is useful as an internal or external nucleic acid standard in
 CC quantitative assays, e.g. PCR or RT-PCR for the presence of a tested
 CC nucleic acid in blood samples
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 23
 AA223536
 ID AA223536 standard; DNA; 24 BP.
 XX
 AC AA223536;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE HCV wild type genome primer KY80.
 XX
 KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
 KW cellular; yeast; fungal; primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 PN DE19814828-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 02-APR-1998; 98DE-01014828.

XX
 PR 02-APR-1998; 98DE-01014828.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Kessler C, Haberhausen G, Batz H, Oerum H;
 XX
 DR WPI; 1999-552286/47.
 XX
 PT Nucleic acid amplification assay for detecting viral, bacterial,
 PT cellular, yeast or fungal nucleic acids.
 XX
 PS Example 1; Page 19; 28pp; German.
 XX
 CC This invention describes a novel assay for a nucleic acid comprises: (a)
 CC generating amplification products from a fragment of the nucleic acid,
 CC (b) contacting the amplification products with a probe; and (c) detecting
 CC hybridization between the amplification product and the probe. The assay
 CC is useful for detection of viral, bacterial, cellular, yeast or fungal
 CC nucleic acids in human, animal, bacterial, plant, yeast or fungal
 CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
 CC or liquid biopsy samples. This sequence represents a primer used in the
 CC method of the invention
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 24
 AA223968
 ID AA223968 standard; DNA; 24 BP.
 XX
 AC AA223968;
 XX
 DT 28-JUN-1999 (first entry)
 XX
 DE PCR primer KY80.
 XX
 KW Amplification; medical; forensic; diagnosis; food analysis; blood;
 KW environmental analysis; plant protection; veterinary medicine;
 KW human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia;
 KW screening; PCR primer; detection; probe; ss.
 XX
 OS Synthetic.
 XX
 PN DE19748690-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 04-NOV-1997; 97DE-01048690.
 XX
 PR 04-NOV-1997; 97DE-01048690.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 DR WPI; 1999-278780/24.
 XX
 PT Detecting nucleic acid by generating short amplicons and probing e.g. for
 PT diagnosis, food and environmental analysis and plant protection.
 XX
 PS Example 1; Page 16; 22pp; German.
 XX
 CC This invention describes a method for the detection of nucleic acid which
 CC comprises amplification and reaction of the amplicon with a probe. The
 CC method is used to detect nucleic acid e.g. for medical or forensic
 CC diagnosis, in food and environmental analysis, in plant protection and

CC veterinary medicine, e.g. for detecting human immune deficiency virus,
 CC hepatitis B or C viruses, or Chlamydia, in blood screening. The method
 CC provides target-dependent, exponential amplification for highly specific
 CC and sensitive, reproducible and quantitative detection of one or more
 CC nucleic acids (single or double stranded). The design of primers and
 CC probes is sufficiently flexible to allow many nucleic acids to be
 CC detected in a standardized reaction format using partly the same primers
 CC and probes. Only small amplicons are produced (requiring short
 CC amplification cycles), there is no competition/displacement between the
 CC short counter-strand of the amplicon and the detection probe, and
 CC specificity is high because the relative proportion of the internal
 CC detection region is increased with respect to the total amplicon length,
 CC allowing better differentiation between (viral) subtypes. Also short
 CC amplicons are less likely to undergo non-specific hybridization, so
 CC background is low, and short RNA sequences are more stable, with reduced
 CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
 CC PCR primers and probes used in the method of the invention
 CC
 CC Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGCTAGCCATGGCGT 24
 |||||
 Db 1 GCAGAAAGCGCTAGCCATGGCGT 24

RESULT 25
 AAX78451
 ID AAX78451 standard; DNA; 24 BP.
 AC AAX78451;
 XX
 XX
 XX 26-AUG-1999 (first entry)
 DT HCV PCR primer 1.
 XX
 XX RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
 KW ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV; HTLV-1;
 KW HTLV-2; hepatitis B; enterovirus; blood-borne pathogen; ss.
 XX
 XX Synthetic.
 OS Hepatitis C virus.
 XX
 XX US5919625-A.
 XX
 XX 06-JUL-1999.
 XX
 XX 29-APR-1997; 97US-00841252.
 XX
 XX 03-JUL-1996; 96US-00675153.
 XX (AMBI-) AMBION INC.
 PA (CENE-) CENETRON DIAGNOSTICS LLC.
 XX
 XX Pasloske BL, Dubois DB, Winkler MM;
 FI
 XX WPI; 1999-394617/33.
 XX
 XX Ribonuclease resistant viral RNA standards.
 PT
 XX Example V; Col 31-32; 22pp; English.

CC This invention describes the construction of novel RNA standards for the
 CC quantification of human immunodeficiency virus (HIV) and hepatitis C
 CC virus (HCV) from e.g. cerebrospinal fluids. The method involves (1)
 CC obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
 CC RNA standard, encapsulated in a bacteriophage viral coat protein, which
 CC comprises an RNA segment having a segment encoding a sequence that serves
 CC as a standard in detection or quantification of the RNA of interest; (3)
 CC mixing the sample with the standard; (4) isolating RNA from the mixture,

CC and (5) assaying for the presence of the RNA. The method is useful for
 CC the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1, HTLV-2,
 CC hepatitis G, an enterovirus or a blood-borne pathogen. This sequence
 CC represents a PCR primer used to amplify a region of the Hepatitis C
 CC genome which is used in the method of the invention
 CC
 CC Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGCTAGCCATGGCGT 24
 |||||
 Db 1 GCAGAAAGCGCTAGCCATGGCGT 24

RESULT 26
 AAZ09797
 ID AAZ09797 standard; DNA; 24 BP.
 XX
 AC AAZ09797;
 XX
 XX 26-NOV-1999 (first entry)
 DT HCV PCR primer KY80.
 XX
 XX Probe; amplification; primer; reporter group; quencher group; PCR;
 KW amplicon; detection; ss.
 XX
 XX Synthetic.
 OS Hepatitis C virus.
 XX
 XX DE19814001-A1.
 XX
 XX 30-SEP-1999.
 XX
 XX 28-MAR-1998; 98DE-01014001.
 XX
 XX 28-MAR-1998; 98DE-01014001.
 XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA
 XX Kessler C, Haberhausen G, Batz H, Orum H;
 PI WPI; 1999-552213/47.
 XX
 XX Fluorescent nucleic acid amplification assay, useful for detection of
 PT viral, bacterial, cellular, yeast or fungal nucleic acids.

Example 1; Page 19; 16pp; German.

CC This invention describes a novel assay for a nucleic acid which comprises
 CC an amplification reaction using two non-overlapping primers, a polymerase
 CC with 5'-nuclease activity and a probe with reporter groups and quencher
 CC groups that binds a region other than that bound by the primers. The
 CC reaction generates products of less than 100 nucleotides. The assay is
 CC useful for detection of viral, bacterial, cellular, yeast or fungal
 CC nucleic acids in human, animal, bacterial, plant, yeast or tissue, cell
 CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
 CC or liquid biopsy samples. Compared with assays in which longer
 CC amplification products are generated, the assay can be performed more
 CC rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
 CC may be increased due to reduced competition between the short
 CC counterstrand of the amplicon and the detector probe. Specificity may
 CC also be increased because of the increased relative length of sequence B
 CC compared with the total length of the amplicon and the differentiability
 CC of subtypes may be increased. In addition signal-to-noise ratios may be
 CC increased with the new method because short amplicons have reduced
 CC potential for nonspecific hybridization. In addition reproducibility may
 CC be increased because small target regions on RNA genomes are less
 CC sensitive to RNA degradation, and the possibilities for secondary
 CC structure formation are reduced. This sequence represents a PCR primer

CC used in the amplification of a region of HCV which is used to illustrate
CC the method of the invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 27
AAH25403
ID AAH25403 standard; DNA; 24 BP.
XX
AC AAH25403;
XX
DT 22-AUG-2001 (first entry)
XX
DE PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-EP011459.
XX
PR 17-NOV-1999; 99EP-00122853.
PR 12-MAY-2000; 2000EP-00110165.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 2001-381247/40.
XX
PT Novel composition of magnetic glass particles for purification of DNA or
PT RNA in automated processes.
XX
PS Example 7; Page 94; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between 5
CC -500 nm. The composition is useful for the purification of nucleic acids.
CC The composition can be used to process large quantities of nucleic acid
CC samples, because it does not involve the particles being centrifuged or
CC the fluids being drawn through glass fiber filters. PCR primers AAH25403-
CC 04 were used to amplify HCV DNA fragments. The amplified fragment can be
CC purified using the method of the invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 28
AAD19056
ID AAD19056 standard; DNA; 24 BP.
XX
AC AAD19056;

CC used in the amplification of a region of HCV which is used to illustrate
CC the method of the invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 29
ABN83648
ID ABN83648 standard; DNA; 24 BP.
XX
AC ABN83648;
XX
DT 27-AUG-2002 (first entry)
XX
DE Hepatitis C virus PCR primer KY80.
XX
KW Nucleic acid detection; infection; subtilisin; esperase; diagnosis; PCR;
KW primer; ss.
XX
OS Hepatitis C virus.
XX

XX 18-DEC-2001 (first entry)
XX Hepatitis viral DNA amplifying forward PCR primer #30.
XX
XX Hepatitis virus; bacterial infection; fungi; protozoa; PCR primer;
KW amplification; blood-borne pathogen; sexually transmitted disease;
KW respiratory disease; ss.
XX
OS Hepatitis virus.
XX
PN WO200168921-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-US008110.
XX
PR 14-MAR-2000; 2000US-0189344P.
XX
PA (INVE-) INVESTIGEN.
XX
PI Koshinsky H, Zwick MS, Mccue KF;
XX
DR WPI; 2001-611396/70.
XX
PT Simultaneous detection of biological entities such as bacteria, fungi and
PT viruses by specific nucleic acid amplification.
XX
PS Disclosure; Page 31; 55pp; English.
XX
CC The invention relates to a method and apparatus for the simultaneous
CC detection of multiple biological entities such as bacteria, fungi and
CC viruses by specific nucleic acid amplification. The invention also
CC relates to a kit for simultaneous detection of biological entities. The
CC kit is employed for detecting blood-borne pathogens, associated with a
CC variety of infectious diseases such as respiratory and sexually
CC transmitted diseases. The methods and apparatus are used for the
CC simultaneous detection of biological entities present in biological and
CC environment samples. In particular, they are used for monitoring diseases
CC caused by microorganisms associated with a respiratory or sexually
CC transmitted disease such as a bacterium (Staphylococcus, Pneumococcus,
CC Gonococcus, Haemophilus, Bacteroides, Escherichia or Salmonella), virus
CC (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV,
CC HDV, HEV, HGV or TTV), fungus (Aspergillus fumigatus, Blastomycosis,
CC dermatitis, Candida albicans) or protozoa (Entamoeba histolytica). The
CC present sequence is a PCR primer used for amplifying Hepatitis viral DNA
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 29
ABN83648
ID ABN83648 standard; DNA; 24 BP.
XX
AC ABN83648;
XX
DT 27-AUG-2002 (first entry)
XX
DE Hepatitis C virus PCR primer KY80.
XX
KW Nucleic acid detection; infection; subtilisin; esperase; diagnosis; PCR;
KW primer; ss.
XX
OS Hepatitis C virus.
XX

PN EP1201752-A1.
XX
PD 02-MAY-2002.
XX
PF 31-OCT-2000; 2000EP-00123728.
XX
PR 31-OCT-2000; 2000EP-00123728.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Schmuck R, Staepels J, Meier T, Wehnes U, Russmann E;
XX WPI; 2002-396808/43.
DR
XX
XX Use of Bacillus lentus subtilisin 147 to analyze one or more target non-
PT proteinaceous components from a mixture of non-proteinaceous and
PT proteinaceous components derived from a biological sample useful e.g.
PT diagnostically.
XX
PS Example; Page 22; 36pp; English.
XX
CC The present sequence is hepatitis C virus (HCV) PCR primer KY80. This was
CC used with biotinylated primer KY78 (see ABN83649) and a capture probe
CC (see ABN83650) in an example from the invention for the amplification and
CC detection of HCV RNA in a plasma sample. The invention provides a method
CC for the analysis of non-proteinaceous components, especially DNA and/or
CC RNA, in a mixture of proteinaceous and non-proteinaceous components in a
CC biological sample. The sample is incubated with protease subtilisin 147
CC (see ABN76400) of Bacillus lentus variant 147 (NCIB 10147), and the
CC target DNA or RNA is then amplified by PCR and determined or detected. In
CC the present example, the ruthenium-tris(bipyridyl)-labeled capture probe
CC provided a sensitive nonisotopic approach to detection based on
CC electrochemiluminescence following specific hybridisation to biotinylated
CC denatured HCV amplicons. The method is useful in environmental, food and
CC medical analysis, e.g. to detect viral infection, and in molecular
CC biological research, and can be performed using a high throughput format
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
RESULT 30
ABK51599
ID ABK51599 standard; DNA; 24 BP.
XX
AC ABK51599;
XX
DT 13-AUG-2002 (first entry)
XX
DE Hepatitis C virus protease, PCR primer KY80.
XX
KW Subtilisin 147; medical analysis; environmental analysis; food analysis;
KW diagnostic; virus infection; PCR; primer; ss; hepatitis C virus;
KW protease.
XX
OS Hepatitis C virus.
XX
FN EP1201753-A1.
XX
PD 02-MAY-2002.
XX
PF 26-OCT-2001; 2001EP-00125322.
XX
PR 31-OCT-2000; 2000EP-00123728.
PR 15-MAR-2001; 2001EP-00106308.
XX

PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Russmann E, Schmuck R, Meier T, Staepels J, Wehnes U;
XX WPI; 2002-428566/46.
DR
XX
XX Use of Bacillus lentus subtilisin 147 to analyze a target non-
PT proteinaceous component from a mixture of non-proteinaceous and
PT proteinaceous components derived from a biological sample useful e.g.
PT diagnostically to detect viruses.
XX
PS Example 2; Page 24; 38pp; English.
XX
CC The invention describes a target non-proteinaceous component is analysed
CC from a mixture of non-proteinaceous and proteinaceous components derived
CC from a biological sample by incubating the mixture with a protease having
CC at least 80 % identity to the known amino acid sequence for subtilisin
CC 147 from Bacillus lentus. The methods are useful for analysis of
CC biological samples e.g. in medical, environmental or food analysis or in
CC molecular biological research. They are especially useful in diagnostics
CC e.g. to detect virus infections. They can be used to enrich a mixture for
CC a target non-proteinaceous component or purify/isolate the component, the
CC component can especially be a nucleic acid, e.g. from a
CC virus/microorganism. The methods can be used to isolate non-proteinaceous
CC components useful as substrates in enzymatic reactions, or (in the case
CC of nucleic acids) for sequencing, as probes etc. They can be used in high
CC throughput formats, enabling analysis of large numbers of samples in a
CC short time. Kits for undertaking the methods, comprising the preferred
CC polypeptide, optionally a material with an affinity to nucleic acids
CC (especially preferred materials as above) and/or optionally lysis,
CC washing and elution buffers are provided. This sequence represents a
CC primer used to isolate DNA sequences encoding Hepatitis C virus proteases
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
RESULT 31
ABZ75890
ID ABZ75890 standard; DNA; 24 BP.
XX
AC ABZ75890;
XX
DT 15-MAY-2003 (first entry)
XX
DE HCV RNA detecting RT-PCR primer RJD-1 (KY80) .
XX
KW .HCV; hepatic disorder; envelope glycoprotein; DC-SIGN; DC-SIGNR; primer;
KW hepatoprotective; virucide; cytostatic; protein therapy; RT-PCR; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003000024-A2.
XX
PD 03-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-US020875.
XX
PR 26-JUN-2001; 2001US-00891894.
XX
PA (PROG-) PROGENICS PHARM INC.
XX
PI Olson WC, Maddon PJ;
XX WPI; 2003-267852/26.
DR

Wed Nov 24 08:46:07 2004

us-10-087-631b-6.max.rng

Best Local Similarity 100.0%; Pred. No. 0.051; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 34
ADM24824
ID ADM24824 standard; DNA; 24 BP.
XX AC ADM24824;
XX DT 20-MAY-2004 (first entry)
XX DE Hepatitis C virus (HCV) RNA specific RT-PCR primer, RJD-1.
XX KW Hepatotropic; virucide; antiinflammatory; cytostatic; Hepatitis C virus;
KW HCV; HCV infection; DC-SIGN; DC-SIGN related; DC-SIGNR; therapy;
KW liver disease; hepatitis; cirrhosis; hepatocellular carcinoma;
KW reverse transcription; RT; PCR; primer; ss.
XX OS Hepatitis C virus.
XX PN US2003134297-A1.
XX PD 17-JUL-2003.
XX PF 26-JUN-2002; 2002US-00184150.
XX PR 26-JUN-2001; 2001US-0300971P.
XX PA (OLSO/) OLSON W C.
XX PI (MADD/) MADDON P J.
XX PI Olson WC, Maddon PJ;
XX DR WPI; 2003-829636/77.
XX QY Inhibiting hepatitis C virus infection of susceptible cell or target cell
PT comprises contacting cell with compound to inhibit binding of hepatitis C
PT virus envelope glycoprotein to specified intracellular adhesion proteins.
PS Disclosure; Page 31; 47pp; English.
XX CC The invention relates to a method for inhibiting Hepatitis C virus (HCV)
CC infection using dendritic cell-specific intracellular adhesion molecule 3
CC -grabbing nonintegrin (DC-SIGN) or DC-SIGN related (DC-SIGNR) protein.
CC The method is useful for inhibiting HCV infection of a susceptible cell
CC or a target cell, e.g. a primary cell, a dendritic cell, endometrial cell
CC in liver or placenta cell. It is useful for diagnosing and treating HCV
CC infection. The method is useful for treating or preventing a liver
CC disease, e.g., hepatitis, cirrhosis and hepatocellular carcinoma. The
CC present sequence is HCV RNA specific reverse transcription (RT)-PCR
CC primer. This sequence is used to illustrate the method of the invention.
XX QY Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
XX DE DC-SIGN; HCV infection; liver disease; hepatocellular carcinoma;
KW hepatitis; cirrhosis; DC-SIGNR; HCV envelope glycoprotein; cytostatic;
KW antiinflammatory; hepatotropic; virucide; RT-PCR; reverse transcriptase;
KW primer; ss; RJD-1; KY80.
XX OS Hepatitis C virus.
XX PN US2003232745-A1.
XX PD 18-DEC-2003.
XX PF 24-DEC-2002; 2002US-00328997.
XX PR 26-JUN-2001; 2001US-0300971P.
XX AC ADE91309;

XX DT 12-FEB-2004 (first entry)
XX DE PCR primer #1 for hepatitis C virus (HCV) polyprotein gene.
XX KW Hepatitis C virus infection; HCV infection; clinical diagnosis;
KW polyprotein; PCR; primer; ss.
XX OS Hepatitis C virus.
XX PN US2003124654-A1.
XX PD 03-JUL-2003.
XX PF 03-JAN-2002; 2002US-00037990.
XX PR 03-JAN-2002; 2002US-00037990.
XX PA (RELI-) RELIANCE LIFE SCI PRIVATE LTD.
XX PI Sharma V, Kondiboyina VR;
XX DR WPI; 2004-009143/01.
XX QY Detecting hepatitis C virus by amplification using primers which amplify
PT transcripts of the polyprotein gene of hepatitis C virus is useful for
PT clinical diagnosis of hepatitis C virus.
XX PS Claim 1; Page 5; 7pp; English.
XX CC The present invention relates to a method for detecting hepatitis C virus
CC (HCV) in a biological sample. The method comprises amplification using
CC PCR primers which amplify the HCV polyprotein gene and detection with an
CC oligonucleotide probe. The method is useful for rapid clinical diagnosis
CC of HCV infection. Also disclosed is a kit for carrying out the detection
CC method. The present sequence represents a PCR primer used in the method
CC of the present invention.
XX QY Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
XX DE DC-SIGN; HCV infection; liver disease; hepatocellular carcinoma;
KW hepatitis; cirrhosis; DC-SIGNR; HCV envelope glycoprotein; cytostatic;
KW antiinflammatory; hepatotropic; virucide; RT-PCR; reverse transcriptase;
KW primer; ss; RJD-1; KY80.
XX OS Hepatitis C virus.
XX PN US2003232745-A1.
XX PD 18-DEC-2003.
XX PF 24-DEC-2002; 2002US-00328997.
XX PR 26-JUN-2001; 2001US-0300971P.

Query Match 92.3%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 36
ADH79950
ID ADH79950 standard; DNA; 24 BP.
XX AC ADH79950;
XX DT 22-APR-2004 (first entry)
XX DE HCV RT-PCR primer RJD-1 (KY80).
XX KW DC-SIGN; HCV infection; liver disease; hepatocellular carcinoma;
KW hepatitis; cirrhosis; DC-SIGNR; HCV envelope glycoprotein; cytostatic;
KW antiinflammatory; hepatotropic; virucide; RT-PCR; reverse transcriptase;
KW primer; ss; RJD-1; KY80.
XX OS Hepatitis C virus.
XX PN US2003232745-A1.
XX PD 18-DEC-2003.
XX PF 24-DEC-2002; 2002US-00328997.
XX PR 26-JUN-2001; 2001US-0300971P.

PR 26-JUN-2002; 2002US-00184150.
 XX (OLSON/) OLSON W C.
 PA (MADD/) MADDON P J.
 PA (GARD/) GARDNER J P.
 XX Olson WC, Maddon PJ, Gardner JP;
 XX WPI; 2004-061306/06.
 XX Use of DC-SIGN and DC-SIGNR proteins for inhibiting, preventing or
 PT treating HCV infection and liver disease e.g. hepatitis or cirrhosis or
 PT hepatocellular carcinoma.
 XX Disclosure; Page 33; 55pp; English.
 XX The invention relates to the use of DC-SIGN and DC-SIGNR proteins for
 CC inhibiting, treating or preventing HCV infection and liver diseases such
 CC as hepatocellular carcinoma, hepatitis or cirrhosis. The DC-SIGN and DC-
 CC SIGNR protein are useful for inhibiting HCV infection, treating HCV
 CC infection or treating or preventing liver disease e.g. hepatitis,
 CC cirrhosis or hepatocellular carcinoma. Antibodies to the polypeptides,
 CC the polypeptides or non-peptidyl agents can be used for inhibiting
 CC binding of a DC-SIGN or DC-SIGNR protein to an HCV envelope glycoprotein.
 CC This sequence represents an HCV reverse transcriptase PCR (RT-PCR) primer
 CC used in the scope of the invention.
 XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 SQ Query Match 92.3%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 37
 ADO05656
 ID ADO05656 standard; DNA; 24 BP.
 AC ADO05656;
 XX 15-JUL-2004 (first entry)
 XX HCV 5' NCR (non coding region) fragment amplifying forward primer 7.
 XX Nucleic acid amplification; mutation detection; cytostatic;
 KW antiinflammatory; hepatotropic; virucide; cancer; PCR; primer; ss.
 XX Hepatitis C virus.
 OS Synthetic.
 XX WO2004035832-A1.
 PN 29-APR-2004.
 PD 17-OCT-2003; 2003WO-KR002179.
 PF 18-OCT-2002; 2002KR-00063832.
 PR 02-SEP-2003; 2003KR-00061066.
 XX (GENE-) GENEMATRIX INC.
 PA Kim N, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;
 PI Jee M, Hwang S, Hong S;
 XX WPI; 2004-348478/32.
 XX Detecting a mutation, useful in diagnosing and treating e.g. cancer or
 PT hepatitis, comprises generating fragments of polynucleotides using
 PT specific primers and measuring molecular weight of cleaved fragments.

XX Claim 13; SEQ ID NO 17; 58pp; English.
 XX The invention relates to detecting a mutation. The method involves
 CC amplifying a target polynucleotide using a forward primer and a reverse
 CC primer, generating fragments of two or more single-stranded
 CC polynucleotides including one or more mutations sequence having the size
 CC of 2-32 bases by cleaving the amplified target polynucleotide with
 CC restriction enzymes, where the second restriction enzyme does not react
 CC while a first restriction enzyme is reacted with the amplified
 CC polynucleotide; and measuring the molecular weight of the cleaved
 CC fragments. The polynucleotide is cleaved to include one mutation among
 CC two or more different mutations in only one single stranded
 CC polynucleotide fragment and all mutations in the other single stranded
 CC nucleotide fragment. Restrictions enzyme treatment step is performed
 CC using restriction enzymes having different optimum temperatures. The
 CC method is useful in detecting a mutation. The method and primer are
 CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.
 CC cancer or hepatitis B or C virus. The present sequence represents a
 CC primer for amplifying the HCV 5' NCR (non coding region) DNA fragment.
 XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 SQ Query Match 92.3%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 38
 ADO52627
 ID ADO52627 standard; DNA; 24 BP.
 XX ADO52627;
 AC ADO52627;
 XX 26-AUG-2004 (first entry)
 XX HCV real time, RT-PCR primer KV80.
 XX HCV; ss; acute hepatitis; chronic liver disease; cirrhosis; liver cancer;
 KW real time PCR; reverse transcriptase PCR; PCR; primer; RT-PCR.
 XX Hepatitis C virus.
 OS US2004106099-A1.
 XX 03-JUN-2004.
 XX 02-DEC-2002; 2002US-00307523.
 XX 02-DEC-2002; 2002US-00307523.
 XX (LEET/) LEE T H.
 XX Lee TH;
 XX WPI; 2004-460064/43.
 XX Detecting hepatitis C virus in sample such as serum collected from humans
 PT infected with HCV, by performing real time PCR and detecting amplified
 PT product using nucleic acid binding fluorescent entity.
 XX Disclosure; Page 4; 5pp; English.
 XX The invention relates to detecting hepatitis C virus (HCV) in a sample,
 CC involving extracting RNA and synthesizing cDNA using reverse
 CC transcriptase, forming an amplification medium along with a nucleic acid
 CC binding fluorescent entity and thermally cycling it, illuminating the
 CC medium, determining amount of fluorescence generated, and detecting
 CC presence of target nucleic acid by analysing amount of luminescence

determined after the amplification cycle. The fluorescent entity comprises a double strand specific nucleic acid binding dye. The method is useful for detecting the hepatitis C virus (HCV) in a sample and to determine the quantity of the HCV RNA in a sample (by determining a threshold cycle number at which the amount of fluorescent generated by the fluorescent entity in a sample reaches a fixed threshold value above a baseline value, and calculating the quantity of the HCV RNA in the sample by comparing the threshold cycle number determined for the target nucleic acid in the sample with the threshold cycle number determined for target nucleic acid of known amounts in standard solutions). The method is also useful for evaluating the effectiveness of antiviral drugs, for assaying cell cultures comprising HCV, and for detecting HCV in a biological sample. The method is a real-time PCR assay for directly detecting or quantifying HCV in a sample in which detection steps are minimized resulting in a method which may be performed quickly, accurately, and easily with minimal operator skill. HCV is a major cause of human acute hepatitis, chronic liver disease, cirrhosis and liver cancer. The present sequence is an HCV real time, reverse transcriptase (RT)-PCR primer used in the method of the invention.

Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 39
ADD67940
ID ADD67940 standard; DNA; 25 BP.
XX
AC ADD67940;
XX
DT 15-JAN-2004 (first entry)
XX
DE Hepatitis C virus detection probe seq id 12.
XX
KW antiviral; hepatitis C virus; HCV; viral replication inhibitor;
KW replication competent HCV; 3' non-translated region; probe; ss;
KW lightcycler RT-PCR.
XX
OS Hepatitis C virus.
XX
PN US2003125541-A1.
XX
PD 03-JUL-2003.
XX
PF 27-SEP-2002; 2002US-00259275.
XX
PR 23-DEC-1999; 99US-0171909P.
PR 23-DEC-2000; 2000US-00747419.
PR 27-SEP-2001; 2001US-0325236P.
PR 13-NOV-2001; 2001US-0338123P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Lemon SM, Yi M;
XX
WPI; 2003-811006/76.
XX
XX Identifying a compound that inhibits replication of a hepatitis C virus (HCV) RNA comprises contacting a cell comprising a replication competent HCV RNA containing a heterologous polynucleotide encoding a transactivator, with a compound.
XX
XX Example 6; SEQ ID NO 12; 95pp; English.
XX The invention describes a method of identifying a compound that inhibits replication of a hepatitis C virus (HCV) RNA. The method comprises

contacting a cell comprising a replication competent HCV RNA containing a heterologous polynucleotide having a first coding sequence encoding a transactivator, with a compound. The method is useful for identifying a compound that inhibits replication of HCV RNA. The kit is useful for detecting replication competent HCV RNA. This sequence represents a probe used to detect DNA encoding HCV in order to detect the production of the viral RNA in cell lines.

Sequence 25 BP; 7 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.052; 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

Qy 3 AGAAGCGTCTAGCCATGGCGTTA 26
Db 1 AGAAGCGTCTAGCCATGGCGTTA 24

RESULT 40
ABX10612
ID ABX10612 standard; DNA; 25 BP.
XX
AC ABX10612;
XX
DT 11-APR-2003 (first entry)
XX
DE Light Cycler fluor PCR probe used to detect Viral RNA.
XX
KW PCR; probe; ss; replication competent; hepatitis C virus; HCV;
KW 3' non-translated RNA; 3'NTR; chronic viral hepatitis; hepatic fibrosis;
KW cirrhosis; hepatocellular carcinoma; secretory alkaline phosphatase;
KW SEAP.
XX
OS Hepatitis c virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 25 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= labelled with fluorescein"
XX
PN US2002155582-A1.
XX
PD 24-OCT-2002.
XX
PF 23-DEC-2000; 2000US-00747419.
XX
PR 23-DEC-1999; 99US-0171909P.
XX
PA (LEMO/) LEMON S M.
PA (YINN/) YI M.
XX
PI Lemon SM, Yi M;
XX
WPI; 2003-182640/18.
XX
XX Novel replication competent hepatitis C virus for producing infectious viral particles and as antigen for detecting hepatitis C virus antibodies, comprises hepatitis C virus genome and heterologous polynucleotide.
XX
XX Example 6; Page 16; 37pp; English.
XX The invention discloses a replication competent hepatitis C virus (HCV) comprising a HCV virus genome and a heterologous polynucleotide, where the HCV genome comprises a 3' non-translated RNA and the heterologous polynucleotide is present in the 3' non-translated RNA. HCV is a cause of chronic viral hepatitis, hepatic fibrosis, cirrhosis and/or the development of hepatocellular carcinoma. A cell comprising the HCV is useful for selecting or detecting a replication competent HCV, for identifying a compound that inhibits replication of HCV, for producing

CC infectious viral particles which are useful as a source of virus
CC particles for various assays, including evaluating methods for
CC inactivating particles, excluding particles from serum, identifying a
CC neutralising compound and as an antigen for use in detecting anti-HCV
CC antibodies in an animal. The cell comprising the HCV is also useful for
CC identifying a variant HCV. An HCV particle is useful as an antigen, as a
CC positive-control in assays that test for the presence of anti-HCV
CC antibodies, to produce antibodies to detect the presence of viral
CC particles in biological samples (e.g. blood products and cell-free blood
CC products) and as a source of viral antigen to measure the presence and
CC amount of antibody present in an animal. The sequence presented is the
CC Light Cycler fluor PCR probe which was used to detect viral RNA in Huh-
CC secretory alkaline phosphatase (SEAP)-o10 cell lines
XX
SQ Sequence 25 BP; 7 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGCGTCTAGCCATGCGGTTA 26
|||||
Db 1 AGAAGCGTCTAGCCATGCGGTTA 24

Search completed: November 23, 2004, 17:29:13
Job time : 162.543 secs

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OM nucleic - nucleic search, using sw model

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Title: US-10-087-631B-6

Perfect score: 26

Sequence: 1 gcagaaagcgtctagccatgcggtta 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents_NA*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	2	US-08-738-928-1
2	26	100.0	26	3	US-09-039-866-3
3	26	100.0	30	4	US-10-353-589-1
4	26	100.0	30	4	US-10-029-907-17
5	25	96.2	28	4	US-09-493-353-1
6	24	92.3	24	1	US-08-240-547-5
7	24	92.3	24	1	US-08-449-050-17
8	24	92.3	24	1	US-08-332-616A-9
9	24	92.3	24	1	US-08-317-220-9
10	24	92.3	24	1	US-08-675-153-7
11	24	92.3	24	2	US-08-738-928-4
12	24	92.3	24	2	US-08-841-252-7
13	24	92.3	24	2	US-08-881-571-7
14	24	92.3	24	3	US-09-078-290A-9
15	24	92.3	24	3	US-09-282-054-7
16	24	92.3	24	3	US-09-665-638-7
17	24	92.3	24	4	US-10-007-389-4
18	24	92.3	26	1	US-08-240-547-6
19	24	92.3	37	5	PCT-US94-05407-14
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21	21	80.8	21	3	US-08-934-097A-25
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23	21	80.8	21	3	US-09-677-218B-25
24	21	80.8	21	3	US-09-677-192-25
25	21	80.8	21	4	US-09-402-618B-25
26	21	80.8	21	4	US-09-825-574-25
27	21	80.8	21	4	US-09-676-768-25

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20	76.9	20	3	US-08-650-093C-33	Sequence 33, Appl
21	76.9	21	2	US-08-735-381-4	Sequence 4, Appl
21	76.9	21	3	US-09-183-619-3	Sequence 3, Appl
21	76.9	21	3	US-09-201-674-4	Sequence 4, Appl
21	76.9	21	3	US-09-210-657-1	Sequence 1, Appl
30	73.1	30	1	US-08-240-547-4	Sequence 4, Appl
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33	73.1	33	1	US-08-438-639-44	Sequence 44, Appl
33	73.1	33	1	US-07-813-338A-44	Sequence 44, Appl
33	73.1	33	2	US-08-470-124-77	Sequence 77, Appl
33	73.1	33	3	US-08-441-971-120	Sequence 120, Appl
33	73.1	33	3	US-08-221-653-120	Sequence 120, Appl
33	73.1	33	3	US-08-442-144A-120	Sequence 120, Appl
33	73.1	33	3	US-08-441-970-120	Sequence 120, Appl
33	73.1	33	3	US-08-397-220B-10	Sequence 10, Appl
33	73.1	33	3	US-08-650-093C-10	Sequence 10, Appl
33	73.1	33	4	US-08-823-895A-10	Sequence 10, Appl
25	69.2	25	1	US-08-361-442-3	Sequence 3, Appl
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28	69.2	28	3	US-08-474-700B-31	Sequence 31, Appl
28	69.2	28	5	PCT-US95-05812-4	Sequence 4, Appl
28	69.2	28	5	PCT-US95-05812-31	Sequence 31, Appl
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16	61.5	16	4	US-09-431-419A-16	Sequence 16, Appl
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26	61.5	26	3	US-09-038-369B-3	Sequence 3, Appl
26	61.5	26	4	US-09-378-900A-3	Sequence 3, Appl
26	61.5	26	4	US-09-899-044-3	Sequence 3, Appl
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48	60.8	48	1	US-08-475-231-18	Sequence 18, Appl
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20	57.7	20	1	US-08-157-235-9	Sequence 9, Appl
20	57.7	20	1	US-08-244-116B-25	Sequence 25, Appl
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20	57.7	20	2	US-08-242-580-3	Sequence 3, Appl
20	57.7	20	2	US-08-470-426B-6	Sequence 6, Appl
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24	57.7	24	4	US-09-539-601-40	Sequence 40, Appl
26	57.7	26	5	PCT-US96-05611A-14	Sequence 14, Appl
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28	54.6	28	4	US-08-397-220B-34	Sequence 34, Appl
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33	53.8	33	3	US-09-202-316-39	Sequence 39, Appl
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27	53.1	27	1	US-08-199-509-1	Sequence 1, Appl
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28	53.1	28	1	US-08-475-231-41	Sequence 41, Appl
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36	53.1	36	1	US-08-095-726-40	Sequence 40, Appl
36	53.1	36	1	US-08-096-043-37	Sequence 37, Appl
36	53.1	36	1	US-08-093-577-33	Sequence 33, Appl
36	53.1	36	1	US-08-331-004A-7	Sequence 7, Appl
36	53.1	36	1	US-08-096-623A-45	Sequence 45, Appl
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48	53.1	48	1	US-08-475-231-16	Sequence 16, Appl
39	52.3	39	3	US-09-232-479-23	Sequence 23, Appl
39	52.3	39	4	US-09-784-990-23	Sequence 23, Appl
44	51.5	44	1	US-07-936-163-38	Sequence 38, Appl

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102	13.2	50.8	33	1	US-08-285-936-14	Sequence 14, Appli	175	12.2	46.9	20	1	US-08-231-990-8	Sequence 8, Appli
103	13.2	50.8	33	1	US-08-487-860-14	Sequence 14, Appli	176	12.2	46.9	20	1	US-08-367-122-8	Sequence 8, Appli
104	13.2	50.8	36	4	US-10-083-304-11	Sequence 11, Appli	177	12.2	46.9	20	3	US-09-165-264-9	Sequence 9, Appli
105	13.2	50.8	40	3	US-09-147-550-1	Sequence 1, Appli	c 178	12.2	46.9	20	4	US-09-600-932-22	Sequence 22, Appli
106	13.2	50.8	40	3	US-09-557-917-1	Sequence 1, Appli	179	12.2	46.9	20	4	US-09-600-932-24	Sequence 24, Appli
107	13.2	50.8	40	3	US-09-355-947-1	Sequence 1, Appli	c 180	12.2	46.9	21	4	US-09-657-472-1474	Sequence 1474, Ap
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109	13.2	50.8	44	3	US-08-656-664-3	Sequence 3, Appli	c 182	12.2	46.9	27	4	US-09-623-326-26	Sequence 26, Appli
110	13.2	50.8	44	3	US-08-656-664-3	Sequence 3, Appli	c 183	12.2	46.9	30	4	US-09-386-642-31	Sequence 31, Appli
111	13.2	50.8	47	4	US-09-422-978-1436	Sequence 1436, Ap	c 184	12.2	46.9	33	4	US-07-829-461A-18	Sequence 18, Appli
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116	13.2	50.8	31	1	US-09-946-678-27	Sequence 27, Appli	c 189	12.2	46.9	44	3	US-08-484-661A-6	Sequence 6, Appli
117	13.2	50.8	31	6	5254799-27	Patent No. 5254799	c 190	12.2	46.9	44	3	US-08-656-664-6	Sequence 6, Appli
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127	12.8	49.2	34	2	US-08-389-564B-7	Sequence 7, Appli	c 200	12.2	46.2	17	4	US-09-866-108A-7460	Sequence 7460, Ap
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132	12.6	48.5	30	3	US-08-687-421-43	Sequence 43, Appli	c 205	12.2	46.2	17	4	US-09-866-108A-7465	Sequence 7465, Ap
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136	12.6	48.5	37	2	US-08-855-213-48	Sequence 48, Appli	c 209	12.2	46.2	20	3	US-08-650-093C-32	Sequence 32, Appli
137	12.6	48.5	37	3	US-09-201-474-48	Sequence 48, Appli	c 210	12.2	46.2	22	1	US-08-445-289B-24	Sequence 24, Appli
138	12.6	48.5	41	3	US-09-351-814-55	Sequence 55, Appli	c 211	12.2	46.2	23	4	US-09-611-627-27	Sequence 27, Appli
139	12.4	47.7	24	1	US-08-186-895-6	Sequence 6, Appli	c 212	12.2	46.2	24	4	US-09-611-627-25	Sequence 25, Appli
140	12.4	47.7	25	1	US-08-628-665-4	Sequence 4, Appli	c 213	12.2	46.2	25	1	US-09-015-876-5	Sequence 5, Appli
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142	12.4	47.7	27	1	US-07-731-157A-29	Sequence 29, Appli	c 215	12.2	46.2	25	1	US-08-271-880A-130	Sequence 130, App
143	12.4	47.7	27	2	US-08-541-780-29	Sequence 29, Appli	c 216	12.2	46.2	25	2	US-08-910-408-130	Sequence 130, App
144	12.4	47.7	28	3	US-08-676-818-14	Sequence 14, Appli	c 217	12.2	46.2	25	3	US-09-249-215-130	Sequence 130, App
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152	12.4	47.7	30	3	US-09-133-521-28	Sequence 28, Appli	c 225	12.2	46.2	25	4	US-09-866-108A-12360	Sequence 12360, A
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155	12.4	47.7	31	4	US-06-620-412C-204	Sequence 204, App	c 228	12.2	46.2	25	4	US-09-866-108A-12363	Sequence 12363, A
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157	12.4	47.7	32	1	US-08-444-231-8	Sequence 8, Appli	c 230	12.2	46.2	25	4	US-09-866-108A-12365	Sequence 12365, A
158	12.4	47.7	32	1	US-08-152-443A-8	Sequence 5, Appli	c 231	12.2	46.2	27	1	US-07-661-378A-13	Sequence 13, Appli
159	12.4	47.7	33	1	US-08-186-895-5	Sequence 37, Appli	c 232	12.2	46.2	30	4	US-09-857-475A-1	Sequence 1, Appli
160	12.4	47.7	33	3	US-09-202-316-37	Sequence 14, Appli	c 233	12.2	46.2	30	4	US-09-857-475A-2	Sequence 2, Appli
161	12.4	47.7	34	3	US-08-836-561-14	Sequence 14, Appli	c 234	12.2	46.2	30	4	US-09-050-739-164	Sequence 164, App
162	12.4	47.7	34	3	US-08-836-561-14	Sequence 14, Appli	c 235	12.2	46.2	30	4	US-08-876-078-4	Sequence 4, Appli
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164	12.4	47.7	38	1	US-08-399-412A-115	Sequence 26, Appli	c 237	12.2	46.2	33	3	US-08-185-827-1	Sequence 1, Appli
165	12.4	47.7	41	3	US-08-639-857-26	Sequence 9, Appli	c 238	12.2	46.2	35	5	PCT-US94-13798A-1	Sequence 1, Appli
166	12.4	47.7	41	3	US-08-836-561-9	Sequence 87, Appli	c 239	12.2	46.2	36	1	US-07-955-905A-16	Sequence 16, Appli
167	12.4	47.7	41	3	US-09-464-453-87	Sequence 87, Appli	c 240	12.2	46.2	36	1	US-09-552-950-22	Sequence 22, Appli
168	12.4	47.7	41	3	US-09-434-122-9	Sequence 9, Appli	c 241	12.2	46.2	37	4	US-09-936-572-31	Sequence 31, Appli
169	12.4	47.7	42	3	US-08-879-565-8	Sequence 8, Appli	c 242	12.2	46.2	37	4	US-09-232-479-27	Sequence 27, Appli
170	12.4	47.7	45	4	US-09-878-766A-6	Sequence 6, Appli	c 243	12.2	46.2	38	4	US-09-784-990-27	Sequence 27, Appli
171	12.4	47.7	47	4	US-09-641-638-1257	Sequence 1257, Ap	c 244	12.2	46.2	38	4	US-08-976-413A-356	Sequence 356, App
172	12.4	47.7	47	4	US-10-170-097-1257	Sequence 1257, Ap	c 245	12.2	46.2	43	1	US-07-744-282C-27	Sequence 27, Appli
173	12.4	47.7	48	4	US-09-578-634A-56	Sequence 56, Appli	c 246	12.2	46.2	43	5	PCT-US92-06821A-33	Sequence 33, Appli

C 247	12	46.2	48	2	US-09-133-774-23	Sequence 23, Appl	320	11.8	45.4	46	3	US-08-977-378-19	Sequence 19, Appl
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C 249	12	46.2	49	4	US-09-611-627-28	Sequence 28, Appl	C 322	11.8	45.4	47	4	US-09-422-978-2982	Sequence 2982, Ap
C 250	11.8	45.4	20	3	US-08-813-507-20	Sequence 20, Appl	C 323	11.8	45.4	47	4	US-09-422-978-3606	Sequence 3606, Ap
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C 252	11.8	45.4	20	4	US-09-198-432A-2105	Sequence 2105, Ap	C 325	11.8	45.4	49	1	US-08-487-426B-6	Sequence 6, Appli
C 253	11.8	45.4	20	4	US-09-198-452A-3610	Sequence 3610, Ap	C 326	11.8	45.4	49	2	US-08-487-720A-6	Sequence 6, Appli
C 254	11.8	45.4	20	4	US-09-112-580-102	Sequence 102, App	C 327	11.8	45.4	49	2	US-08-945-734-6	Sequence 6, Appli
C 255	11.8	45.4	22	1	US-08-592-126-16	Sequence 16, Appl	C 328	11.8	45.4	49	3	US-09-258-797-6	Sequence 6, Appli
C 256	11.8	45.4	22	1	US-08-687-080-16	Sequence 16, Appl	C 329	11.8	45.4	49	3	US-09-538-709-924	Sequence 924, App
C 257	11.8	45.4	22	4	US-09-632-538C-25	Sequence 25, Appl	C 330	11.8	45.4	49	5	PCT-US96-09451-6	Sequence 6, Appli
C 258	11.8	45.4	22	4	US-09-168-595-16	Sequence 16, Appl	C 331	11.8	45.4	50	4	US-08-956-171E-2687	Sequence 2687, Ap
C 259	11.8	45.4	24	2	US-08-432-871C-41	Sequence 41, Appl	C 332	11.8	45.4	50	4	US-09-863-859-18	Sequence 18, Appl
C 260	11.8	45.4	24	4	US-09-270-956-41	Sequence 41, Appl	C 333	11.8	45.4	50	4	US-09-863-859-18	Sequence 18, Appl
C 261	11.8	45.4	25	4	US-09-050-739-106	Sequence 106, App	C 334	11.8	45.4	50	4	US-08-781-986A-2687	Sequence 2687, Ap
C 262	11.8	45.4	25	4	US-09-866-108A-11899	Sequence 11899, A	C 335	11.6	44.6	23	3	US-09-205-995-8	Sequence 8, Appli
C 263	11.8	45.4	25	4	US-09-866-108A-11900	Sequence 11900, A	C 336	11.6	44.6	23	6	5208144-42	Patent No. 5208144
C 264	11.8	45.4	25	4	US-09-866-108A-11901	Sequence 11901, A	C 337	11.6	44.6	25	1	US-08-400-256-5	Sequence 5, Appli
C 265	11.8	45.4	26	2	US-08-502-535B-9	Sequence 9, Appli	C 338	11.6	44.6	25	1	US-08-400-256-8	Sequence 8, Appli
C 266	11.8	45.4	26	2	US-08-908-005A-9	Sequence 9, Appli	C 339	11.6	44.6	25	3	US-08-975-365-5	Sequence 5, Appli
C 267	11.8	45.4	26	3	US-09-253-523-9	Sequence 9, Appli	C 340	11.6	44.6	25	3	US-08-975-365-8	Sequence 8, Appli
C 268	11.8	45.4	26	3	US-09-251-911-9	Sequence 9, Appli	C 341	11.6	44.6	27	3	US-08-651-472-68	Sequence 68, Appl
C 269	11.8	45.4	26	4	US-09-506-286B-37	Sequence 37, Appl	C 342	11.6	44.6	27	3	US-08-358-928-68	Sequence 68, Appl
C 270	11.8	45.4	26	4	US-09-762-861B-37	Sequence 37, Appl	C 343	11.6	44.6	27	4	US-08-793-381A-5	Sequence 5, Appli
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C 273	11.8	45.4	27	1	US-07-692-995B-32	Sequence 32, Appl	C 346	11.6	44.6	30	4	US-09-170-496D-248	Sequence 248, App
C 274	11.8	45.4	27	1	US-08-488-457-32	Sequence 32, Appl	C 347	11.6	44.6	32	4	US-09-510-238A-56	Sequence 56, Appl
C 275	11.8	45.4	27	3	US-08-558-818-9	Sequence 9, Appli	C 348	11.6	44.6	35	3	US-09-039-198A-22	Sequence 22, Appl
C 276	11.8	45.4	27	3	US-08-974-469A-9	Sequence 9, Appli	C 349	11.6	44.6	35	3	US-03-267-574-22	Sequence 22, Appl
C 277	11.8	45.4	27	4	US-09-711-899-9	Sequence 9, Appli	C 350	11.6	44.6	36	1	US-07-934-373C-12	Sequence 12, Appl
C 278	11.8	45.4	29	2	US-08-639-857-18	Sequence 18, Appl	C 351	11.6	44.6	36	3	US-08-437-642B-12	Sequence 12, Appl
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C 282	11.8	45.4	30	5	PCT-US93-09695-22	Sequence 22, Appl	C 355	11.6	44.6	36	5	PCT-US93-07832-12	Sequence 12, Appl
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C 284	11.8	45.4	31	2	US-08-995-161-2	Sequence 2, Appli	C 357	11.6	44.6	38	4	US-09-402-923A-204	Sequence 204, App
C 285	11.8	45.4	31	2	US-09-063-927-2	Sequence 2, Appli	C 358	11.6	44.6	39	3	US-08-961-810-103	Sequence 103, App
C 286	11.8	45.4	31	3	US-09-202-316-38	Sequence 38, Appl	C 359	11.6	44.6	39	3	US-08-352-902D-103	Sequence 103, App
C 287	11.8	45.4	32	2	US-08-484-891-1	Sequence 1, Appli	C 360	11.6	44.6	39	3	US-09-249-180-2	Sequence 2, Appli
C 288	11.8	45.4	32	4	US-09-150-811-1	GENERAL INFORMA	C 361	11.6	44.6	39	4	US-03-255-503B-103	Sequence 103, App
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C 292	11.8	45.4	35	3	US-09-232-278A-17	Sequence 17, Appl	C 365	11.6	44.6	45	2	US-08-494-151-2	Sequence 2, Appli
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C 294	11.8	45.4	36	4	US-08-923-940-19	Sequence 19, Appl	C 367	11.6	44.6	47	4	US-03-641-638-778	Sequence 778, App
C 295	11.8	45.4	36	4	US-09-462-625-19	Sequence 19, Appl	C 368	11.6	44.6	47	4	US-10-170-097-778	Sequence 778, App
C 296	11.8	45.4	36	5	PCT-US95-03940-19	Sequence 19, Appl	C 369	11.6	44.6	48	4	US-09-475-947A-306	Sequence 306, App
C 297	11.8	45.4	38	3	US-08-170-113-16	Sequence 16, Appl	C 370	11.6	44.6	50	4	US-09-313-221A-23	Sequence 23, Appl
C 298	11.8	45.4	38	3	US-09-552-613-16	Sequence 16, Appl	C 371	11.4	43.8	18	4	US-09-856-662-58	Sequence 58, Appl
C 299	11.8	45.4	38	4	US-09-371-772B-13857	Sequence 13857, A	C 372	11.4	43.8	22	4	US-09-054-281-6	Sequence 6, Appli
C 300	11.8	45.4	38	4	US-09-166-265-9	Sequence 9, Appli	C 373	11.4	43.8	23	6	5212866-15	Patent No. 5212866
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C 302	11.8	45.4	39	4	US-09-596-248D-26	Sequence 26, Appl	C 375	11.4	43.8	24	4	US-09-371-307-15	Sequence 15, Appl
C 303	11.8	45.4	39	4	US-09-596-248D-48	Sequence 48, Appl	C 376	11.4	43.8	25	4	US-09-595-684B-6	Sequence 6, Appli
C 304	11.8	45.4	40	3	US-09-367-012-7	Sequence 7, Appli	C 377	11.4	43.8	25	4	US-09-060-299-82	Sequence 82, Appl
C 305	11.8	45.4	40	4	US-09-777-157A-7	Sequence 7, Appli	C 378	11.4	43.8	25	4	US-09-402-923A-82	Sequence 82, Appl
C 306	11.8	45.4	40	4	US-09-673-896-6	Sequence 6, Appli	C 379	11.4	43.8	25	4	US-03-712-368-20	Sequence 20, Appl
C 307	11.8	45.4	42	1	US-08-173-497-27	Sequence 27, Appl	C 380	11.4	43.8	25	4	US-09-823-549-21	Sequence 21, Appl
C 308	11.8	45.4	42	1	US-08-286-889-27	Sequence 27, Appl	C 381	11.4	43.8	25	4	US-09-866-108A-11897	Sequence 11897, A
C 309	11.8	45.4	42	1	US-08-485-618-27	Sequence 27, Appl	C 382	11.4	43.8	25	4	US-09-866-108A-11898	Sequence 11898, A
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C 316	11.8	45.4	42	4	US-09-688-307A-27	Sequence 27, Appl	C 389	11.4	43.8	27	4	US-09-578-515-15	Sequence 15, Appl
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C 318	11.8	45.4	43	4	US-09-940-244-147	Sequence 147, App	C 391	11.4	43.8	28	3	US-09-411-977-11	Sequence 11, Appl
C 319	11.8	45.4	43	2	US-08-846-338-16	Sequence 16, Appl	C 392	11.4	43.8	29	4	US-09-304-232-91	Sequence 91, Appl

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402	11.4	43.8	33	3	US-08-485-740-3	Sequence 3, Appli	Sequence 3, Appli	Sequence 504, App
403	11.4	43.8	33	3	US-09-162-184-3	Sequence 3, Appli	Sequence 3, Appli	Sequence 504, App
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409	11.4	43.8	35	3	US-08-570-140A-3	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli
410	11.4	43.8	36	2	US-08-585-684B-430	Sequence 430, App	Sequence 430, App	Sequence 13, Appl
411	11.4	43.8	36	3	US-08-491-954-49	Sequence 49, Appl	Sequence 49, Appl	Sequence 11, Appl
412	11.4	43.8	36	3	US-09-038-073-430	Sequence 430, App	Sequence 430, App	Sequence 24, Appl
413	11.4	43.8	37	3	US-09-202-316-35	Sequence 35, Appl	Sequence 35, Appl	Sequence 10, Appl
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415	11.4	43.8	38	4	US-09-371-772B-9690	Sequence 9690, Ap	Sequence 9690, Ap	Sequence 206, App
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417	11.4	43.8	38	4	US-09-371-772B-9773	Sequence 9773, Ap	Sequence 9773, Ap	Sequence 2, Appli
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420	11.4	43.8	39	4	US-09-912-733-34	Sequence 34, Appl	Sequence 34, Appl	Sequence 8, Appli
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422	11.4	43.8	39	4	US-09-950-634-12	Sequence 12, Appl	Sequence 12, Appl	Sequence 5, Appli
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424	11.4	43.8	40	2	US-08-425-684-132	Sequence 132, App	Sequence 132, App	Sequence 31, Appl
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426	11.4	43.8	40	4	US-09-245-802-132	Sequence 132, App	Sequence 132, App	Sequence 70, Appl
427	11.4	43.8	41	1	US-08-252-057-33	Sequence 33, Appl	Sequence 33, Appl	Sequence 25, Appl
428	11.4	43.8	41	2	US-08-786-555-5	Sequence 5, Appli	Sequence 5, Appli	Sequence 25, App
429	11.4	43.8	41	2	US-08-375-116A-13	Sequence 13, Appl	Sequence 13, Appl	Sequence 285, App
430	11.4	43.8	42	1	US-08-930-274-16	Sequence 16, Appl	Sequence 16, Appl	Sequence 285, App
431	11.4	43.8	46	1	US-08-093-884-31	Sequence 31, Appl	Sequence 31, Appl	Sequence 265, App
432	11.4	43.8	47	3	US-09-526-542-7	Sequence 7, Appli	Sequence 7, Appli	Sequence 265, App
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434	11.4	43.8	47	4	US-09-422-978-1451	Sequence 1451, Ap	Sequence 1451, Ap	Sequence 1125, Ap
435	11.4	43.8	47	4	US-09-422-978-3789	Sequence 3789, Ap	Sequence 3789, Ap	Sequence 927, App
436	11.4	43.8	47	4	US-10-117-087-7	Sequence 7, Appli	Sequence 7, Appli	Sequence 1196, Ap
437	11.4	43.8	49	3	US-09-025-769B-70	Sequence 70, Appl	Sequence 70, Appl	Sequence 2187, Ap
438	11.4	43.8	49	4	US-09-490-070A-70	Sequence 70, Appl	Sequence 70, Appl	Sequence 2388, Ap
439	11.4	43.8	49	4	US-09-490-153-70	Sequence 41, Appl	Sequence 41, Appl	Sequence 832, App
440	11.4	43.8	49	4	US-09-627-465B-41	Sequence 14, Appl	Sequence 14, Appl	Sequence 832, App
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444	11.4	43.8	50	2	US-08-821-559A-18	Sequence 18, Appl	Sequence 18, Appl	Sequence 404, App
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446	11.4	43.8	50	3	US-09-400-541-17	Sequence 17, Appl	Sequence 17, Appl	Sequence 53, Appl
447	11.4	43.8	50	3	US-09-899-999-17	Sequence 18, Appl	Sequence 18, Appl	Sequence 526, App
448	11.4	43.8	50	3	US-09-899-999-17	Sequence 18, Appl	Sequence 18, Appl	Sequence 526, App
449	11.4	43.8	50	3	US-09-899-999-18	Sequence 18, Appl	Sequence 18, Appl	Sequence 526, App
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451	11.2	43.1	20	4	US-09-887-145-31	Sequence 31, Appl	Sequence 31, Appl	Sequence 526, App
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453	11.2	43.1	21	3	US-08-448-894-5	Sequence 5, Appli	Sequence 5, Appli	Sequence 404, App
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456	11.2	43.1	23	1	US-08-528-363-2	Sequence 2, Appli	Sequence 2, Appli	Sequence 138, App
457	11.2	43.1	23	1	US-08-451-318-2	Sequence 2, Appli	Sequence 2, Appli	Sequence 138, App
458	11.2	43.1	23	4	US-08-191-225-2	Sequence 5, Appli	Sequence 5, Appli	Sequence 138, App
459	11.2	43.1	23	4	US-08-486-602-5	Sequence 5, Appli	Sequence 5, Appli	Sequence 138, App
460	11.2	43.1	24	1	US-08-485-602-79	Sequence 79, Appl	Sequence 79, Appl	Sequence 404, App
461	11.2	43.1	24	1	US-08-757-180-5	Sequence 5, Appli	Sequence 5, Appli	Sequence 526, App
462	11.2	43.1	24	1	US-08-757-180-5	Sequence 5, Appli	Sequence 5, Appli	Sequence 526, App
463	11.2	43.1	24	1	US-08-745-638-5	Sequence 75, Appl	Sequence 75, Appl	Sequence 2, Appli
464	11.2	43.1	24	1	US-08-745-638-5	Sequence 75, Appl	Sequence 75, Appl	Sequence 2, Appli
465	11.2	43.1	25	2	US-09-050-739-104	Sequence 104, App	Sequence 104, App	Sequence 4, Appli
466	11.2	43.1	25	2	US-08-855-998-1139	Sequence 1139, App	Sequence 1139, App	Sequence 4, Appli

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C 685	10.8	41.5	28	3	US-09-218-444-4	Sequence 4, Appli	758	10.8	41.5	35	2	US-07-829-461A-14	Sequence 14, Appl
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C 687	10.8	41.5	28	4	US-09-853-666-4	Sequence 4, Appli	C 760	10.8	41.5	35	3	US-08-691-045-38	Sequence 38, Appl
C 688	10.8	41.5	28	4	US-09-610-651-57	Sequence 57, Appl	C 761	10.8	41.5	35	3	US-09-197-649-15	Sequence 15, Appl
C 689	10.8	41.5	30	2	US-08-670-175-5	Sequence 5, Appli	C 762	10.8	41.5	35	3	US-09-532-594B-21	Sequence 21, Appl
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C 691	10.8	41.5	30	2	US-08-995-927-8	Sequence 8, Appli	C 764	10.8	41.5	35	4	US-09-784-982-14	Sequence 18, Appl
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C 693	10.8	41.5	30	4	US-09-553-690-45	Sequence 45, Appl	C 766	10.8	41.5	35	5	PCT-US93-07645A-5	Sequence 5, Appli
C 694	10.8	41.5	30	4	US-09-125-576B-3	Sequence 3, Appli	C 767	10.8	41.5	35	5	PCT-US93-07645-5	Sequence 1, Appli
C 695	10.8	41.5	31	1	US-07-971-819A-34	Sequence 34, Appl	C 768	10.8	41.5	36	1	US-08-689-823-4	Sequence 4, Appli
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C 699	10.8	41.5	31	1	US-08-254-359A-18	Sequence 18, Appl	C 772	10.8	41.5	36	3	US-09-311-743-23	Sequence 17, Appl
C 700	10.8	41.5	31	1	US-08-475-231-34	Sequence 34, Appl	C 773	10.8	41.5	36	3	US-08-943-136-17	Sequence 17, Appl
C 701	10.8	41.5	31	1	US-08-475-231-40	Sequence 40, Appl	C 774	10.8	41.5	36	3	US-09-344-888A-16	Sequence 16, Appl
C 702	10.8	41.5	31	1	US-08-483-043-18	Sequence 18, Appl	C 775	10.8	41.5	36	3	US-08-973-518-17	Sequence 17, Appl
C 703	10.8	41.5	31	1	US-08-458-819-30	Sequence 30, Appl	C 776	10.8	41.5	36	3	US-09-448-310-58	Sequence 58, Appl
C 704	10.8	41.5	31	1	US-08-481-238-18	Sequence 18, Appl	C 777	10.8	41.5	36	4	US-09-479-005A-1055	Sequence 1055, Ap
C 705	10.8	41.5	31	2	US-08-471-066B-18	Sequence 18, Appl	C 778	10.8	41.5	36	4	US-09-479-005A-1056	Sequence 1056, Ap
C 706	10.8	41.5	31	2	US-08-484-956-18	Sequence 18, Appl	C 779	10.8	41.5	36	4	US-09-479-005A-1059	Sequence 1059, Ap
C 707	10.8	41.5	31	2	US-08-757-653-18	Sequence 18, Appl	C 780	10.8	41.5	36	4	US-09-479-005A-1059	Sequence 1059, Ap
C 708	10.8	41.5	31	2	US-08-599-491-18	Sequence 18, Appl	C 781	10.8	41.5	37	1	US-08-330-535A-27	Sequence 27, Appl
C 709	10.8	41.5	31	2	US-08-756-386-18	Sequence 18, Appl	C 782	10.8	41.5	37	1	US-08-688-145-2	Sequence 2, Appl
C 710	10.8	41.5	31	2	US-08-823-516-18	Sequence 18, Appl	C 783	10.8	41.5	37	1	US-08-688-145-2	Sequence 2, Appl
C 711	10.8	41.5	31	2	US-08-890-980-82	Sequence 80, Appl	C 784	10.8	41.5	37	2	US-08-838-844-27	Sequence 2, Appli
C 712	10.8	41.5	31	2	US-08-890-980-82	Sequence 82, Appl	C 785	10.8	41.5	37	2	US-08-776-944-2	Sequence 34, Appl
C 713	10.8	41.5	31	3	US-08-682-853A-18	Sequence 18, Appl	C 786	10.8	41.5	37	2	US-08-700-670A-34	Sequence 51, Appl
C 714	10.8	41.5	31	3	US-08-890-979-71	Sequence 71, Appl	C 787	10.8	41.5	37	3	US-09-202-316-51	Sequence 11, Appl
C 715	10.8	41.5	31	3	US-08-890-979-73	Sequence 73, Appl	C 788	10.8	41.5	37	4	US-09-375-975-33	Sequence 33, Appl
C 716	10.8	41.5	31	3	US-08-759-038-18	Sequence 18, Appl	C 789	10.8	41.5	38	2	US-08-292-620A-2198	Sequence 2198, Ap
C 717	10.8	41.5	31	3	US-08-758-314-18	Sequence 18, Appl	C 790	10.8	41.5	38	2	US-09-071-845-2198	Sequence 19, Appl
C 718	10.8	41.5	31	3	US-09-234-163-7	Sequence 7, Appli	C 791	10.8	41.5	38	4	US-09-337-307A-19	Sequence 9776, Ap
C 719	10.8	41.5	31	3	US-09-032-894-80	Sequence 80, Appl	C 792	10.8	41.5	38	4	US-09-371-772B-9776	Sequence 10654, A
C 720	10.8	41.5	31	3	US-09-198-839-6	Sequence 82, Appl	C 793	10.8	41.5	38	4	US-09-371-772B-10654	Sequence 29, Appl
C 721	10.8	41.5	31	3	US-08-901-379-7	Sequence 6, Appli	C 794	10.8	41.5	38	4	US-09-375-975-29	Sequence 35, Appl
C 722	10.8	41.5	31	3	US-08-901-379-7	Sequence 7, Appli	C 795	10.8	41.5	38	4	US-09-375-975-35	Sequence 36, Appl
C 723	10.8	41.5	31	3	US-09-031-626-80	Sequence 80, Appl	C 796	10.8	41.5	38	4	US-09-375-975-36	Sequence 133, App
C 724	10.8	41.5	31	3	US-09-031-626-82	Sequence 82, Appl	C 797	10.8	41.5	38	4	US-09-354-138-133	Sequence 3, Appli
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C 729	10.8	41.5	31	4	US-09-684-938-18	Sequence 18, Appl	C 802	10.8	41.5	39	4	US-09-621-275-19	Sequence 20, Appl
C 730	10.8	41.5	31	4	US-09-308-825A-18	Sequence 6, Appli	C 803	10.8	41.5	39	4	US-09-621-275-20	Sequence 41, Appl
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C 732	10.8	41.5	31	4	US-09-655-378A-18	Sequence 18, Appl	C 805	10.8	41.5	41	3	US-08-813-507-54	Sequence 54, Appl
C 733	10.8	41.5	31	4	US-09-940-244-18	Sequence 18, Appl	C 806	10.8	41.5	41	3	US-09-464-453-54	Sequence 74, Appl
C 734	10.8	41.5	31	4	US-09-333-145-18	Sequence 18, Appl	C 807	10.8	41.5	42	1	US-08-464-136-74	Sequence 74, Appl
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C 736	10.8	41.5	32	1	US-08-433-924-14	Sequence 42, Appl	C 809	10.8	41.5	42	3	US-08-470-297A-74	Sequence 74, Appl
C 737	10.8	41.5	32	1	US-08-471-791-42	Sequence 17, Appl	C 810	10.8	41.5	42	3	US-08-470-297A-74	Sequence 5, Appli
C 738	10.8	41.5	32	3	US-08-722-719-17	Sequence 17, Appl	C 811	10.8	41.5	42	5	PCT-US91-07149-74	Sequence 74, Appl
C 739	10.8	41.5	32	4	US-09-334-951-17	Sequence 17, Appl	C 812	10.8	41.5	42	5	PCT-US91-07149-74	Sequence 24, Appl
C 740	10.8	41.5	32	4	US-09-334-923A-17	Sequence 17, Appl	C 813	10.8	41.5	43	2	US-08-418-897-24	Sequence 24, Appl
C 741	10.8	41.5	32	4	US-09-689-693-18	Sequence 18, Appl	C 814	10.8	41.5	43	2	US-08-418-897-28	Sequence 28, Appl
C 742	10.8	41.5	32	4	US-09-334-954A-17	Sequence 17, Appl	C 815	10.8	41.5	43	2	US-08-418-897-32	Sequence 32, Appl
C 743	10.8	41.5	32	5	PCT-US91-01746-42	Sequence 42, Appl	C 816	10.8	41.5	43	3	US-09-351-814-26	Sequence 26, Appl
C 744	10.8	41.5	33	1	US-08-138-608-7	Sequence 7, Appli	C 817	10.8	41.5	43	3	US-09-351-814-26	Sequence 9, Appli
C 745	10.8	41.5	33	1	US-08-094-534-20	Sequence 20, Appl	C 818	10.8	41.5	44	4	US-09-050-559C-9	Sequence 9, Appli
C 746	10.8	41.5	33	5	PCT-US94-08000-20	Sequence 20, Appl	C 819	10.8	41.5	44	4	US-09-313-221A-47	Sequence 47, Appl
C 747	10.8	41.5	34	2	US-08-422-333-19	Sequence 19, Appl	C 820	10.8	41.5	44	4	US-09-736-116-18	Sequence 18, Appl
C 748	10.8	41.5	34	3	US-09-270-140A-53	Sequence 53, Appl	C 821	10.8	41.5	45	3	US-08-863-813A-56	Sequence 56, Appl
C 749	10.8	41.5	34	3	US-09-556-877-198	Sequence 198, App	C 822	10.8	41.5	45	3	US-08-863-813A-59	Sequence 59, Appl
C 750	10.8	41.5	34	4	US-09-620-412C-198	Sequence 198, App	C 823	10.8	41.5	45	4	US-09-839-477-2	Sequence 2, Appli
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C 752	10.8	41.5	34	4	US-09-721-908-62	Sequence 62, Appl	C 825	10.8	41.5	45	4	US-09-500-700-59	Sequence 59, Appl
C 753	10.8	41.5	34	4	US-09-451-739H-18	Sequence 18, Appl	C 826	10.8	41.5	46	4	US-08-944-410-57	Sequence 57, Appl
C 754	10.8	41.5	35	1	US-09-913-524-32	Sequence 32, Appl	C 827	10.8	41.5	46	6	5240845-12	Patent No. 5240845
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C 756	10.8	41.5	35	1	US-08-012-543-5	Sequence 5, Appli	C 829	10.8	41.5	47	4	US-09-671-317-733	Sequence 733, App
							C 830	10.8	41.5	47	4	US-09-422-978-781	Sequence 781, App

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C 832	10.8	41.5	47	4	US-09-422-978-3857	Sequence 3857, App	C 905	10.6	40.8	25	4	US-08-806-708B-6	Sequence 6, Appl
C 833	10.8	41.5	49	2	US-07-916-098A-17	Sequence 17, App	C 906	10.6	40.8	26	2	US-08-859-998-1257	Sequence 1257, Ap
C 834	10.8	41.5	50	1	US-08-259-612A-7	Sequence 7, Appl	C 907	10.6	40.8	26	3	US-09-225-928-1257	Sequence 1257, Ap
C 835	10.8	41.5	50	1	US-08-644-291-7	Sequence 7, Appl	C 908	10.6	40.8	26	4	US-09-225-201B-1257	Sequence 1257, Ap
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C 840	10.6	40.8	18	1	US-08-444-803-55	Sequence 55, Appl	C 913	10.6	40.8	27	3	US-08-482-369A-1	Sequence 1, Appl
C 841	10.6	40.8	18	1	US-08-449-043-55	Sequence 55, Appl	C 914	10.6	40.8	27	3	US-09-009-217-15	Sequence 15, Appl
C 842	10.6	40.8	18	1	US-08-456-265A-55	Sequence 55, Appl	C 915	10.6	40.8	27	3	US-09-009-656-15	Sequence 15, Appl
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C 844	10.6	40.8	18	1	US-08-455-244-55	Sequence 55, Appl	C 917	10.6	40.8	27	4	US-09-743-980-10	Sequence 10, Appl
C 845	10.6	40.8	18	1	US-08-454-876-55	Sequence 55, Appl	C 918	10.6	40.8	27	5	PCT-US95-07439-1	Sequence 1, Appl
C 846	10.6	40.8	18	2	US-08-457-364-55	Sequence 55, Appl	C 919	10.6	40.8	28	1	US-08-140-729A-16	Sequence 16, Appl
C 847	10.6	40.8	18	2	US-08-456-262-55	Sequence 55, Appl	C 920	10.6	40.8	28	1	US-08-546-666-16	Sequence 16, Appl
C 848	10.6	40.8	18	2	US-08-456-240-55	Sequence 55, Appl	C 921	10.6	40.8	28	2	US-08-916-745-16	Sequence 16, Appl
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C 852	10.6	40.8	18	2	US-08-996-306-39	Sequence 39, Appl	C 925	10.6	40.8	28	3	US-09-198-650-16	Sequence 16, Appl
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C 856	10.6	40.8	18	3	US-09-218-207-39	Sequence 39, Appl	C 929	10.6	40.8	28	4	US-09-260-629-5	Sequence 5, Appl
C 857	10.6	40.8	18	3	US-09-218-207-360	Sequence 360, App	C 930	10.6	40.8	28	4	US-09-227-614-16	Sequence 16, Appl
C 858	10.6	40.8	18	4	US-09-422-978-5490	Sequence 5490, App	C 931	10.6	40.8	29	1	US-08-466-033-129	Sequence 129, App
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C 860	10.6	40.8	18	4	US-09-906-234-55	Sequence 55, Appl	C 933	10.6	40.8	29	2	US-08-464-134-129	Sequence 129, App
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C 865	10.6	40.8	20	2	US-08-505-377-9	Sequence 9, Appl	C 938	10.6	40.8	29	5	PCT-US95-06266-109	Sequence 109, App
C 866	10.6	40.8	20	2	US-08-748-104-6	Sequence 6, Appl	C 939	10.6	40.8	30	1	US-08-461-773-8	Sequence 8, Appl
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C 868	10.6	40.8	20	3	US-09-045-106-12	Sequence 12, Appl	C 941	10.6	40.8	30	2	US-08-921-382-4	Sequence 4, Appl
C 869	10.6	40.8	20	3	US-08-798-269-9	Sequence 9, Appl	C 942	10.6	40.8	30	2	US-08-859-998-290	Sequence 290, App
C 870	10.6	40.8	20	3	US-08-813-507-18	Sequence 18, Appl	C 943	10.6	40.8	30	3	US-09-102-371-3	Sequence 3, Appl
C 871	10.6	40.8	20	3	US-09-490-692-19	Sequence 19, Appl	C 944	10.6	40.8	30	3	US-09-225-928-290	Sequence 290, App
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C 875	10.6	40.8	20	4	US-09-967-665-60	Sequence 60, Appl	C 948	10.6	40.8	30	4	US-09-616-430-4	Sequence 4, Appl
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C 877	10.6	40.8	21	4	US-09-493-784-6	Sequence 6, Appl	C 950	10.6	40.8	31	3	US-09-575-602-8	Sequence 8, Appl
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C 879	10.6	40.8	22	3	US-08-943-731-552	Sequence 552, App	C 952	10.6	40.8	32	3	US-08-996-441B-103	Sequence 103, App
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C 884	10.6	40.8	23	4	US-09-602-586-40	Sequence 40, Appl	C 957	10.6	40.8	32	4	US-09-427-770-103	Sequence 103, App
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C 888	10.6	40.8	23	4	US-09-825-244A-18	Sequence 18, Appl	C 961	10.6	40.8	33	3	US-09-232-468A-26	Sequence 26, Appl
C 889	10.6	40.8	23	5	PCT-US92-07916-15	Sequence 15, Appl	C 962	10.6	40.8	33	4	US-09-597-877-17	Sequence 17, Appl
C 890	10.6	40.8	24	1	US-08-029-404-3	Sequence 3, Appl	C 963	10.6	40.8	33	4	US-09-597-877-18	Sequence 18, Appl
C 891	10.6	40.8	24	1	US-08-290-933-2	Sequence 3, Appl	C 964	10.6	40.8	33	4	US-09-311-784A-58	Sequence 58, Appl
C 892	10.6	40.8	24	3	US-08-459-953A-3	Sequence 3, Appl	C 965	10.6	40.8	33	4	US-09-784-984B-20	Sequence 20, Appl
C 893	10.6	40.8	24	4	US-09-475-947A-307	Sequence 307, App	C 966	10.6	40.8	34	2	US-08-793-229-4	Sequence 4, Appl
C 894	10.6	40.8	24	4	US-09-393-212-3	Sequence 3, Appl	C 967	10.6	40.8	34	2	US-08-521-871A-7	Sequence 7, Appl
C 895	10.6	40.8	25	1	US-08-343-379-1	Sequence 1, Appl	C 968	10.6	40.8	34	3	US-09-285-957-4	Sequence 4, Appl
C 896	10.6	40.8	25	1	US-09-478-122-11	Sequence 11, Appl	C 969	10.6	40.8	36	1	US-08-450-384-20	Sequence 20, Appl
C 897	10.6	40.8	25	4	US-09-484-997-11	Sequence 11, Appl	C 970	10.6	40.8	36	3	US-09-050-559C-23	Sequence 23, Appl
C 898	10.6	40.8	25	4	US-09-481-355-11	Sequence 11, Appl	C 971	10.6	40.8	36	3	US-09-101-629A-13	Sequence 13, Appl
C 899	10.6	40.8	25	4	US-09-481-282-11	Sequence 11, Appl	C 972	10.6	40.8	36	3	US-09-101-629A-14	Sequence 14, Appl
C 900	10.6	40.8	25	4	US-09-455-659A-11	Sequence 11, Appl	C 973	10.6	40.8	36	4	US-09-810-502-6	Sequence 6, Appl
C 901	10.6	40.8	25	4	US-09-484-996-11	Sequence 11, Appl	C 974	10.6	40.8	37	2	US-08-561-521-18	Sequence 18, Appl
C 902	10.6	40.8	25	4	US-09-827-998-1559	Sequence 1559, App	C 975	10.6	40.8	37	2	US-08-561-521-20	Sequence 20, Appl
C 903	10.6	40.8	25	4	US-09-479-123-11	Sequence 11, Appl	C 976	10.6	40.8	37	4	US-09-301-593-63	Sequence 63, Appl

US-10-353-589-1

Query Match 100.0%; Score 26; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
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DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 4

US-10-029-907-17
; Sequence 17, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: HCV
US-10-029-907-17

Query Match 100.0%; Score 26; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||||
DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 5

US-09-493-353-1
; Sequence 1, Application US/09493353
; Patent No. 6638714
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; APPLICANT: Linnen, J.M.
; APPLICANT: Gorman, K.M.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT
; TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2094/1E286-US1
; CURRENT APPLICATION NUMBER: US/09/493,353
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/118,497
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-493-353-1

Query Match 96.2%; Score 25; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
|||||

DB 1 CAGAAAGCGTCTAGCCATGGCGTTA 25

RESULT 6

US-08-240-547-5
; Sequence 5, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2977
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-5

Query Match 92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24

DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 7

US-08-449-050-17
; Sequence 17, Application US/08449050
; Patent No. 5561058
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David
; APPLICANT: Myers, Thomas
; APPLICANT: Sigua, Christopher
; TITLE OF INVENTION: Reagents and Methods for Coupled High
; TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain
; NUMBER OF SEQUENCES: 19
; TITLE OF INVENTION: Reactions
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley


```

US-08-332-616A-9
Query Match          92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||||

RESULT 9
US-08-317-220-9
; Sequence 9, Application US/08317220
; Patent No. 5654179
; GENERAL INFORMATION:
; APPLICANT: LIN, LILY
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETER G. CARROLL
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,220
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,649
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,545
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/614,921
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: HRI-00542
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-317-220-9
Query Match          92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||||

```



```
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, DWIGHT
; APPLICANT: WINKLER, MATTHEW
; APPLICANT: PASLOSKE, BRITTAN L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
; TITLE OF INVENTION: RNA STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,153
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-675-153-7

Query Match          92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    ||||||||||||||||||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 11
US-08-738-928-4
; Sequence 4, Application US/08/738928
; Patent No. 5837442
; GENERAL INFORMATION:
; APPLICANT: Teang, Sue Y.
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
; TITLE OF INVENTION: HCV Nucleic Acid
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-738-928-4

Query Match          92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    ||||||||||||||||||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 12
US-08-841-252-7
; Sequence 7, Application US/08841252
; Patent No. 5919625
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, DWIGHT
; APPLICANT: WINKLER, MATTHEW
; APPLICANT: PASLOSKE, BRITTAN L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
; TITLE OF INVENTION: STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,252
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,677,124
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI-026--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-300
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-841-252-7

Query Match          92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-282-054-7

Query Match      92.3%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 16
US-09-665-638-7
; Sequence 7, Application US/09665638
; Patent No. 6399307
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; DuBois, Dwight
; Brown, David
; Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/665,638
; FILING DATE: 19-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-665-638-7
Query Match      92.3%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 17
US-10-007-389-4
; Sequence 4, Application US/10007389
; Patent No. 6727067
; GENERAL INFORMATION:
; APPLICANT: Ruesman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-007-389-4

Query Match      92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 18
US-08-240-547-6
; Sequence 6, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-240-547-6
;
Query Match 92.3%; Score 24; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 3 GCAGAAAGCGTCTAGCCATGGCGT 26

RESULT 19
PCT-US94-05407-14
; Sequence 14, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; PCT-US94-05407-14
;
Query Match 92.3%; Score 24; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTT 25
Db 14 CAGAAAGCGTCTAGCCATGGCGTT 37

RESULT 20
US-09-034-205-25
; Sequence 25, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-240-547-6
;
Query Match 92.3%; Score 24; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGG 21
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 21
US-08-934-097A-25
; Sequence 25, Application US/08934097A
; Patent No. 6210880
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Fors, Lance
; APPLICANT: Brow, Mary Ann D.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing With Structure-Bridging
; TITLE OF INVENTION: Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,205
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-09-034-205-25
;
Query Match 80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,097A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-934-097A-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 22
US-08-851-588-25
; Sequence 25, Application US/08851588
; Patent No. 6214545
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Prudent, James R.
; APPLICANT: Dahlberg, James E.
; APPLICANT: Fors, Lance
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/851,588
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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```
; DESCRIPTION: /desc = "DNA"
US-08-851-588-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 23
US-09-677-218B-25
; Sequence 25, Application US/09677218B
; Patent No. 6355437
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESS: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/677,218B
; FILING DATE: 02-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/034,205
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-677-218B-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 24
US-09-677-192-25
; Sequence 25, Application US/09677192
```

```
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichiev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-677-192-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 25
US-09-402-618B-25
; Sequence 25, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-402-618B-25

Query Match      80.8%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 26
US-09-825-574-25
; Sequence 25, Application US/09825574
```

```
; Patent No. 6709819
; GENERAL INFORMATION:
; APPLICANT: Lyamichiev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing With Structure-Bridging
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/825,574
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
; US-09-825-574-25

Query Match      80.8%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 27
US-09-676-768-25
; Sequence 25, Application US/09676768
; Patent No. 6780585
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichiev, Victor I.
; APPLICANT: Prudent, James R.
; APPLICANT: Dahlberg, James E.
; APPLICANT: Fors, Lance
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
```

STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/676,768
FILING DATE: 02-Oct-2000
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/851,588
FILING DATE: 05-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-676-768-25

Query Match 80.8%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGG 21
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 28
US-08-397-220B-33/c
Sequence 33, Application US/08397220B
Patent No. 6284458
GENERAL INFORMATION:
APPLICANT: Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,220B
FILING DATE: 09-Mar-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01293
FILING DATE: 10-Sep-93
APPLICATION NUMBER: JP 5-87195
FILING DATE: 14-Apr-93
APPLICATION NUMBER: 07/945,289

FILING DATE: 10-Sep-92
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-397-220B-33

Query Match 76.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGCGTCTAGCCATGGC 22
Db 20 AGAAGCGTCTAGCCATGGC 1

RESULT 29
US-08-650-093C-33/c
Sequence 33, Application US/08650093C
Patent No. 6391542
GENERAL INFORMATION:
APPLICANT: Kevin P. Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: LICATA & TYRRELL P.C.
STREET: 66 E. Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WORDPERFECT 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,093C
FILING DATE: 17-May-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/452,841
FILING DATE: May 30, 1995
APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes

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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-650-093C-33
Query Match          76.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGAAGCGTCTAGCCATGCG 22
Db 20 AGAAGCGTCTAGCCATGCG 1

RESULT 30
US-08-735-381-4/c
; Sequence 4, Application US/08735381
; Patent No. 5853993
; GENERAL INFORMATION:
; APPLICANT: Dellinger, Douglas J.
; APPLICANT: Dahm, SueAnn
; APPLICANT: Troll, Mark
; TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hewlett-Packard Company, Legal Dept.,
; STREET: 1501 Page Mill Road, MS 4U-10
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1126
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,381
; FILING DATE: 21-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10950427-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-857-4125
; TELEFAX: 650-852-8063
; TELEX: 348-461
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OLIGONUCLEOTIDE"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-735-381-4

Query Match          76.9%; Score 20; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATG 20
Db 20 GCAGAAAGCGTCTAGCCATG 1

RESULT 31
US-09-183-619-3/c
; Sequence 3, Application US/09183619
; Patent No. 6103474
; GENERAL INFORMATION:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OLIGONUCLEOTIDE"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-201-674-4

Query Match          76.9%; Score 20; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATG 20
Db 20 GCAGAAAGCGTCTAGCCATG 1

RESULT 33
US-09-210-657-1
; Sequence 1, Application US/09210657
; Patent No. 6248526
; GENERAL INFORMATION:
; APPLICANT: Weimer, Thomas
; TITLE OF INVENTION: LABELED PRIMER FOR USE IN AND DETECTION OF TARGET
; FILE REFERENCE: 06478-1421
; CURRENT APPLICATION NUMBER: US/09/210,657
; CURRENT FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-210-657-1

Query Match          73.1%; Score 19; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGTCTAGCCATGGCGTTA 26
Db 1 GCGTCTAGCCATGGCGTTA 19

RESULT 34
US-08-240-547-4
; Sequence 4, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-4

Query Match          73.1%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
Db 12 GCAGAAAGCGTCTAGCCAT 30

RESULT 35
US-09-014-416-16
; Sequence 16, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-16

Query Match          73.1%; Score 19; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
Db 12 GCAGAAAGCGTCTAGCCAT 30

RESULT 36
US-08-438-639-44/c
; Sequence 44, Application US/08438639
; Patent No. 5712383
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
; TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,639
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,338
; FILING DATE: 23-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth, M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0232.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-438-639-44
Query Match 73.1%; Score 19; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 37
US-07-813-338A-44/c
; Sequence 44, Application US/07813338A
; Patent No. 5747244
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
; TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,338A
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth, M.

```

```

; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0232.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-813-338A-44
Query Match 73.1%; Score 19; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 38
US-08-470-124-77/c
; Sequence 77, Application US/08470124
; Patent No. 5849481
; GENERAL INFORMATION:
; APPLICANT: Urdea, Michael S.
; APPLICANT: Horn, Thomas
; APPLICANT: Chang, Chu-An
; APPLICANT: Warner, Brian
; APPLICANT: Fultz, Timothy J.
; TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
; TITLE OF INVENTION: POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,588
; FILING DATE: 23 December 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ciotti, Thomas E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20104.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-470-124-77
Query Match 73.1%; Score 19; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;

```

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
|
Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 39

US-08-441-971-120/c
; Sequence 120, Application US/08441971
; Patent No. 6071693
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,971
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,653
; FILING DATE:
; APPLICATION NUMBER: US/07/881,528
; FILING DATE:
; APPLICATION NUMBER: 07/697,326
; FILING DATE: 8 May 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 720-3500
; TELEFAX: (617) 720-2441
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-441-971-120

Query Match 73.1%; Score 19; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
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Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 40

US-08-221-653-120/c
; Sequence 120, Application US/08221653
; Patent No. 6190864
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; DIAGNOSTICS AND THERAPEUTICS

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; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,653
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/881,528
; FILING DATE:
; APPLICATION NUMBER: 07/697,326
; FILING DATE: 8 May 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 720-3500
; TELEFAX: (617) 720-2441
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-221-653-120

Query Match 73.1%; Score 19; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19 GCAGAAAGCGTCTAGCCAT 1

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Job time : 38.0899 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-6

Perfect score: 26

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	26	100.0	30	13	US-10-029-907-17
5	26	100.0	30	15	US-10-309-561-17
6	26	100.0	30	15	US-10-198-680A-2
7	26	100.0	30	15	US-10-320-978-1
8	26	100.0	30	15	US-10-353-563-1
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14	26	100.0	30	17	US-10-789-355-17	Sequence 17, Appl
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16	26	100.0	30	18	US-10-791-318-1	Sequence 1, Appli
17	24	92.3	24	13	US-10-120-013-7	Sequence 7, Appli
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19	24	92.3	24	15	US-10-037-990-1	Sequence 1, Appli
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24	24	92.3	24	16	US-10-688-272-17	Sequence 17, Appli
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27	24	92.3	25	15	US-10-259-275-12	Sequence 12, Appli
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31	21	80.8	21	15	US-10-240-460-10	Sequence 10, Appli
32	21	80.8	25	15	US-10-182-126-7	Sequence 7, Appli
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38	19	73.1	19	18	US-10-667-271-104	Sequence 104, App
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40	19	73.1	19	18	US-10-667-271-113	Sequence 113, App
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43	19	73.1	19	18	US-10-667-271-795	Sequence 795, App
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51	19	73.1	22	16	US-10-407-897-38	Sequence 38, Appli
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53	19	73.1	24	17	US-10-451-882-34	Sequence 34, Appli
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58	18	69.2	19	18	US-10-667-271-111	Sequence 111, App
59	18	69.2	19	18	US-10-667-271-801	Sequence 801, App
60	18	69.2	19	18	US-10-667-271-807	Sequence 807, App
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70	17	65.4	17	10	US-09-817-879-14	Sequence 14, Appli
71	17	65.4	17	10	US-09-817-879-15	Sequence 15, Appli
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c 98	16	61.5	19	18	US-10-667-271-823	Sequence 823, App	c 171	50.8	20	17	US-10-688-706-1658	Sequence 1658, Ap
c 99	16	61.5	22	16	US-10-407-897-3	Sequence 3, Appli	c 172	50.8	22	15	US-10-459-970-8	Sequence 8, Appli
c 100	16	61.5	26	9	US-09-294-121A-3	Sequence 3, Appli	c 173	50.8	25	17	US-10-717-597-1103	Sequence 1103, Ap
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c 145	14	53.8	17	10	US-09-740-332-17	Sequence 17, Appl	c 218	50.0	42	16	US-10-179-940-48	Sequence 48, Appl
c 146	14	53.8	17	10	US-09-817-879-17	Sequence 17, Appl	c 219	50.0	47	16	US-10-462-645-4	Sequence 4, Appli
c 147	14	53.8	17	17	US-10-669-841-2610	Sequence 2610, Ap	c 220	12.8	20	9	US-09-752-639-30	Sequence 30, Appl
c 148	14	53.8	19	10	US-09-848-269-2	Sequence 2, Appli	c 221	49.2	20	9	US-09-984-198-30	Sequence 30, Appl
c 149	14	53.8	19	18	US-10-667-271-95	Sequence 95, Appl	c 222	49.2	30	10	US-09-954-987B-156	Sequence 156, App
c 150	14	53.8	19	18	US-10-667-271-121	Sequence 121, App	c 223	49.2	30	10	US-09-954-987B-157	Sequence 157, App
c 151	14	53.8	19	18	US-10-667-271-791	Sequence 791, App	c 224	49.2	30	15	US-10-265-072-23	Sequence 23, Appl
c 152	14	53.8	19	18	US-10-667-271-817	Sequence 817, App	c 225	12.8	30	15	US-10-265-072-24	Sequence 24, Appl
c 153	14	53.8	30	15	US-10-289-135A-92	Sequence 92, Appl	c 226	49.2	31	9	US-09-801-274-1424	Sequence 1424, Ap
c 154	13.8	53.1	25	17	US-10-230-026-99	Sequence 99, Appl	c 227	49.2	31	10	US-09-877-478-5186	Sequence 5186, Ap
c 155	13.8	53.1	25	17	US-10-717-597-4121	Sequence 4121, Ap	c 228	49.2	31	16	US-10-342-902-5186	Sequence 5186, Ap
c 156	13.8	53.1	25	17	US-10-717-597-4122	Sequence 4122, Ap	c 229	49.2	31	17	US-10-712-672-4888	Sequence 4888, Ap
c 157	13.8	53.1	31	15	US-10-156-306-3372	Sequence 3372, Ap	c 230	49.2	31	17	US-10-669-841-10077	Sequence 10077, A
c 158	13.8	53.1	31	15	US-10-238-700-3943	Sequence 3943, Ap	c 231	49.2	36	17	US-10-644-355A-64	Sequence 64, Appl

C 232	12.8	49.2	39	14	US-10-006-593-78	Sequence 78, Appl	305	12.2	46.9	36	15	US-10-050-902-301	Sequence 301, App
C 233	12.8	49.2	39	15	US-10-307-724-78	Sequence 78, Appl	306	12.2	46.9	36	15	US-10-050-898-301	Sequence 301, App
C 234	12.6	48.5	25	15	US-10-098-2638-3931	Sequence 3931, Ap	307	12.2	46.9	36	16	US-10-617-876-80	Sequence 80, Appl
C 235	12.6	48.5	25	15	US-10-098-2638-4567	Sequence 4567, Ap	308	12.2	46.9	37	10	US-09-894-799-1	Sequence 1, Appli
C 236	12.6	48.5	25	15	US-10-098-2638-111917	Sequence 111917, Ap	309	12.2	46.9	37	16	US-10-648-984-1	Sequence 1, Appli
C 237	12.6	48.5	25	15	US-10-098-2638-111918	Sequence 111918, Ap	310	12.2	46.9	38	15	US-10-050-902-302	Sequence 302, App
C 238	12.6	48.5	30	15	US-10-261-078-16	Sequence 16, Appl	311	12.2	46.9	38	15	US-10-050-898-302	Sequence 302, App
C 239	12.6	48.5	37	9	US-09-935-371-48	Sequence 48, Appl	312	12.2	46.9	38	16	US-10-371-472-51	Sequence 51, Appl
C 240	12.6	48.5	38	10	US-09-877-478-4209	Sequence 4209, Ap	313	12.2	46.9	38	16	US-10-617-876-81	Sequence 81, Appl
C 241	12.6	48.5	38	16	US-10-342-902-4209	Sequence 4209, Ap	314	12.2	46.9	39	15	US-10-094-749-3292	Sequence 3292, Ap
C 242	12.6	48.5	38	16	US-10-467-431-4	Sequence 4, Appli	315	12.2	46.9	39	15	US-10-104-047-3950	Sequence 3950, Ap
C 243	12.6	48.5	38	17	US-10-669-841-9100	Sequence 9100, Ap	316	12.2	46.9	39	16	US-10-108-2608-4896	Sequence 4896, Ap
C 244	12.6	48.5	38	17	US-10-466-695A-4	Sequence 4, Appli	317	12.2	46.9	39	16	US-10-609-775-21	Sequence 21, Appl
C 245	12.6	48.5	41	14	US-10-038-723-55	Sequence 55, Appl	318	12.2	46.9	44	16	US-10-282-122A-2112	Sequence 212, Ap
C 246	12.4	47.7	25	9	US-09-791-171-106	Sequence 106, App	319	12.2	46.9	44	17	US-10-706-229-6	Sequence 6, Appli
C 247	12.4	47.7	25	10	US-09-943-443-106	Sequence 106, App	320	12.2	46.9	47	16	US-10-349-143-1691	Sequence 4, Appli
C 248	12.4	47.7	25	10	US-09-804-980-106	Sequence 106, App	321	12.2	46.9	48	14	US-10-023-066A-4	Sequence 4, Appli
C 249	12.4	47.7	25	14	US-10-215-112-5596	Sequence 5596, Ap	322	12.2	46.9	48	15	US-10-161-547-38	Sequence 38, Appl
C 250	12.4	47.7	25	14	US-10-215-112-6086	Sequence 5596, Ap	323	12.2	46.9	50	16	US-10-131-827-5585	Sequence 5585, Ap
C 251	12.4	47.7	25	17	US-10-620-246-106	Sequence 106, App	324	12	46.2	13	10	US-09-740-332-4598	Sequence 4598, Ap
C 252	12.4	47.7	27	17	US-10-469-552-13	Sequence 13, Appl	325	12	46.2	13	10	US-09-817-879-4598	Sequence 4598, Ap
C 253	12.4	47.7	30	15	US-10-142-283-104	Sequence 104, App	326	12	46.2	13	17	US-10-569-841-7191	Sequence 7191, Ap
C 254	12.4	47.7	30	15	US-10-289-135A-102	Sequence 102, App	327	12	46.2	15	10	US-09-825-805-3	Sequence 3, Appli
C 255	12.4	47.7	30	17	US-10-651-674-3	Sequence 3, Appli	328	12	46.2	17	9	US-09-866-108-7460	Sequence 7460, Ap
C 256	12.4	47.7	30	17	US-10-651-674-4	Sequence 4, Appli	329	12	46.2	17	9	US-09-866-108-7461	Sequence 7461, Ap
C 257	12.4	47.7	31	9	US-09-841-132-204	Sequence 204, App	330	12	46.2	17	9	US-09-866-108-7462	Sequence 7462, Ap
C 258	12.4	47.7	31	10	US-09-740-332-5474	Sequence 5474, Ap	331	12	46.2	17	9	US-09-866-108-7463	Sequence 7463, Ap
C 259	12.4	47.7	31	10	US-09-817-879-5474	Sequence 5474, Ap	332	12	46.2	17	9	US-09-866-108-7464	Sequence 7464, Ap
C 260	12.4	47.7	31	17	US-10-712-672-4662	Sequence 4662, Ap	333	12	46.2	17	9	US-09-866-108-7465	Sequence 7465, Ap
C 261	12.4	47.7	31	17	US-10-712-672-4845	Sequence 4845, Ap	334	12	46.2	17	10	US-09-740-332-18	Sequence 18, Appli
C 262	12.4	47.7	31	17	US-10-669-841-12019	Sequence 12019, A	335	12	46.2	17	10	US-09-817-879-18	Sequence 18, Appl
C 263	12.4	47.7	33	15	US-10-289-135A-109	Sequence 109, App	336	12	46.2	17	17	US-10-669-841-2611	Sequence 2611, Ap
C 264	12.4	47.7	34	14	US-10-283-349-14	Sequence 14, Appl	337	12	46.2	17	17	US-10-723-361-7460	Sequence 7460, Ap
C 265	12.4	47.7	35	10	US-09-986-033-1	Sequence 1, Appli	338	12	46.2	17	17	US-10-723-361-7461	Sequence 7461, Ap
C 266	12.4	47.7	38	10	US-09-848-754A-4463	Sequence 4463, Ap	339	12	46.2	17	17	US-10-723-361-7462	Sequence 7462, Ap
C 267	12.4	47.7	38	15	US-10-156-306-2061	Sequence 2061, Ap	340	12	46.2	17	17	US-10-723-361-7463	Sequence 7463, Ap
C 268	12.4	47.7	41	14	US-10-043-573-87	Sequence 87, Appl	341	12	46.2	17	17	US-10-723-361-7464	Sequence 7464, Ap
C 269	12.4	47.7	41	14	US-10-283-349-9	Sequence 9, Appli	342	12	46.2	17	18	US-10-667-271-103	Sequence 103, App
C 270	12.4	47.7	42	16	US-10-162-743-8	Sequence 8, Appli	343	12	46.2	19	18	US-10-667-271-137	Sequence 137, App
C 271	12.4	47.7	45	9	US-09-878-766A-6	Sequence 6, Appli	344	12	46.2	19	18	US-10-667-271-199	Sequence 199, App
C 272	12.4	47.7	45	16	US-10-650-369-6	Sequence 6, Appli	345	12	46.2	19	18	US-10-667-271-833	Sequence 833, App
C 273	12.4	47.7	47	14	US-10-136-841-17	Sequence 17, Appl	346	12	46.2	19	18	US-10-786-720-7515	Sequence 7515, Ap
C 274	12.4	47.7	47	15	US-10-170-097-1257	Sequence 1257, Ap	347	12	46.2	21	18	US-10-786-720-7515	Sequence 7515, Ap
C 275	12.4	47.7	47	16	US-10-272-531A-13	Sequence 17, Appl	348	12	46.2	21	18	US-10-323-463-6	Sequence 6, Appli
C 276	12.4	47.7	47	16	US-10-272-483A-17	Sequence 17, Appl	349	12	46.2	23	15	US-10-632-658-27	Sequence 27, Appl
C 277	12.4	47.7	47	16	US-10-333-429-128	Sequence 128, App	350	12	46.2	23	16	US-10-605-708A-23	Sequence 23, Appl
C 278	12.4	47.7	48	15	US-10-309-630-56	Sequence 56, Appl	351	12	46.2	23	17	US-09-962-318-9	Sequence 9, Appli
C 279	12.4	47.7	50	10	US-09-308-683-5	Sequence 5, Appli	352	12	46.2	24	9	US-09-962-318-15	Sequence 15, Appl
C 280	12.4	47.7	50	14	US-10-136-841-13	Sequence 13, Appl	353	12	46.2	24	16	US-10-632-658-25	Sequence 25, Appl
C 281	12.4	47.7	50	16	US-10-272-531A-13	Sequence 13, Appl	354	12	46.2	24	16	US-09-866-108-12352	Sequence 12352, A
C 282	12.4	47.7	50	16	US-10-272-483A-13	Sequence 13, Appl	355	12	46.2	25	9	US-09-866-108-12353	Sequence 12353, A
C 283	12.2	46.9	18	15	US-10-044-115A-1	Sequence 1, Appli	356	12	46.2	25	9	US-09-866-108-12354	Sequence 12354, A
C 284	12.2	46.9	20	15	US-10-033-662A-27	Sequence 27, Appl	357	12	46.2	25	9	US-09-866-108-12355	Sequence 12355, A
C 285	12.2	46.9	20	17	US-10-688-706-704	Sequence 704, App	358	12	46.2	25	9	US-09-866-108-12356	Sequence 12356, A
C 286	12.2	46.9	20	17	US-10-688-706-1762	Sequence 1762, Ap	359	12	46.2	25	9	US-09-866-108-12357	Sequence 12357, A
C 287	12.2	46.9	22	10	US-09-931-936-1949	Sequence 1949, Ap	360	12	46.2	25	9	US-09-866-108-12358	Sequence 12358, A
C 288	12.2	46.9	25	15	US-10-098-263B-44798	Sequence 44798, A	361	12	46.2	25	9	US-09-866-108-12359	Sequence 12359, A
C 289	12.2	46.9	25	15	US-10-098-263B-87902	Sequence 87902, A	362	12	46.2	25	9	US-09-866-108-12360	Sequence 12360, A
C 290	12.2	46.9	25	17	US-10-223-646-31	Sequence 31, Appl	363	12	46.2	25	9	US-09-866-108-12361	Sequence 12361, A
C 291	12.2	46.9	25	17	US-10-717-597-4120	Sequence 4120, Ap	364	12	46.2	25	9	US-09-866-108-12362	Sequence 12362, A
C 292	12.2	46.9	26	14	US-10-096-718-76	Sequence 76, Appl	365	12	46.2	25	9	US-09-866-108-12363	Sequence 12363, A
C 293	12.2	46.9	27	16	US-10-456-129-26	Sequence 26, Appl	366	12	46.2	25	9	US-09-866-108-12364	Sequence 12364, A
C 294	12.2	46.9	29	10	US-09-862-393-20	Sequence 20, Appl	367	12	46.2	25	9	US-09-866-108-12365	Sequence 12365, A
C 295	12.2	46.9	29	18	US-10-777-010-4	Sequence 4, Appli	368	12	46.2	25	14	US-10-215-112-3129	Sequence 3129, Ap
C 296	12.2	46.9	30	15	US-10-300-699-9	Sequence 9, Appli	369	12	46.2	25	14	US-10-215-112-10461	Sequence 10461, A
C 297	12.2	46.9	30	15	US-10-418-820-9	Sequence 9, Appli	370	12	46.2	25	15	US-10-098-263B-49153	Sequence 49153, A
C 298	12.2	46.9	33	16	US-09-790-399-19	Sequence 19, Appl	371	12	46.2	25	15	US-10-098-263B-115494	Sequence 115494, A
C 299	12.2	46.9	33	16	US-10-343-766-2	Sequence 2, Appli	372	12	46.2	25	17	US-10-318-416B-7	Sequence 7, Appli
C 300	12.2	46.9	34	18	US-10-784-880-191	Sequence 191, App	373	12	46.2	25	17	US-10-723-361-12352	Sequence 12352, A
C 301	12.2	46.9	35	15	US-10-094-749-3291	Sequence 3291, Ap	374	12	46.2	25	17	US-10-723-361-12353	Sequence 12353, A
C 302	12.2	46.9	35	15	US-10-104-047-3949	Sequence 3949, Ap	375	12	46.2	25	17	US-10-723-361-12354	Sequence 12354, A
C 303	12.2	46.9	35	16	US-10-108-260A-4895	Sequence 4895, Ap	376	12	46.2	25	17	US-10-723-361-12355	Sequence 12355, A
C 304	12.2	46.9	36	15	US-10-053-662A-25	Sequence 25, Appl	377	12	46.2	25	17	US-10-723-361-12355	Sequence 12355, A

670	11.4	43.8	40	18	US-10-469-851-255	Sequence 255, App	c 743	11.2	43.1	25	15	US-10-098-263B-65714	Sequence 65714, A
671	11.4	43.8	41	16	US-10-035-833A-118	Sequence 118, App	744	11.2	43.1	25	15	US-10-098-263B-66326	Sequence 66326, A
c 672	11.4	43.8	41	16	US-10-035-833A-186	Sequence 186, App	745	11.2	43.1	25	15	US-10-098-263B-90688	Sequence 90688, A
673	11.4	43.8	41	16	US-10-035-833A-573	Sequence 573, App	746	11.2	43.1	25	15	US-10-098-263B-95129	Sequence 95129, A
674	11.4	43.8	41	16	US-10-035-833A-5457	Sequence 5457, App	747	11.2	43.1	25	15	US-10-098-263B-96129	Sequence 96129, A
c 675	11.4	43.8	41	16	US-10-035-833A-5525	Sequence 5525, App	c 748	11.2	43.1	25	15	US-10-098-263B-108488	Sequence 108488, A
676	11.4	43.8	41	16	US-10-035-833A-5525	Sequence 5525, App	c 749	11.2	43.1	25	15	US-10-098-263B-115732	Sequence 115732, A
677	11.4	43.8	42	13	US-10-090-983-11	Sequence 11, App	750	11.2	43.1	25	15	US-10-098-263B-116716	Sequence 116716, A
c 678	11.4	43.8	47	16	US-10-117-087-7	Sequence 7, Appli	751	11.2	43.1	25	15	US-10-098-263B-130089	Sequence 130089, A
679	11.4	43.8	47	16	US-10-349-143-618	Sequence 618, App	752	11.2	43.1	25	15	US-10-098-263B-130090	Sequence 130090, A
680	11.4	43.8	47	16	US-10-349-143-1451	Sequence 1451, App	c 753	11.2	43.1	25	17	US-10-717-597-2438	Sequence 2438, App
c 681	11.4	43.8	47	16	US-10-349-143-3789	Sequence 3789, App	c 754	11.2	43.1	25	17	US-10-620-246-104	Sequence 104, App
c 682	11.4	43.8	48	9	US-09-761-534A-19	Sequence 19, Appl	c 755	11.2	43.1	26	15	US-10-228-629A-5	Sequence 5, Appli
c 683	11.4	43.8	49	15	US-10-300-011-5	Sequence 5, Appli	c 756	11.2	43.1	26	17	US-10-746-167-29	Sequence 29, Appl
c 684	11.4	43.8	50	16	US-10-131-827-2712	Sequence 2712, App	757	11.2	43.1	27	15	US-10-214-670-10	Sequence 10, Appl
c 685	11.4	43.8	50	16	US-10-131-827-3650	Sequence 3650, App	758	11.2	43.1	27	15	US-10-317-444-35	Sequence 35, Appl
c 686	11.4	43.8	50	16	US-10-131-827-3726	Sequence 3726, App	c 759	11.2	43.1	27	15	US-10-317-444-36	Sequence 36, Appl
687	11.4	43.8	50	16	US-10-131-827-6023	Sequence 6023, App	c 760	11.2	43.1	28	9	US-09-836-607-23	Sequence 23, Appl
688	11.4	43.8	50	16	US-10-131-827-6327	Sequence 6327, App	c 761	11.2	43.1	28	10	US-09-894-799-23	Sequence 23, Appl
689	11.4	43.8	50	16	US-10-131-827-7940	Sequence 7940, App	c 762	11.2	43.1	28	10	US-09-421-112-23	Sequence 23, Appl
690	11.2	43.1	17	16	US-10-138-674-9165	Sequence 9165, App	c 763	11.2	43.1	28	15	US-10-138-473-154	Sequence 154, App
691	11.2	43.1	17	16	US-10-287-949A-9165	Sequence 9165, App	c 764	11.2	43.1	28	15	US-10-648-984-23	Sequence 23, Appl
692	11.2	43.1	17	18	US-10-712-633-4436	Sequence 4436, App	765	11.2	43.1	29	15	US-10-373-667-13	Sequence 13, Appl
693	11.2	43.1	18	9	US-09-888-615-137	Sequence 137, App	c 766	11.2	43.1	30	15	US-10-235-079B-1	Sequence 1, Appli
694	11.2	43.1	20	10	US-09-887-145-31	Sequence 31, Appl	c 767	11.2	43.1	30	15	US-10-214-417A-105	Sequence 105, App
c 695	11.2	43.1	20	17	US-10-688-706-1019	Sequence 1019, App	c 768	11.2	43.1	30	15	US-10-214-417A-121	Sequence 121, App
c 696	11.2	43.1	20	17	US-10-473-254-12	Sequence 12, Appl	c 769	11.2	43.1	30	15	US-10-214-417A-124	Sequence 124, App
697	11.2	43.1	21	8	US-08-983-605-451	Sequence 451, App	c 770	11.2	43.1	30	15	US-10-214-417A-125	Sequence 125, App
698	11.2	43.1	21	10	US-09-931-486-5	Sequence 5, Appli	c 771	11.2	43.1	30	15	US-10-214-417A-126	Sequence 126, App
699	11.2	43.1	21	16	US-10-420-194-474	Sequence 474, App	c 772	11.2	43.1	30	15	US-10-214-417A-128	Sequence 128, App
c 700	11.2	43.1	21	16	US-10-420-194-984	Sequence 984, App	c 773	11.2	43.1	30	15	US-10-214-417A-129	Sequence 129, App
c 701	11.2	43.1	21	18	US-10-786-720-16705	Sequence 16705, A	c 774	11.2	43.1	30	15	US-10-214-417A-136	Sequence 136, App
c 702	11.2	43.1	21	18	US-10-786-720-16706	Sequence 16706, A	c 775	11.2	43.1	30	16	US-10-602-350-14	Sequence 14, Appl
703	11.2	43.1	21	18	US-10-786-720-16707	Sequence 16707, A	c 776	11.2	43.1	30	16	US-10-419-020-159	Sequence 159, App
c 704	11.2	43.1	21	18	US-10-786-720-16708	Sequence 16708, A	777	11.2	43.1	30	18	US-10-419-020-160	Sequence 160, App
c 705	11.2	43.1	21	18	US-10-786-720-16710	Sequence 16710, A	778	11.2	43.1	31	9	US-09-841-132-206	Sequence 206, App
c 706	11.2	43.1	21	18	US-10-786-720-17338	Sequence 17338, A	779	11.2	43.1	31	10	US-09-730-289B-3268	Sequence 3268, App
c 707	11.2	43.1	21	18	US-10-786-720-17340	Sequence 17340, A	780	11.2	43.1	31	10	US-09-927-046-4404	Sequence 4404, App
c 708	11.2	43.1	21	18	US-10-786-720-17800	Sequence 17800, A	781	11.2	43.1	31	10	US-09-877-478-4993	Sequence 4993, App
709	11.2	43.1	21	18	US-10-786-720-17802	Sequence 17802, A	782	11.2	43.1	31	10	US-09-740-332-7687	Sequence 7687, App
c 710	11.2	43.1	21	18	US-10-786-720-17884	Sequence 17884, A	783	11.2	43.1	31	10	US-09-817-879-7687	Sequence 7687, App
c 711	11.2	43.1	21	18	US-10-786-720-17885	Sequence 17885, A	784	11.2	43.1	31	15	US-10-163-552-1921	Sequence 1921, App
712	11.2	43.1	21	18	US-10-786-720-17886	Sequence 17886, A	785	11.2	43.1	31	15	US-10-156-306-3347	Sequence 3347, App
c 713	11.2	43.1	21	18	US-10-786-720-17887	Sequence 17887, A	786	11.2	43.1	31	15	US-10-238-700-4386	Sequence 4386, App
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; Publication No. US20020142350A1
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; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; NUMBER OF SEQ ID NOS: 25
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RESULT 5
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; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/309,561
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: HCV
US-10-309-561-17
Query Match          100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGCGGTTA 28

RESULT 6
US-10-198-680A-2
; Sequence 2, Application US/10198680A
; Publication No. US20030176433A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Viral Polymerase Inhibitors
; FILE REFERENCE: 13/095
; CURRENT APPLICATION NUMBER: US/10/198,680A
; CURRENT FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/338,061
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/307,674
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-198-680A-2
Query Match          100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGCGGTTA 28

RESULT 7
US-10-320-978-1
; Sequence 1, Application US/10320978
; Publication No. US20030181363A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: MARCOCYCIC PEPTIDES ACTIVE AGAINST THE HEPATITIS C VIRUS
; FILE REFERENCE: 13/092
; CURRENT APPLICATION NUMBER: US/10/320,978
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 2,369,711
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-320-978-1
Query Match          100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGCGGTTA 28

RESULT 8
US-10-353-563-1
; Sequence 1, Application US/10353563
; Publication No. US20030186895A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM INTERNATIONAL GmbH
; TITLE OF INVENTION: HEPATITIS C INHIBITOR TRI-PEPTIDES
; FILE REFERENCE: 13/107
; CURRENT APPLICATION NUMBER: US/10/353,563
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 2,369,970
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Forward primer
US-10-353-563-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 9
US-10-353-589-1
; Sequence 1, Application US/10353589
; Publication No. US20030187018A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM INTERNATIONAL GmbH
; TITLE OF INVENTION: HEPATITIS C INHIBITOR TRI-PEPTIDES
; FILE REFERENCE: 13/106
; CURRENT APPLICATION NUMBER: US/10/353,589
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 2,370,396
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-353-589-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 10
US-10-320-979-1
; Sequence 1, Application US/10320979
; Publication No. US20030191067A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM INTERNATIONAL GmbH
; TITLE OF INVENTION: HEPATITIS C INHIBITOR TRI-PEPTIDES
; FILE REFERENCE: 13/107
; CURRENT APPLICATION NUMBER: US/10/320,979
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 2,369,970
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-320-979-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 11
US-10-353-894-1
; Sequence 1, Application US/10353894
; Publication No. US20030224977A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: MARCROCYCLIC PEPTIDES ACTIVE AGAINST THE HEPATITIS C VIRUS
; FILE REFERENCE: 13/092
; CURRENT APPLICATION NUMBER: US/10/353,894
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 2,369,711
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-353-894-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 12
US-10-198-259A-2
; Sequence 2, Application US/10198259A
; Publication No. US20030236251A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Viral Polymerase Inhibitors
; FILE REFERENCE: 13/089
; CURRENT APPLICATION NUMBER: US/10/198,259A
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,669
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/338,324
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-198-259A-2
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 13
US-10-198-384A-2
; Sequence 2, Application US/10198384A
; Publication No. US20040024190A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Viral Polymerase inhibitors
; FILE REFERENCE: 13/090
```

; CURRENT APPLICATION NUMBER: US/10/198,384A
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/338,061
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/307,674
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-198-384A-2

Query Match 100.0%; Score 26; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 14
US-10-789-355-17
; Sequence 17, Application US/10789355
; Publication No. US2004018033A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: HCV
US-10-789-355-17

Query Match 100.0%; Score 26; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 15
US-10-686-835-17
; Sequence 17, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukulj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT APPLICATION NUMBER: US/10/686,835
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: HCV
US-10-686-835-17

Query Match 100.0%; Score 26; DB 18; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 16
US-10-791-318-1
; Sequence 1, Application US/10791318
; Publication No. US20040224900A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Bailey, Murray D.
; APPLICANT: Llinas-Brunet, Montse
; TITLE OF INVENTION: Hepatitis C Inhibitor Peptide Analogs
; FILE REFERENCE: 13/112
; CURRENT APPLICATION NUMBER: US/10/791,318
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US 60/452,187
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-791-318-1

Query Match 100.0%; Score 26; DB 18; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 17
US-10-120-013-7
; Sequence 7, Application US/10120013
; Publication No. US20020192689A1
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; DuBois, Dwight
; Brown, David
; Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/120,013
; FILING DATE: 10-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMB1:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-120-013-7
Query Match          92.3%; Score 24; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 18
US-10-011-855-1
; Sequence 1, Application US/10011855
; Publication No. US20030104582A1
; GENERAL INFORMATION:
; APPLICANT: BAUMANN, RUSSELL
; APPLICANT: HAMDAN, HASNAH
; APPLICANT: LEWINSKI, MICHAEL
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS FOR DETECTING HEPATITIS C
; FILE REFERENCE: 034827/0702
; CURRENT APPLICATION NUMBER: US/10/011,855
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-011-855-1
Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 19
US-10-037-990-1
; Sequence 1, Application US/10037990
; Publication No. US20030124654A1
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Sharma, Vijay
; APPLICANT: Kondiboyina, Venkat Ramana
; TITLE OF INVENTION: Method and Device for the Rapid Clinical Diagnosis of Hepatitis C
; FILE REFERENCE: RELIA P-106
; CURRENT APPLICATION NUMBER: US/10/037,990
; CURRENT FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-037-990-1
Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 20
US-10-007-389-4
; Sequence 4, Application US/10007389
; Publication No. US20030165855A1
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-007-389-4
Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 21
US-10-322-138-1
; Sequence 1, Application US/10322138
; Publication No. US20030175765A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Christoph
; APPLICANT: Haberhausen, Gerd
; APPLICANT: Bartl, Knut
; APPLICANT: Orum, Henrik
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS
; FILE REFERENCE: 4817/OQ
; CURRENT APPLICATION NUMBER: US/10/322,138
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/530,746B
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 95
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```
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amplification primer
US-10-322-138-1

Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 22
US-10-147-679A-5
; Sequence 5, Application US/10147679A
; Publication No. US20030224366A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Kiedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide primer (HCV forward)
US-10-147-679A-5

Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 23
US-10-655-508-4
; Sequence 4, Application US/10655508
; Publication No. US20040063155A1
; GENERAL INFORMATION:
; APPLICANT: Ruseman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Rainer
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperease
; CURRENT APPLICATION NUMBER: US/10/655,508
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/10/007,389
; PRIOR FILING DATE: CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
```

```
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-508-4

Query Match          92.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 24
US-10-688-272-17
; Sequence 17, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: GeneMatrix Inc.; Kim, Nam-Keun
; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 17
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer of 5'NCR of HCV
US-10-688-272-17

Query Match          92.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 25
US-10-307-523B-3
; Sequence 3, Application US/10307523B
; Publication No. US20040106099A1
; GENERAL INFORMATION:
; APPLICANT: LEE, TZONG H
; TITLE OF INVENTION: METHOD FOR DETECTING HEPATITIS C VIRUS
; FILE REFERENCE: APV 31601
; CURRENT APPLICATION NUMBER: US/10/307,523B
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: TW 091134394
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-307-523B-3

Query Match          92.3%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||

RESULT 26
 US-09-747-419-12
 ; Sequence 12, Application US/09747419
 ; Patent No. US2002015582A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lemon, Stanley
 ; APPLICANT: Yi, MinKyung
 ; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
 ; FILE REFERENCE: 265.0007 0101
 ; CURRENT APPLICATION NUMBER: US/09/747,419
 ; CURRENT FILING DATE: 2000-12-23
 ; PRIOR APPLICATION NUMBER: US 60/171,909
 ; PRIOR FILING DATE: 1999-12-23
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 ; NAME/KEY: misc_difference
 ; LOCATION: (25)..(25)
 ; OTHER INFORMATION: Labeled with fluorescein
 US-09-747-419-12

Query Match 92.3%; Score 24; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGCGTCTAGCCATGGCGTTA 26
|||||
pb 1 AGAAGCGTCTAGCCATGGCGTTA 24
|||||

```

RESULT 27
US-10-259-275-12
; Sequence 12, Application US/10259275
; Publication No. US2003012541A1
; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley M.
; APPLICANT: Yi, Minkyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0120
; CURRENT APPLICATION NUMBER: US/10/259,275
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 09/747,419
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/325,236
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/338,123
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Probe
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: (25)..(25)
; OTHER INFORMATION: Labeled with fluorescein
US-10-259-275-12

```

Query Match 92.3%; Score 24; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 24; Conservative 0; Mismatches 0; Indels

Qy 3 AGAAAGCGTCTAGCCATGGCGTTA 26
1 AGAAAGCGTCTAGCCATGGCGTTA 24

```

RESULT 28
US-10-451-882-35
Sequence 35, Application US/10451882
Publication No. US20040185455A1
GENERAL INFORMATION:
APPLICANT: Takara Shuzo Co., Ltd.
TITLE OF INVENTION: Method for detection of virulent organisms
FILE REFERENCE: 662981
CURRENT APPLICATION NUMBER: US/10/451,882
CURRENT FILING DATE: 2004-01-05
PRIORITY APPLICATION NUMBER: JP 2000-396321
PRIORITY FILING DATE: 2000-12-26
PRIORITY APPLICATION NUMBER: JP 2000-396222
PRIORITY FILING DATE: 2000-12-26
PRIORITY APPLICATION NUMBER: JP 2001-199552
PRIORITY FILING DATE: 2001-06-29
PRIORITY APPLICATION NUMBER: JP 2001-278920
PRIORITY FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 35
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Designed oligonucleotide probe to detect a
OTHER INFORMATION: portion of HCV.
US-10-451-882-35

```

Query Match	84.6%	Score 22;	DB 17;	Length 36;
Best Local Similarity	100.0%;	Pred. No. 0.64;		
Matches 22: Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 5 AAAGCGTCTAGCCATGGCGTTA 26
|||
7 AAAGCGTCTAGCCATGGCGTTA 28
pb

RESULT 29
US-09-825-574-25
; Sequence 25, Application US/09825574
; Patent No. US20020119454A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; Brow, Mary Ann D.
; Fors, Lance
; Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing With Structure-Bridging
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEULEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/825,574

; FILING DATE: 03-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/POCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-825-574-25

Query Match 80.8%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGG 21
|||||
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 30

US-09-882-945A-25
; Sequence 25, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-25

Query Match 80.8%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGG 21
|||||
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 31

US-10-240-460-10
; Sequence 10, Application US/10240460
; Publication No. US20030207292A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030207292Alomi, Tsugunori
; APPLICANT: Nagamine, Kentaro
; TITLE OF INVENTION: METHOD FOR AMPLIFYING NUCLEIC ACID BY USING

; TITLE OF INVENTION: DOUBLE-STRANDED NUCLEIC ACID AS TEMPLATE
; FILE REFERENCE: 201487/1110
; CURRENT APPLICATION NUMBER: US/10/240,460
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/JP01/02771
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-111939
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-240-460-10

Query Match 80.8%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGG 21
|||||
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 32

US-10-182-126-7
; Sequence 7, Application US/10182126
; Publication No. US20030175691A1
; GENERAL INFORMATION:
; APPLICANT: ELAISSARI, Abdelhamid
; APPLICANT: MANDRAND, Bernard
; APPLICANT: DELAIR, Thierry
; APPLICANT: SPENCER, Doran
; APPLICANT: ARKIS, Ahmed
; TITLE OF INVENTION: METHOD FOR ISOLATING PROTEINS OR PROTEIN AND NUCLEIC ACID ASSOCIAT
; FILE REFERENCE: 113339
; CURRENT APPLICATION NUMBER: US/10/182,126
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/FR01/00205
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: FR 00.00862
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-182-126-7

Query Match 80.8%; Score 21; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AAGCGTCTAGCCATGGCGTTA 26
|||||
Db 1 AAGCGTCTAGCCATGGCGTTA 21

RESULT 33

US-08-887-505-69/c
; Sequence 69, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilkuskie, Robert E.
; APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John
APPLICANT: Wolfe, Jia L.
APPLICANT: Roberts, Peter C.
APPLICANT: Hamlin, Jr., Henry A.
APPLICANT: Walther, No. US20020081577A1 A.
APPLICANT: Roberts, Debra M.
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 172
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,505
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-040CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-887-505-69

Query Match 76.9%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATG 20
Db 20 GCAGAAAGCGTCTAGCCATG 1

RESULT 34

US-09-935-338-227
Sequence 227, Application US/09935338
Publication No. US20030073081A1
GENERAL INFORMATION:
APPLICANT: MUKAI, Hiroyuki
APPLICANT: SAGAWA, Hiroaki
APPLICANT: UEMORI, Takashi
APPLICANT: YAMAMOTO, Junko
APPLICANT: TOMONO, Jun
APPLICANT: KOBAYASHI, Ei-ji
APPLICANT: ENOKI, Tatsuji
APPLICANT: TAKEDA, Osamu
APPLICANT: MIYAKE, Kazuo
APPLICANT: SATO, Yoshiaki
APPLICANT: MORIYAMA, Mariko
APPLICANT: SAWARAGI, Haruhisa
APPLICANT: HAGIYA, Michio

APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: A method for amplification of nucleic acids
FILE REFERENCE: MUKAI-1
CURRENT APPLICATION NUMBER: US/09/935,338
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: JP11-076966
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: JP11-370035
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP2000-251981
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: JP2000-284419
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: JP2000-288750
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: JP2001-104191
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: PCT/JP00/01534
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn version 3.2
SEQ ID NO 227
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Designed chimeric oligonucleotide primer designated as HCV-P3 to amplify a portion of HCV. "nucleotides 17 to 19 are ribonucleotides-other nucleotides are deoxyribonucleotides"
US-09-935-338-227

Query Match 73.1%; Score 19; DB 10; Length 19;
Best Local Similarity 89.5%; Pred. No. 19;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCGTCTAGCCATGCGGTTA 26
Db 1 GCGTCTAGCCATGCGGTTA 19

RESULT 35

US-10-667-271-99
Sequence 99, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBHE02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378

```

; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-99

Query Match          73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 78.9%; Pred. No. 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGCGTCTAGCCATGGCGT 24
Db 1 AAGCGUCUAGCCAUAGGCGU 19

RESULT 36
US-10-667-271-101
; Sequence 101, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-101

Query Match          73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

US-10-087-631b-6.max.rnpb
```

```

Qy 5 AAGCGTCTAGCCATGGCG 23
Db 1 AAGCGUCUAGCCAUAGGCG 19

RESULT 37
US-10-667-271-102
; Sequence 102, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-102

Query Match          73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 73.7%; Pred. No. 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGTCTAGCCATGGCGTTA 26
Db 1 GCGUCUAGCCAUAGGCGUUA 19

RESULT 38
US-10-667-271-104
; Sequence 104, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
```

; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-104

Query Match 73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 73.1%; Pred. No. 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCGTCTAGCATGGCGTT 25
|||||:|||||:|||||:
DB 1 AGCGUCUAGCGGCGUU 19

RESULT 39
US-10-667-271-107
; Sequence 107, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-107

Query Match 73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAAAGCGTCTAGCCATGGC 22
|||||:|||||:|||||:
DB 1 GAAAGCGUCUAGCCAUAGC 19

RESULT 40
US-10-667-271-113
; Sequence 113, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
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; Remaining Prior Application data removed - See File Wrapper or PALM.
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OM nucleic - nucleic search, using sw model

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C 192	13	61.9	18	2	PCT-US03-21410-29	Sequence 29, Appl	C 265	13	61.9	37	39	US-09-930-423-2899	Sequence 2899, Ap
C 193	13	61.9	18	18	US-09-235-463-182	Sequence 182, Appl	C 266	13	61.9	43	2	PCT-US04-27793-39	Sequence 39, Appl
C 194	13	61.9	18	35	US-09-857-290-29	Sequence 29, Appl	C 267	13	61.9	43	64	US-10-926-542-39	Sequence 39, Appl
C 195	13	61.9	18	48	US-10-137-290-29	Sequence 29, Appl	C 268	13	61.9	50	51	US-10-321-854-1043	Sequence 1043, Ap
C 196	13	61.9	18	52	US-10-388-263-182	Sequence 182, Appl	C 269	13	61.9	50	51	US-10-321-854-1044	Sequence 1044, Ap
C 197	13	61.9	19	59	US-10-714-333A-30595	Sequence 30595, A	C 270	13	61.9	50	124	US-60-585-352-12759	Sequence 12759, A
198	13	61.9	20	51	US-10-317-278-17	Sequence 17, Appl	C 271	13	61.9	50	124	US-60-585-352-100213	Sequence 100213, A
C 199	13	61.9	20	51	US-10-317-278-51	Sequence 51, Appl	C 272	12.8	61.0	18	51	US-10-310-188-15695	Sequence 15695, A
200	13	61.9	25	42	US-09-956-584A-191086	Sequence 191086,	C 273	12.8	61.0	19	59	US-10-714-333A-75057	Sequence 75057, A

274	12.8	61.0	19	59	US-10-714-333A-340332	Sequence 340332,	347	12.8	61.0	25	88	US-60-234-049-133938	Sequence 133938,
C 275	12.8	61.0	19	59	US-10-714-333A-342124	Sequence 342124,	348	12.8	61.0	25	88	US-60-234-049-133939	Sequence 133939,
276	12.8	61.0	19	59	US-10-714-333A-468849	Sequence 468849,	349	12.8	61.0	25	108	US-60-427-808-168516	Sequence 168516,
277	12.8	61.0	19	59	US-10-714-333A-765106	Sequence 765106,	350	12.8	61.0	25	108	US-60-427-808-169722	Sequence 169722,
278	12.8	61.0	19	59	US-10-714-333A-1085773	Sequence 1085773,	351	12.8	61.0	25	108	US-60-427-808-173391	Sequence 173391,
279	12.8	61.0	19	59	US-10-714-333A-1151256	Sequence 1151256,	C 352	12.8	61.0	25	108	US-60-427-808-177539	Sequence 177539,
280	12.8	61.0	19	59	US-10-714-333A-1326778	Sequence 1326778,	C 353	12.8	61.0	25	108	US-60-427-808-248519	Sequence 248519,
281	12.8	61.0	19	59	US-10-714-333A-1473642	Sequence 1473642,	C 354	12.8	61.0	25	108	US-60-427-808-360624	Sequence 360624,
C 282	12.8	61.0	24	2	PCI-US02-40227A-8	Sequence 8, Appli	C 355	12.8	61.0	25	108	US-60-427-808-401285	Sequence 401285,
C 283	12.8	61.0	24	51	US-09-940-185-787	Sequence 787, App	C 356	12.8	61.0	25	108	US-60-427-808-401286	Sequence 401286,
C 284	12.8	61.0	24	51	US-10-320-231A-8	Sequence 8, Appli	C 357	12.8	61.0	25	108	US-60-427-808-513324	Sequence 513324,
C 285	12.8	61.0	24	62	US-10-819-039-20	Sequence 20, Appl	C 358	12.8	61.0	25	108	US-60-427-808-522969	Sequence 522969,
C 286	12.8	61.0	24	63	US-10-867-506-8	Sequence 8, Appli	C 359	12.8	61.0	25	108	US-60-427-808-559261	Sequence 559261,
C 287	12.8	61.0	25	40	US-09-940-185-4752	Sequence 4752, Ap	C 360	12.8	61.0	25	108	US-60-427-808-706664	Sequence 706664,
C 288	12.8	61.0	25	41	US-09-953-570A-28434	Sequence 28434, A	C 361	12.8	61.0	25	108	US-60-427-808-838207	Sequence 838207,
C 289	12.8	61.0	25	41	US-09-953-570A-77409	Sequence 77409, A	C 362	12.8	61.0	25	108	US-60-427-808-857738	Sequence 857738,
C 290	12.8	61.0	25	41	US-09-953-570A-116523	Sequence 116523,	C 363	12.8	61.0	25	108	US-60-427-808-902357	Sequence 902357,
C 291	12.8	61.0	25	41	US-09-954-427A-34193	Sequence 34193, A	C 364	12.8	61.0	25	108	US-60-427-808-905085	Sequence 905085,
C 292	12.8	61.0	25	41	US-09-954-427A-46948	Sequence 46948, A	C 365	12.8	61.0	25	108	US-60-427-836-99339	Sequence 99339, A
C 293	12.8	61.0	25	41	US-09-954-427A-48691	Sequence 48691, A	C 366	12.8	61.0	25	108	US-60-427-836-509311	Sequence 509311,
C 294	12.8	61.0	25	41	US-09-954-427A-312531	Sequence 312531,	C 367	12.8	61.0	25	108	US-60-427-836-584226	Sequence 584226,
C 295	12.8	61.0	25	41	US-09-954-429-18604	Sequence 18604, A	C 368	12.8	61.0	25	116	US-60-507-481-16692	Sequence 16692, A
C 296	12.8	61.0	25	41	US-09-954-429-18604	Sequence 18604, A	C 369	12.8	61.0	25	116	US-60-507-481-77247	Sequence 77247, A
C 297	12.8	61.0	25	41	US-09-954-445A-79773	Sequence 79773, A	C 370	12.8	61.0	25	116	US-60-507-481-96989	Sequence 96989, A
C 298	12.8	61.0	25	41	US-09-954-445A-79773	Sequence 79773, A	C 371	12.8	61.0	25	116	US-60-507-481-159211	Sequence 159211,
C 299	12.8	61.0	25	42	US-09-956-584A-24300	Sequence 24300, A	C 372	12.8	61.0	25	116	US-60-507-481-180069	Sequence 180069,
C 300	12.8	61.0	25	42	US-09-956-584A-211684	Sequence 211684,	C 373	12.8	61.0	25	116	US-60-507-481-180069	Sequence 180069,
C 301	12.8	61.0	25	42	US-09-956-584A-248616	Sequence 248616,	C 374	12.8	61.0	25	116	US-60-507-511-45091	Sequence 45091, A
C 302	12.8	61.0	25	42	US-09-956-584A-248618	Sequence 248618,	C 375	12.8	61.0	25	116	US-60-507-511-45105	Sequence 45105, A
C 303	12.8	61.0	25	42	US-09-956-584A-248630	Sequence 248630,	C 376	12.8	61.0	25	116	US-60-507-511-93827	Sequence 93827, A
C 304	12.8	61.0	25	42	US-09-956-604-139744	Sequence 139744,	C 377	12.8	61.0	25	120	US-60-545-213-121605	Sequence 121605,
C 305	12.8	61.0	25	42	US-09-956-604-139745	Sequence 139745,	C 378	12.8	61.0	25	120	US-60-545-213-12015	Sequence 12015,
C 306	12.8	61.0	25	42	US-09-956-604A-139744	Sequence 139744,	C 379	12.8	61.0	25	120	US-60-545-213-298921	Sequence 298921,
C 307	12.8	61.0	25	42	US-09-956-604B-139745	Sequence 139745,	C 380	12.8	61.0	25	120	US-60-545-213-298922	Sequence 298922,
C 308	12.8	61.0	25	42	US-09-956-604B-139744	Sequence 139744,	C 381	12.8	61.0	33	63	US-10-891-260-3420	Sequence 3420, Ap
C 309	12.8	61.0	25	42	US-09-956-604B-139745	Sequence 139745,	C 382	12.8	61.0	39	101	US-60-353-790-1988	Sequence 1988, Ap
C 310	12.8	61.0	25	42	US-09-956-604D-59826	Sequence 59826, A	C 383	12.8	61.0	50	93	US-60-278-561-15270	Sequence 15270, A
C 311	12.8	61.0	25	42	US-09-956-604D-120818	Sequence 120818,	C 384	12.8	61.0	50	124	US-60-585-353-60091	Sequence 60091, A
C 312	12.8	61.0	25	42	US-09-956-604D-136040	Sequence 136040,	C 385	12.8	61.0	50	124	US-60-585-353-63349	Sequence 63349, A
C 313	12.8	61.0	25	60	US-10-719-900-168516	Sequence 168516,	C 386	12.8	61.0	50	124	US-60-585-353-67967	Sequence 67967, A
C 314	12.8	61.0	25	60	US-10-719-900-168516	Sequence 168516,	C 387	12.8	61.0	50	124	US-60-585-353-68574	Sequence 68574, A
C 315	12.8	61.0	25	60	US-10-719-900-169722	Sequence 169722,	C 388	12.8	61.0	50	124	US-60-585-353-82268	Sequence 82268, A
C 316	12.8	61.0	25	60	US-10-719-900-173391	Sequence 173391,	C 389	12.6	60.0	19	59	US-10-714-333A-1194033	Sequence 1194033,
C 317	12.8	61.0	25	60	US-10-719-900-177539	Sequence 177539,	C 390	12.6	60.0	20	50	US-10-289-762-3669	Sequence 3669, Ap
C 318	12.8	61.0	25	60	US-10-719-900-248519	Sequence 248519,	C 391	12.6	60.0	21	61	US-10-770-726-13622	Sequence 13622, A
C 319	12.8	61.0	25	60	US-10-719-900-360624	Sequence 360624,	C 392	12.6	60.0	21	61	US-10-770-726-14630	Sequence 14630, A
C 320	12.8	61.0	25	60	US-10-719-900-401285	Sequence 401285,	C 393	12.6	60.0	21	61	US-10-770-726-14631	Sequence 14631, A
C 321	12.8	61.0	25	60	US-10-719-900-401286	Sequence 401286,	C 394	12.6	60.0	21	61	US-10-770-726-14631	Sequence 14631, A
C 322	12.8	61.0	25	60	US-10-719-900-513324	Sequence 513324,	C 395	12.6	60.0	25	20	US-09-396-196F-95290	Sequence 95290, A
C 323	12.8	61.0	25	60	US-10-719-900-522969	Sequence 522969,	C 396	12.6	60.0	25	20	US-09-396-196G-95290	Sequence 95290, A
C 324	12.8	61.0	25	60	US-10-719-900-559261	Sequence 559261,	C 397	12.6	60.0	25	20	US-09-396-196G-103159	Sequence 103159,
C 325	12.8	61.0	25	60	US-10-719-900-706664	Sequence 706664,	C 398	12.6	60.0	25	32	US-09-754-853A-418	Sequence 418, App
C 326	12.8	61.0	25	60	US-10-719-900-838207	Sequence 838207,	C 399	12.6	60.0	25	41	US-09-953-115A-14594	Sequence 14594, A
C 327	12.8	61.0	25	60	US-10-719-900-857738	Sequence 857738,	C 400	12.6	60.0	25	41	US-09-953-115A-27664	Sequence 27664, A
C 328	12.8	61.0	25	60	US-10-719-900-902357	Sequence 902357,	C 401	12.6	60.0	25	41	US-09-953-115A-29320	Sequence 29320, A
C 329	12.8	61.0	25	60	US-10-719-900-905065	Sequence 905065,	C 402	12.6	60.0	25	41	US-09-953-570A-18971	Sequence 18971, A
C 330	12.8	61.0	25	60	US-10-719-956-297399	Sequence 297399, A	C 403	12.6	60.0	25	41	US-09-953-570A-103452	Sequence 103452,
C 331	12.8	61.0	25	60	US-10-719-956-509311	Sequence 509311,	C 404	12.6	60.0	25	41	US-09-953-570A-107848	Sequence 107848,
C 332	12.8	61.0	25	60	US-10-719-956-584226	Sequence 584226,	C 405	12.6	60.0	25	41	US-09-954-427-291622	Sequence 291622,
C 333	12.8	61.0	25	64	US-10-933-982-20490	Sequence 20490, A	C 406	12.6	60.0	25	41	US-09-954-427A-29655	Sequence 29655, A
C 334	12.8	61.0	25	64	US-10-933-982-68451	Sequence 68451, A	C 407	12.6	60.0	25	41	US-09-954-427A-226137	Sequence 226137,
C 335	12.8	61.0	25	64	US-10-933-982-68452	Sequence 68452, A	C 408	12.6	60.0	25	41	US-09-954-427A-118507	Sequence 118507, A
C 336	12.8	61.0	25	64	US-10-933-982-71405	Sequence 71405, A	C 409	12.6	60.0	25	42	US-09-956-584-95687	Sequence 95687, A
C 337	12.8	61.0	25	64	US-10-933-982-102015	Sequence 102015,	C 410	12.6	60.0	25	42	US-09-956-584-183108	Sequence 183108,
C 338	12.8	61.0	25	64	US-10-933-982-115459	Sequence 115459,	C 411	12.6	60.0	25	42	US-09-956-584-220109	Sequence 220109,
C 339	12.8	61.0	25	64	US-10-933-982-115461	Sequence 115461,	C 412	12.6	60.0	25	42	US-09-956-584-247123	Sequence 247123,
C 340	12.8	61.0	25	64	US-10-933-982-15462	Sequence 15462,	C 413	12.6	60.0	25	42	US-09-956-584A-247135	Sequence 247135,
C 341	12.8	61.0	25	64	US-10-933-982-157093	Sequence 157093,	C 414	12.6	60.0	25	42	US-09-956-584A-320535	Sequence 320535,
C 342	12.8	61.0	25	64	US-10-933-982-209724	Sequence 209724,	C 415	12.6	60.0	25	42	US-09-956-584A-320540	Sequence 320540,
C 343	12.8	61.0	25	64	US-10-933-982-209732	Sequence 209732,	C 416	12.6	60.0	25	42	US-09-956-584A-320545	Sequence 320545,
C 344	12.8	61.0	25	64	US-10-933-982-222479	Sequence 222479,	C 417	12.6	60.0	25	42	US-09-956-584A-417549	Sequence 417549,
C 345	12.8	61.0	25	68	US-60-233-166-34193	Sequence 34193, A	C 418	12.6	60.0	25	42	US-09-956-604-8348	Sequence 8348, Ap
C 346	12.8	61.0	25	88	US-60-233-620-79773	Sequence 79773, A	C 419	12.6	60.0	25	42		

C 420	12.6	60.0	25	42	US-09-956-604A-8348	Sequence 8348, Ap	493	12.6	60.0	25	108	US-60-427-808-775364	Sequence 775364,
C 421	12.6	60.0	25	42	US-09-956-604B-8348	Sequence 8348, Ap	494	12.6	60.0	25	108	US-60-427-808-880950	Sequence 880950,
C 422	12.6	60.0	25	42	US-09-956-604D-49799	Sequence 49799, A	495	12.6	60.0	25	108	US-60-427-808-929175	Sequence 929175,
C 423	12.6	60.0	25	42	US-09-956-604D-71928	Sequence 71928, A	496	12.6	60.0	25	108	US-60-427-836-89990	Sequence 89990, A
C 424	12.6	60.0	25	42	US-09-956-604D-140704	Sequence 140704, A	497	12.6	60.0	25	108	US-60-427-836-142557	Sequence 142557,
C 425	12.6	60.0	25	52	US-10-355-577-270500	Sequence 270500,	C 498	12.6	60.0	25	108	US-60-427-836-145988	Sequence 145988,
C 426	12.6	60.0	25	52	US-10-355-577-422372	Sequence 422372,	C 499	12.6	60.0	25	108	US-60-427-836-173166	Sequence 173166,
C 427	12.6	60.0	25	52	US-10-355-577-437303	Sequence 437303,	C 500	12.6	60.0	25	108	US-60-427-836-234400	Sequence 234400,
C 428	12.6	60.0	25	52	US-10-355-577-594010	Sequence 594010,	C 501	12.6	60.0	25	108	US-60-427-836-234401	Sequence 234401,
C 429	12.6	60.0	25	52	US-10-355-577-889379	Sequence 889379,	C 502	12.6	60.0	25	108	US-60-427-836-329028	Sequence 329028,
C 430	12.6	60.0	25	52	US-10-355-577-952475	Sequence 952475,	C 503	12.6	60.0	25	108	US-60-427-836-340925	Sequence 340925,
C 431	12.6	60.0	25	52	US-10-355-577-952476	Sequence 952476,	C 504	12.6	60.0	25	108	US-60-427-836-583417	Sequence 583417,
C 432	12.6	60.0	25	60	US-10-719-900-116596	Sequence 116596,	C 505	12.6	60.0	25	108	US-60-427-836-645692	Sequence 645692,
C 433	12.6	60.0	25	60	US-10-719-900-122510	Sequence 122510,	C 506	12.6	60.0	25	113	US-60-427-871-137943	Sequence 137943,
C 434	12.6	60.0	25	60	US-10-719-900-126366	Sequence 126366,	C 507	12.6	60.0	25	116	US-60-507-511-7144	Sequence 7144, Ap
C 435	12.6	60.0	25	60	US-10-719-900-172673	Sequence 172673,	C 508	12.6	60.0	25	116	US-60-507-511-90302	Sequence 90302, A
C 436	12.6	60.0	25	60	US-10-719-900-276674	Sequence 276674,	C 509	12.6	60.0	25	116	US-60-507-511-185079	Sequence 185079,
C 437	12.6	60.0	25	60	US-10-719-900-282264	Sequence 282264,	C 510	12.6	60.0	25	120	US-60-545-213-34143	Sequence 34143, A
C 438	12.6	60.0	25	60	US-10-719-900-324816	Sequence 324816,	C 511	12.6	60.0	25	120	US-60-545-213-34168	Sequence 34168, A
C 439	12.6	60.0	25	60	US-10-719-900-340214	Sequence 340214,	C 512	12.6	60.0	25	120	US-60-545-213-34169	Sequence 34169, A
C 440	12.6	60.0	25	60	US-10-719-900-444357	Sequence 444357,	C 513	12.6	60.0	25	120	US-60-545-213-126960	Sequence 126960,
C 441	12.6	60.0	25	60	US-10-719-900-550499	Sequence 550499,	C 514	12.6	60.0	25	120	US-60-545-213-171908	Sequence 171908,
C 442	12.6	60.0	25	60	US-10-719-900-762930	Sequence 762930,	C 515	12.6	60.0	25	120	US-60-545-213-171909	Sequence 171909,
C 443	12.6	60.0	25	60	US-10-719-900-775364	Sequence 775364,	C 516	12.6	60.0	25	120	US-60-545-213-263148	Sequence 263148,
C 444	12.6	60.0	25	60	US-10-719-900-880950	Sequence 880950,	C 517	12.6	60.0	33	63	US-10-891-260-7208	Sequence 7208, Ap
C 445	12.6	60.0	25	60	US-10-719-900-929175	Sequence 929175,	C 518	12.6	60.0	34	36	US-09-869-334-29	Sequence 29, Appl
C 446	12.6	60.0	25	60	US-10-719-956-89990	Sequence 89990, A	C 519	12.6	60.0	34	36	US-09-869-334B-29	Sequence 29, Appl
C 447	12.6	60.0	25	60	US-10-719-956-142557	Sequence 142557,	C 520	12.6	60.0	36	31	US-09-708-690-15043	Sequence 15043, A
C 448	12.6	60.0	25	60	US-10-719-956-145988	Sequence 145988,	C 521	12.6	60.0	36	36	US-09-870-161-15043	Sequence 15043, A
C 449	12.6	60.0	25	60	US-10-719-956-173166	Sequence 173166,	C 522	12.6	60.0	36	47	US-10-138-674-15043	Sequence 15043, A
C 450	12.6	60.0	25	60	US-10-719-956-234400	Sequence 234400,	C 523	12.6	60.0	36	47	US-10-138-674B-15043	Sequence 15043, A
C 451	12.6	60.0	25	60	US-10-719-956-329028	Sequence 329028,	C 524	12.6	60.0	36	47	US-10-138-674B-15043	Sequence 15043, A
C 452	12.6	60.0	25	60	US-10-719-956-340925	Sequence 340925,	C 525	12.6	60.0	36	50	US-10-287-949A-15043	Sequence 15043, A
C 453	12.6	60.0	25	60	US-10-719-956-583417	Sequence 583417,	C 526	12.6	60.0	50	124	US-60-585-352-5268	Sequence 5268, A
C 454	12.6	60.0	25	60	US-10-719-956-645692	Sequence 645692,	C 527	12.6	60.0	50	124	US-60-585-352-5268	Sequence 5268, A
C 455	12.6	60.0	25	62	US-10-809-189-95290	Sequence 95290, A	C 528	12.6	60.0	50	124	US-60-585-352-5268	Sequence 5268, A
C 456	12.6	60.0	25	62	US-10-809-189-95290	Sequence 95290, A	C 529	12.6	60.0	50	124	US-60-585-352-5268	Sequence 5268, A
C 457	12.6	60.0	25	62	US-10-809-189-95290	Sequence 95290, A	C 530	12.6	60.0	50	124	US-60-585-352-5268	Sequence 5268, A
C 458	12.6	60.0	25	62	US-10-809-189-95290	Sequence 95290, A	C 531	12.6	60.0	50	124	US-60-585-352-5268	Sequence 5268, A
C 459	12.6	60.0	25	62	US-10-809-189-95290	Sequence 95290, A	C 532	12.6	60.0	50	124	US-60-585-352-5268	Sequence 5268, A
C 460	12.6	60.0	25	63	US-10-859-198-22331	Sequence 22331, A	C 533	12.6	60.0	19	59	US-10-714-333A-97999	Sequence 97999, A
C 461	12.6	60.0	25	63	US-10-859-198-22331	Sequence 22331, A	C 534	12.6	60.0	19	59	US-10-714-333A-97999	Sequence 97999, A
C 462	12.6	60.0	25	63	US-10-859-198-22331	Sequence 22331, A	C 535	12.6	60.0	19	59	US-10-714-333A-899294	Sequence 899294,
C 463	12.6	60.0	25	64	US-10-933-982-20755	Sequence 20755, A	C 536	12.6	60.0	19	59	US-10-714-333A-1307409	Sequence 1307409,
C 464	12.6	60.0	25	64	US-10-933-982-67868	Sequence 67868, A	C 537	12.6	60.0	51	59	US-10-714-333A-1428136	Sequence 1428136,
C 465	12.6	60.0	25	64	US-10-933-982-87996	Sequence 87996, A	C 538	12.6	60.0	21	31	US-09-715-849-184	Sequence 184, Appl
C 466	12.6	60.0	25	64	US-10-933-982-98901	Sequence 98901, A	C 539	12.6	60.0	23	54	US-10-499-886-8	Sequence 8, Appl
C 467	12.6	60.0	25	88	US-60-232-638-115899	Sequence 115899,	C 540	12.6	60.0	25	20	US-09-396-196F-4324	Sequence 4324, Ap
C 468	12.6	60.0	25	88	US-60-233-166-291622	Sequence 291622,	C 541	12.6	60.0	25	20	US-09-396-196F-52993	Sequence 52993, A
C 469	12.6	60.0	25	88	US-60-233-166-291622	Sequence 291622,	C 542	12.6	60.0	25	20	US-09-396-196F-93995	Sequence 93995, A
C 470	12.6	60.0	25	88	US-60-233-166-291622	Sequence 291622,	C 543	12.6	60.0	25	20	US-09-396-196F-93995	Sequence 93995, A
C 471	12.6	60.0	25	88	US-60-234-017-72587	Sequence 72587, A	C 544	12.6	60.0	25	20	US-09-396-196F-93996	Sequence 93996, A
C 472	12.6	60.0	25	88	US-60-234-017-72587	Sequence 72587, A	C 545	12.6	60.0	25	20	US-09-396-196F-93996	Sequence 93996, A
C 473	12.6	60.0	25	88	US-60-234-017-72587	Sequence 72587, A	C 546	12.6	60.0	25	20	US-09-396-196F-93996	Sequence 93996, A
C 474	12.6	60.0	25	101	US-60-353-987-270500	Sequence 270500,	C 547	12.6	60.0	25	20	US-09-396-196F-93996	Sequence 93996, A
C 475	12.6	60.0	25	101	US-60-353-987-422372	Sequence 422372,	C 548	12.6	60.0	25	29	US-09-660-222-22532	Sequence 22532, A
C 476	12.6	60.0	25	101	US-60-353-987-437303	Sequence 437303,	C 549	12.6	60.0	25	41	US-09-953-115A-6081	Sequence 6081, Ap
C 477	12.6	60.0	25	101	US-60-353-987-594010	Sequence 594010,	C 550	12.6	60.0	25	41	US-09-953-115A-11672	Sequence 11672, A
C 478	12.6	60.0	25	101	US-60-353-987-889379	Sequence 889379,	C 551	12.6	60.0	25	41	US-09-953-570A-27512	Sequence 27512, A
C 479	12.6	60.0	25	101	US-60-353-987-952475	Sequence 952475,	C 552	12.6	60.0	25	41	US-09-953-570A-76315	Sequence 76315, A
C 480	12.6	60.0	25	101	US-60-353-987-952476	Sequence 952476,	C 553	12.6	60.0	25	41	US-09-953-570A-82706	Sequence 82706, A
C 481	12.6	60.0	25	107	US-60-417-190-107293	Sequence 107293,	C 554	12.6	60.0	25	41	US-09-953-570A-82719	Sequence 82719, A
C 482	12.6	60.0	25	108	US-60-427-808-116596	Sequence 116596,	C 555	12.6	60.0	25	41	US-09-953-570A-106360	Sequence 106360,
C 483	12.6	60.0	25	108	US-60-427-808-122510	Sequence 122510,	C 556	12.6	60.0	25	41	US-09-954-427-175728	Sequence 175728,
C 484	12.6	60.0	25	108	US-60-427-808-126366	Sequence 126366,	C 557	12.6	60.0	25	41	US-09-954-427-175739	Sequence 175739,
C 485	12.6	60.0	25	108	US-60-427-808-172673	Sequence 172673,	C 558	12.6	60.0	25	41	US-09-954-427A-12359	Sequence 12359, A
C 486	12.6	60.0	25	108	US-60-427-808-276674	Sequence 276674,	C 559	12.6	60.0	25	41	US-09-954-427A-12360	Sequence 12360, A
C 487	12.6	60.0	25	108	US-60-427-808-282264	Sequence 282264,	C 560	12.6	60.0	25	41	US-09-954-427A-14144	Sequence 14144, A
C 488	12.6	60.0	25	108	US-60-427-808-324816	Sequence 324816,	C 561	12.6	60.0	25	41	US-09-954-427A-98823	Sequence 98823, A
C 489	12.6	60.0	25	108	US-60-427-808-340214	Sequence 340214,	C 562	12.6	60.0	25	41	US-09-954-427A-98825	Sequence 98825, A
C 490	12.6	60.0	25	108	US-60-427-808-444357	Sequence 444357,	C 563	12.6	60.0	25	41	US-09-954-427A-369418	Sequence 369418,
C 491	12.6	60.0	25	108	US-60-427-808-550499	Sequence 550499,	C 564	12.6	60.0	25	42	US-09-956-584-203927	Sequence 203927,
C 492	12.6	60.0	25	108	US-60-427-808-762930	Sequence 762930,	C 565	12.6	60.0	25	42	US-09-956-584A-3824	Sequence 3824, Ap

C 566	12.4	59.0	25	42	US-09-956-584A-3827	Sequence 3827, Ap	639	12.4	59.0	25	107	US-60-417-190-107295	Sequence 107295,
C 567	12.4	59.0	25	42	US-09-956-584A-3829	Sequence 3829, Ap	640	12.4	59.0	25	107	US-60-417-190-107296	Sequence 107296,
C 568	12.4	59.0	25	42	US-09-956-584A-3830	Sequence 3830, Ap	641	12.4	59.0	25	107	US-60-417-190-107297	Sequence 107297,
C 569	12.4	59.0	25	42	US-09-956-584A-23425	Sequence 23425, A	642	12.4	59.0	25	108	US-60-427-808-161435	Sequence 161435,
C 570	12.4	59.0	25	42	US-09-956-584A-23430	Sequence 23430, A	643	12.4	59.0	25	108	US-60-427-808-233524	Sequence 233524,
C 571	12.4	59.0	25	42	US-09-956-584A-23432	Sequence 23432, A	644	12.4	59.0	25	108	US-60-427-808-344380	Sequence 344380,
C 572	12.4	59.0	25	42	US-09-956-584A-27522	Sequence 27522, A	645	12.4	59.0	25	108	US-60-427-808-359916	Sequence 359916,
C 573	12.4	59.0	25	42	US-09-956-584A-85828	Sequence 85828, A	646	12.4	59.0	25	108	US-60-427-808-562857	Sequence 562857,
C 574	12.4	59.0	25	42	US-09-956-584A-254810	Sequence 254810, A	647	12.4	59.0	25	108	US-60-427-808-664063	Sequence 664063,
C 575	12.4	59.0	25	42	US-09-956-584A-254812	Sequence 254812, A	648	12.4	59.0	25	108	US-60-427-808-747133	Sequence 747133,
C 576	12.4	59.0	25	42	US-09-956-584A-271694	Sequence 271694, A	649	12.4	59.0	25	108	US-60-427-836-155490	Sequence 155490,
C 577	12.4	59.0	25	42	US-09-956-584A-319739	Sequence 319739, A	650	12.4	59.0	25	108	US-60-427-836-308010	Sequence 308010,
C 578	12.4	59.0	25	42	US-09-956-584A-319742	Sequence 319742, A	651	12.4	59.0	25	108	US-60-427-836-322884	Sequence 322884,
C 579	12.4	59.0	25	42	US-09-956-584A-319745	Sequence 319745, A	652	12.4	59.0	25	113	US-60-427-836-348030	Sequence 348030,
C 580	12.4	59.0	25	42	US-09-956-584A-319749	Sequence 319749, A	653	12.4	59.0	25	113	US-60-470-475-29307	Sequence 29307, A
C 581	12.4	59.0	25	42	US-09-956-604-62461	Sequence 62461, A	654	12.4	59.0	25	113	US-60-470-475-32290	Sequence 32290, A
C 582	12.4	59.0	25	42	US-09-956-604-84729	Sequence 84729, A	655	12.4	59.0	25	113	US-60-470-475-77421	Sequence 77421, A
C 583	12.4	59.0	25	42	US-09-956-604-85117	Sequence 85117, A	656	12.4	59.0	25	113	US-60-470-475-93922	Sequence 93922, A
C 584	12.4	59.0	25	42	US-09-956-604-85118	Sequence 85118, A	657	12.4	59.0	25	113	US-60-470-475-93922	Sequence 93922, A
C 585	12.4	59.0	25	42	US-09-956-604-111820	Sequence 111820, A	658	12.4	59.0	25	113	US-60-470-475-118963	Sequence 118963,
C 586	12.4	59.0	25	42	US-09-956-604A-62461	Sequence 62461, A	659	12.4	59.0	25	116	US-60-507-481-47893	Sequence 47893, A
C 587	12.4	59.0	25	42	US-09-956-604A-84729	Sequence 84729, A	660	12.4	59.0	25	116	US-60-507-481-55930	Sequence 55930, A
C 588	12.4	59.0	25	42	US-09-956-604A-85117	Sequence 85117, A	661	12.4	59.0	25	116	US-60-507-481-76438	Sequence 76438, A
C 589	12.4	59.0	25	42	US-09-956-604A-85118	Sequence 85118, A	662	12.4	59.0	25	116	US-60-507-481-158546	Sequence 158546,
C 590	12.4	59.0	25	42	US-09-956-604A-111820	Sequence 111820, A	663	12.4	59.0	25	116	US-60-507-481-167178	Sequence 167178,
C 591	12.4	59.0	25	42	US-09-956-604B-62461	Sequence 62461, A	664	12.4	59.0	25	116	US-60-507-511-189916	Sequence 189916,
C 592	12.4	59.0	25	42	US-09-956-604B-84729	Sequence 84729, A	665	12.4	59.0	25	120	US-60-545-213-89482	Sequence 89482, A
C 593	12.4	59.0	25	42	US-09-956-604B-85117	Sequence 85117, A	666	12.4	59.0	25	120	US-60-545-213-89483	Sequence 89483, A
C 594	12.4	59.0	25	42	US-09-956-604B-85118	Sequence 85118, A	667	12.4	59.0	25	120	US-60-545-213-89489	Sequence 89489, A
C 595	12.4	59.0	25	42	US-09-956-604B-111820	Sequence 111820, A	668	12.4	59.0	25	120	US-60-545-213-89491	Sequence 89491, A
C 596	12.4	59.0	25	46	US-10-098-263B-96896	Sequence 96896, A	669	12.4	59.0	25	120	US-60-545-213-89499	Sequence 89499, A
C 597	12.4	59.0	25	46	US-10-098-263B-96896	Sequence 96896, A	670	12.4	59.0	25	120	US-60-545-213-160082	Sequence 160082,
C 598	12.4	59.0	25	46	US-10-355-577-170459	Sequence 170459, A	671	12.4	59.0	25	120	US-60-545-213-267824	Sequence 267824,
C 599	12.4	59.0	25	52	US-10-355-577-170459	Sequence 170459, A	672	12.4	59.0	32	7	US-08-215-116A-15	Sequence 15, Appl
C 600	12.4	59.0	25	52	US-10-355-577-844405	Sequence 844405, A	673	12.4	59.0	32	7	US-08-215-116A-38	Sequence 38, Appl
C 601	12.4	59.0	25	57	US-10-681-773-29307	Sequence 29307, A	674	12.4	59.0	32	9	US-08-472-988A-15	Sequence 15, Appl
C 602	12.4	59.0	25	57	US-10-681-773-32290	Sequence 32290, A	675	12.4	59.0	32	9	US-08-472-988A-38	Sequence 38, Appl
C 603	12.4	59.0	25	57	US-10-681-773-77421	Sequence 77421, A	676	12.4	59.0	32	9	US-08-472-988B-15	Sequence 15, Appl
C 604	12.4	59.0	25	57	US-10-681-773-77422	Sequence 77422, A	677	12.4	59.0	32	9	US-08-472-988B-38	Sequence 38, Appl
C 605	12.4	59.0	25	57	US-10-681-773-93922	Sequence 93922, A	678	12.4	59.0	32	9	US-08-472-988C-38	Sequence 38, Appl
C 606	12.4	59.0	25	57	US-10-681-773-119863	Sequence 119863, A	679	12.4	59.0	32	9	US-08-472-988C-38	Sequence 38, Appl
C 607	12.4	59.0	25	60	US-10-719-900-161435	Sequence 161435, A	680	12.4	59.0	32	9	US-08-472-988D-15	Sequence 15, Appl
C 608	12.4	59.0	25	60	US-10-719-900-323524	Sequence 323524, A	681	12.4	59.0	32	9	US-08-472-988D-38	Sequence 38, Appl
C 609	12.4	59.0	25	60	US-10-719-900-344380	Sequence 344380, A	682	12.4	59.0	32	9	US-08-485-552A-15	Sequence 15, Appl
C 610	12.4	59.0	25	60	US-10-719-900-359916	Sequence 359916, A	683	12.4	59.0	32	9	US-08-485-552A-38	Sequence 38, Appl
C 611	12.4	59.0	25	60	US-10-719-900-562857	Sequence 562857, A	684	12.4	59.0	32	10	US-08-528-756-15	Sequence 15, Appl
C 612	12.4	59.0	25	60	US-10-719-900-562857	Sequence 562857, A	685	12.4	59.0	32	10	US-08-528-756-38	Sequence 38, Appl
C 613	12.4	59.0	25	60	US-10-719-900-64063	Sequence 64063, A	686	12.4	59.0	32	10	US-08-528-756A-49	Sequence 49, Appl
C 614	12.4	59.0	25	60	US-10-719-900-747133	Sequence 747133, A	687	12.4	59.0	32	10	US-08-528-756A-81	Sequence 81, Appl
C 615	12.4	59.0	25	60	US-10-719-956-155490	Sequence 155490, A	688	12.4	59.0	32	10	US-08-528-756B-49	Sequence 49, Appl
C 616	12.4	59.0	25	60	US-10-719-956-308010	Sequence 308010, A	689	12.4	59.0	32	10	US-08-528-756B-81	Sequence 81, Appl
C 617	12.4	59.0	25	60	US-10-719-956-332284	Sequence 332284, A	690	12.4	59.0	32	10	US-08-528-756B-81	Sequence 81, Appl
C 618	12.4	59.0	25	60	US-10-719-956-348030	Sequence 348030, A	691	12.4	59.0	32	63	PCT-US03-18714-14925	Sequence 14925, A
C 619	12.4	59.0	25	62	US-10-809-189-4324	Sequence 4324, Ap	692	12.4	59.0	42	28	US-09-647-309A-131	Sequence 131, App
C 620	12.4	59.0	25	62	US-10-809-189-59293	Sequence 59293, A	693	12.4	59.0	42	28	US-09-647-309A-133	Sequence 133, App
C 621	12.4	59.0	25	62	US-10-809-189-93995	Sequence 93995, A	694	12.4	59.0	42	28	US-09-752-041-71	Sequence 71, Appl
C 622	12.4	59.0	25	64	US-10-933-982-62995	Sequence 62995, A	695	12.4	59.0	42	32	US-09-752-041-71	Sequence 71, Appl
C 623	12.4	59.0	25	64	US-10-933-982-70055	Sequence 70055, A	696	12.4	59.0	42	57	US-10-655-855-71	Sequence 71, Appl
C 624	12.4	59.0	25	64	US-10-933-982-120889	Sequence 120889, A	697	12.4	59.0	42	57	US-10-655-855-72	Sequence 72, Appl
C 625	12.4	59.0	25	88	US-60-232-638-27511	Sequence 27511, A	698	12.4	59.0	45	4	US-07-948-358-5	Sequence 5, Appl
C 626	12.4	59.0	25	88	US-60-232-638-27512	Sequence 27512, A	699	12.4	59.0	48	7	US-08-215-116A-25	Sequence 25, Appl
C 627	12.4	59.0	25	88	US-60-233-166-175728	Sequence 175728, A	700	12.4	59.0	48	9	US-08-472-988A-25	Sequence 25, Appl
C 628	12.4	59.0	25	88	US-60-233-166-175739	Sequence 175739, A	701	12.4	59.0	48	9	US-08-472-988B-25	Sequence 25, Appl
C 629	12.4	59.0	25	88	US-60-234-017-210332	Sequence 210332, A	702	12.4	59.0	48	9	US-08-472-988C-25	Sequence 25, Appl
C 630	12.4	59.0	25	88	US-60-234-049-11864	Sequence 11864, A	703	12.4	59.0	48	9	US-08-472-988D-25	Sequence 25, Appl
C 631	12.4	59.0	25	88	US-60-234-049-107085	Sequence 107085, A	704	12.4	59.0	48	9	US-08-485-552A-25	Sequence 25, Appl
C 632	12.4	59.0	25	88	US-60-234-049-107631	Sequence 107631, A	705	12.4	59.0	48	10	US-08-528-756A-59	Sequence 59, Appl
C 633	12.4	59.0	25	88	US-60-234-049-107632	Sequence 107632, A	706	12.4	59.0	48	10	US-08-528-756B-59	Sequence 59, Appl
C 634	12.4	59.0	25	88	US-60-234-049-124231	Sequence 124231, A	707	12.4	59.0	49	45	US-10-035-833A-2502	Sequence 2502, Ap
C 635	12.4	59.0	25	101	US-60-353-987-170469	Sequence 170469, A	708	12.4	59.0	49	45	US-10-035-833A-4898	Sequence 4898, Ap
C 636	12.4	59.0	25	101	US-60-353-987-844405	Sequence 844405, A	709	12.4	59.0	49	45	US-60-585-352-9814	Sequence 9814, Ap
C 637	12.4	59.0	25	107	US-60-417-190-448	Sequence 448, App	710	12.4	59.0	50	124	US-60-585-352-9814	Sequence 25464, A
C 638	12.4	59.0	25	107	US-60-417-190-107294	Sequence 107294, A	711	12.4	59.0	50	124	US-60-585-352-25464	Sequence 25464, A

c 712	12.4	59.0	50	124	US-60-585-352-103276	Sequence 103276,	c 785	12.2	58.1	25	42	US-09-956-584-594406	Sequence 594406,
c 713	12.2	58.1	19	26	US-09-614-681-15	Sequence 15, Appl	c 786	12.2	58.1	25	42	US-09-956-584-594408	Sequence 594408,
c 714	12.2	58.1	19	46	US-10-084-639-3754	Sequence 3754, A	c 787	12.2	58.1	25	42	US-09-956-584-594409	Sequence 594409,
c 715	12.2	58.1	19	47	US-10-138-381-15	Sequence 15, Appl	c 788	12.2	58.1	25	42	US-09-956-584-594413	Sequence 594413,
c 716	12.2	58.1	19	49	US-10-714-333A-4841	Sequence 4841, A	c 789	12.2	58.1	25	42	US-09-956-584-594414	Sequence 594414,
c 717	12.2	58.1	19	59	US-10-714-333A-63465	Sequence 63465, A	c 790	12.2	58.1	25	42	US-09-956-584-594417	Sequence 594417,
c 718	12.2	58.1	19	59	US-10-714-333A-411316	Sequence 411316,	c 791	12.2	58.1	25	42	US-09-956-584A-28821	Sequence 28821, A
c 719	12.2	58.1	19	59	US-10-714-333A-473044	Sequence 473044,	c 792	12.2	58.1	25	42	US-09-956-584A-113142	Sequence 113142,
c 720	12.2	58.1	19	59	US-10-714-333A-520235	Sequence 520235,	c 793	12.2	58.1	25	42	US-09-956-584A-113145	Sequence 113145,
c 721	12.2	58.1	19	59	US-10-714-333A-535022	Sequence 535022,	c 794	12.2	58.1	25	42	US-09-956-584A-156969	Sequence 156969,
c 722	12.2	58.1	19	59	US-10-714-333A-835512	Sequence 835512,	c 795	12.2	58.1	25	42	US-09-956-584A-156980	Sequence 156980,
c 723	12.2	58.1	19	59	US-10-714-333A-887909	Sequence 887909,	c 796	12.2	58.1	25	42	US-09-956-584A-211131	Sequence 211131,
c 724	12.2	58.1	19	59	US-10-714-333A-887948	Sequence 887948,	c 797	12.2	58.1	25	42	US-09-956-584A-211141	Sequence 211141,
c 725	12.2	58.1	19	59	US-10-714-333A-1056175	Sequence 1056175,	c 798	12.2	58.1	25	42	US-09-956-584A-218332	Sequence 218332,
c 726	12.2	58.1	19	59	US-10-714-333A-1060741	Sequence 1060741,	c 799	12.2	58.1	25	42	US-09-956-584A-262426	Sequence 262426,
c 727	12.2	58.1	19	59	US-10-714-333A-1547505	Sequence 1547505,	c 800	12.2	58.1	25	42	US-09-956-584A-262427	Sequence 262427,
c 728	12.2	58.1	19	59	US-10-714-333A-1580934	Sequence 1580934,	c 801	12.2	58.1	25	42	US-09-956-584A-262427	Sequence 262427,
c 729	12.2	58.1	19	59	US-10-714-333A-1580964	Sequence 1580964,	c 802	12.2	58.1	25	42	US-09-956-584A-364869	Sequence 364869,
c 730	12.2	58.1	20	17	US-09-201-228A-1856	Sequence 1856, Ap	c 803	12.2	58.1	25	42	US-09-956-584A-36496	Sequence 36496,
c 731	12.2	58.1	20	62	US-10-831-901A-24672	Sequence 24672, A	c 804	12.2	58.1	25	42	US-09-956-584A-396503	Sequence 396503,
c 732	12.2	58.1	20	62	US-10-831-901A-24673	Sequence 24673, A	c 805	12.2	58.1	25	42	US-09-956-584A-416972	Sequence 416972,
c 733	12.2	58.1	20	62	US-10-831-901A-24674	Sequence 24674, A	c 806	12.2	58.1	25	42	US-09-956-584A-485761	Sequence 485761,
c 734	12.2	58.1	20	62	US-10-831-901A-24675	Sequence 24675, A	c 807	12.2	58.1	25	42	US-09-956-584A-533545	Sequence 533545,
c 735	12.2	58.1	21	61	US-10-770-726-1445	Sequence 1445, Ap	c 808	12.2	58.1	25	42	US-09-956-584A-577116	Sequence 577116,
c 736	12.2	58.1	22	46	US-10-085-239A-14	Sequence 14, Appl	c 809	12.2	58.1	25	42	US-09-956-584A-578420	Sequence 578420,
c 737	12.2	58.1	23	2	PCT-US04-04452-1134	Sequence 1134, Ap	c 810	12.2	58.1	25	42	US-09-956-584A-578434	Sequence 578434,
c 738	12.2	58.1	24	50	US-10-293-338-7895	Sequence 7895, Ap	c 811	12.2	58.1	25	42	US-09-956-584A-592898	Sequence 592898,
c 739	12.2	58.1	25	20	US-09-396-196F-4874	Sequence 4874, Ap	c 812	12.2	58.1	25	42	US-09-956-604-23423	Sequence 23423, A
c 740	12.2	58.1	25	20	US-09-396-196F-4875	Sequence 4875, Ap	c 813	12.2	58.1	25	42	US-09-956-604-50440	Sequence 50440, A
c 741	12.2	58.1	25	20	US-09-396-196F-4886	Sequence 4886, Ap	c 814	12.2	58.1	25	42	US-09-956-604-50687	Sequence 50687, A
c 742	12.2	58.1	25	20	US-09-396-196F-4886	Sequence 4886, Ap	c 815	12.2	58.1	25	42	US-09-956-604-50688	Sequence 50688, A
c 743	12.2	58.1	25	20	US-09-396-196F-90438	Sequence 90438, A	c 816	12.2	58.1	25	42	US-09-956-604-122293	Sequence 122293,
c 744	12.2	58.1	25	20	US-09-396-196F-90681	Sequence 90681, A	c 817	12.2	58.1	25	42	US-09-956-604B-23423	Sequence 23423, A
c 745	12.2	58.1	25	20	US-09-396-196F-90682	Sequence 90682, A	c 818	12.2	58.1	25	42	US-09-956-604A-50440	Sequence 50440, A
c 746	12.2	58.1	25	20	US-09-396-196F-90693	Sequence 90693, A	c 819	12.2	58.1	25	42	US-09-956-604A-50687	Sequence 50687, A
c 747	12.2	58.1	25	20	US-09-396-196G-4874	Sequence 4874, Ap	c 820	12.2	58.1	25	42	US-09-956-604A-50688	Sequence 50688, A
c 748	12.2	58.1	25	20	US-09-396-196G-4875	Sequence 4875, Ap	c 821	12.2	58.1	25	42	US-09-956-604A-122293	Sequence 122293,
c 749	12.2	58.1	25	20	US-09-396-196G-4886	Sequence 4886, Ap	c 822	12.2	58.1	25	42	US-09-956-604B-23423	Sequence 23423, A
c 750	12.2	58.1	25	20	US-09-396-196G-4886	Sequence 4886, Ap	c 823	12.2	58.1	25	42	US-09-956-604B-23423	Sequence 23423, A
c 751	12.2	58.1	25	20	US-09-396-196G-90438	Sequence 90438, A	c 824	12.2	58.1	25	42	US-09-956-604B-50687	Sequence 50687, A
c 752	12.2	58.1	25	20	US-09-396-196G-90681	Sequence 90681, A	c 825	12.2	58.1	25	42	US-09-956-604B-50688	Sequence 50688, A
c 753	12.2	58.1	25	20	US-09-396-196G-90682	Sequence 90682, A	c 826	12.2	58.1	25	42	US-09-956-604B-122293	Sequence 122293,
c 754	12.2	58.1	25	20	US-09-660-222-113349	Sequence 113349,	c 827	12.2	58.1	25	42	US-09-956-604B-16700	Sequence 16700, A
c 755	12.2	58.1	25	20	US-09-754-853A-786	Sequence 786, App	c 828	12.2	58.1	25	42	US-09-956-604B-16708	Sequence 16708, A
c 756	12.2	58.1	25	32	US-09-953-115A-22238	Sequence 22238, A	c 829	12.2	58.1	25	42	US-09-956-604B-16856	Sequence 16856, A
c 757	12.2	58.1	25	41	US-09-953-115A-22239	Sequence 22239, A	c 830	12.2	58.1	25	42	US-09-956-604B-16950	Sequence 16950, A
c 758	12.2	58.1	25	41	US-09-953-570-63571	Sequence 63571, A	c 831	12.2	58.1	25	42	US-09-956-604B-16958	Sequence 16958, A
c 759	12.2	58.1	25	41	US-09-953-570A-19760	Sequence 19760, A	c 832	12.2	58.1	25	42	US-09-956-604B-16960	Sequence 16960, A
c 760	12.2	58.1	25	41	US-09-953-570A-19761	Sequence 19761, A	c 833	12.2	58.1	25	42	US-09-956-604B-16991	Sequence 16991, A
c 761	12.2	58.1	25	41	US-09-953-570A-46703	Sequence 46703, A	c 834	12.2	58.1	25	42	US-09-956-604B-17739	Sequence 17739, A
c 762	12.2	58.1	25	41	US-09-953-570A-85246	Sequence 85246, A	c 835	12.2	58.1	25	42	US-09-956-604B-17739	Sequence 17739, A
c 763	12.2	58.1	25	41	US-09-953-570A-131695	Sequence 131695, A	c 836	12.2	58.1	25	42	US-09-956-604B-121227	Sequence 121227,
c 764	12.2	58.1	25	41	US-09-954-427-54081	Sequence 54081, A	c 837	12.2	58.1	25	42	US-09-956-604B-126128	Sequence 126128,
c 765	12.2	58.1	25	41	US-09-954-427-54081	Sequence 54081, A	c 838	12.2	58.1	25	42	US-09-956-604B-126129	Sequence 126129,
c 766	12.2	58.1	25	41	US-09-954-427-208615	Sequence 208615,	c 839	12.2	58.1	25	42	US-09-956-604B-126130	Sequence 126130,
c 767	12.2	58.1	25	41	US-09-954-427-301017	Sequence 301017,	c 840	12.2	58.1	25	42	US-09-956-604B-126147	Sequence 126147,
c 768	12.2	58.1	25	41	US-09-954-427-312470	Sequence 312470,	c 841	12.2	58.1	25	42	US-09-956-604B-126156	Sequence 126156,
c 769	12.2	58.1	25	41	US-09-954-427A-4073	Sequence 4073, Ap	c 842	12.2	58.1	25	42	US-09-956-604B-126177	Sequence 126177,
c 770	12.2	58.1	25	41	US-09-954-427A-29695	Sequence 29695, A	c 843	12.2	58.1	25	42	US-09-956-604B-126178	Sequence 126178,
c 771	12.2	58.1	25	41	US-09-954-427A-64553	Sequence 64553, A	c 844	12.2	58.1	25	46	US-10-084-839-3753	Sequence 3753, Ap
c 772	12.2	58.1	25	41	US-09-954-427A-64562	Sequence 64562, A	c 845	12.2	58.1	25	46	US-10-098-263B-115941	Sequence 115941,
c 773	12.2	58.1	25	41	US-09-954-427A-164216	Sequence 164216,	c 846	12.2	58.1	25	46	US-10-098-263B-119516	Sequence 119516,
c 774	12.2	58.1	25	41	US-09-954-427A-164270	Sequence 164270,	c 847	12.2	58.1	25	52	US-10-355-577-30707	Sequence 30707, A
c 775	12.2	58.1	25	41	US-09-954-427A-180593	Sequence 180593,	c 848	12.2	58.1	25	52	US-10-355-577-119362	Sequence 119362,
c 776	12.2	58.1	25	41	US-09-954-427A-203017	Sequence 203017,	c 849	12.2	58.1	25	52	US-10-355-577-532975	Sequence 532975,
c 777	12.2	58.1	25	41	US-09-954-427A-298795	Sequence 298795,	c 850	12.2	58.1	25	52	US-10-355-577-752574	Sequence 752574,
c 778	12.2	58.1	25	41	US-09-954-427A-402010	Sequence 402010,	c 851	12.2	58.1	25	52	US-10-355-577-892666	Sequence 892666,
c 779	12.2	58.1	25	41	US-09-954-427A-99686	Sequence 99686, A	c 852	12.2	58.1	25	52	US-10-355-577-976139	Sequence 976139,
c 780	12.2	58.1	25	42	US-09-956-584-273258	Sequence 273258,	c 853	12.2	58.1	25	57	US-10-681-773-16400	Sequence 16400, A
c 781	12.2	58.1	25	42	US-09-956-584-273267	Sequence 273267,	c 854	12.2	58.1	25	57	US-10-681-773-20234	Sequence 20234, A
c 782	12.2	58.1	25	42	US-09-956-584-340517	Sequence 340517,	c 855	12.2	58.1	25	57	US-10-681-773-20236	Sequence 20236, A
c 783	12.2	58.1	25	42	US-09-956-584-459039	Sequence 459039,	c 856	12.2	58.1	25	57	US-10-681-773-66520	Sequence 66520, A
c 784	12.2	58.1	25	42	US-09-956-584-459040	Sequence 459040,	c 857	12.2	58.1	25	57	US-10-681-773-66521	Sequence 66521, A


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RESULT 1
US-10-087-631B-1
; SEQUENCE 1, APPLICATION US/10087631B
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exempl
; OTHER INFORMATION: principle
US-10-087-631B-1

Query Match      100.0%; Score 21; DB 46; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
Db 1 AGCGCATGCCAGATTACTGGC 21

RESULT 2
US-10-419-022-1
; SEQUENCE 1, APPLICATION US/10419022
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exempl
; OTHER INFORMATION: principle
US-10-419-022-1

Query Match      100.0%; Score 21; DB 53; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
Db 1 AGCGCATGCCAGATTACTGGC 21

RESULT 3
US-09-953-570A-49187
; SEQUENCE 49187, APPLICATION US/09953570A
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, MICHAEL
; TITLE OF INVENTION: METHODS OF GENETIC ANALYSIS OF YEAST
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-152753

Query Match      72.4%; Score 15.2; DB 60; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 1 AGAGCATGCGTGTGCTGG 20
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; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49187
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-49187

Query Match      73.3%; Score 15.4; DB 41; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACT 18
Db 8 GAGCATGCCAGATTACT 24

RESULT 4
US-09-953-570A-49194
; SEQUENCE 49194, APPLICATION US/09953570A
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, MICHAEL
; TITLE OF INVENTION: METHODS OF GENETIC ANALYSIS OF YEAST
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49194
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-49194

Query Match      73.3%; Score 15.4; DB 41; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACT 18
Db 2 GAGCATGCCAGATTACT 18

RESULT 5
US-10-719-900-152753
; SEQUENCE 152753, APPLICATION US/10719900
; GENERAL INFORMATION:
; APPLICANT: XUE MEI ZHOU
; TITLE OF INVENTION: METHODS OF GENETIC ANALYSIS OF MOUSE
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-152753

Query Match      72.4%; Score 15.2; DB 60; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 1 AGAGCATGCGTGTGCTGG 20
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RESULT 6

US-10-719-956-219125
; Sequence 219125, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219125
; TYPE: DNA
; LENGTH: 25
; ORGANISM: Rattus norvegicus
US-10-719-956-219125

Query Match 72.4%; Score 15.2; DB 60; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
||| ||||| ||||| |||||
Db 3 AGAGCATGCCAGTTTGCTGG 22

RESULT 7

US-60-427-808-152753
; Sequence 152753, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152753
; TYPE: DNA
; LENGTH: 25
; ORGANISM: Mus musculus
US-60-427-808-152753

Query Match 72.4%; Score 15.2; DB 108; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
||| ||||| ||||| |||||
Db 1 AGAGCATGCCAGTTTGCTGG 20

RESULT 8

US-60-427-836-219125
; Sequence 219125, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219125
; TYPE: DNA
; LENGTH: 25
; ORGANISM: Rattus norvegicus
US-60-427-836-219125

Query Match 72.4%; Score 15.2; DB 108; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
||| ||||| ||||| |||||
Db 3 AGAGCATGCCAGTTTGCTGG 22

RESULT 9

US-60-507-511-165285/c
; Sequence 165285, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165285
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-165285

Query Match 71.4%; Score 15; DB 116; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACT 18
||| ||||| ||||| |||||
Db 23 GCATGCCAGATTACT 9

RESULT 10

US-60-507-481-158095
; Sequence 158095, Application US/60507481
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODLES OF INFLAMMATORY DISEASES
; FILE REFERENCE: AM101084
; CURRENT APPLICATION NUMBER: US/60/507,481
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 210107
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-60-507-481-158095

Query Match 70.5%; Score 14.8; DB 116; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACTG 19
||| ||||| ||||| |||||
Db 2 GAGCGTCCAGATTACTG 19

RESULT 11

US-60-507-481-158096
; Sequence 158096, Application US/60507481
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODLES OF INFLAMMATORY DISEASES

; FILE REFERENCE: AM101084
; CURRENT APPLICATION NUMBER: US/60/507,481
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 210107
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-60-507-481-158096

Query Match 70.5%; Score 14.8; DB 116; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACTG 19
| | | | | | | | | | | | | | | | | | | | | |
DB 2 GAGCGTGGCAGATTACTG 19

RESULT 12
US-09-956-604D-44625/c
; Sequence 44625, Application US/09956604D
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604D
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.2
; SEQ ID NO 44625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-09-956-604D-44625

Query Match 68.6%; Score 14.4; DB 42; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACTGGC 21
| | | | | | | | | | | | | | | | | | | | | |
DB 20 ATGCCAGTTTACTGGC 5

RESULT 13
US-09-956-604D-61437/c
; Sequence 61437, Application US/09956604D
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604D
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.2
; SEQ ID NO 61437
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-09-956-604D-61437

Query Match 68.6%; Score 14.4; DB 42; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACTGGC 21
| | | | | | | | | | | | | | | | | | | | | |

Db 16 ATGCCAGATAACTGGC 1

RESULT 14
US-60-585-352-61322
; Sequence 61322, Application US/60585352
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690
; CURRENT APPLICATION NUMBER: US/60/585,352
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: TBD
; PRIOR FILING DATE: TBD
; NUMBER OF SEQ ID NOS: 116211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61322
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-60-585-352-61322

Query Match 68.6%; Score 14.4; DB 124; Length 50;
Best Local Similarity 83.3%; Pred. No. 8.8e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGGC 21
| | | | | | | | | | | | | | | | | | | | | |
DB 23 GCAGCCCAATTATTGGC 40

RESULT 15
US-10-708-204-1327/c
; Sequence 1327, Application US/10708204
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1327
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-1327

Query Match 67.6%; Score 14.2; DB 58; Length 22;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACTGG 20
| | | | | | | | | | | | | | | | | | | | | |
DB 21 GCACATCCAGATGACTGG 3

RESULT 16
US-09-953-570-116813/c
; Sequence 116813, Application US/09953570
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 116813
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces Cerevisiae
US-09-953-570-116813

Query Match      67.6%; Score 14.2; DB 41; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCATGCCAGATTACTGCG 21
    ||||| ||||| ||||| |||||
Db 24 CGCATGCCAGATTACTAGC 6

RESULT 17
US-09-953-570A-90293/c
; Sequence 90293, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90293
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-90293

Query Match      67.6%; Score 14.2; DB 41; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCATGCCAGATTACTGCG 21
    ||||| ||||| ||||| |||||
Db 25 CGCATGCCAGATTACTGAC 7

RESULT 18
US-09-956-584A-596217
; Sequence 596217, Application US/09956584A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Genetic Analysis of Mouse
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 596217
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584A-596217

Query Match      67.6%; Score 14.2; DB 42; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTG 19
    ||||| ||||| ||||| |||||
Db 7 AGCACATTCAGATCACTG 25

RESULT 21
US-09-956-604D-42268/c
; Sequence 42268, Application US/09956604D
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604D
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.2
; SEQ ID NO 42268
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-09-956-604D-42268
```

```
Query Match      67.6%; Score 14.2; DB 42; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGG 20
   ||||| ||||| |||||
Db 19 GCGGATGCCGTTACTGG 1

RESULT 22
US-10-719-900-116595/c
; Sequence 116595, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 116595
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-116595

Query Match      67.6%; Score 14.2; DB 60; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGG 20
   ||||| ||||| |||||
Db 23 GCACATGCCAGATTACTGG 5

RESULT 23
US-10-719-900-122509
; Sequence 122509, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 122509
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-122509

Query Match      67.6%; Score 14.2; DB 60; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGCATGCCAGATTACTGG 21
   ||||| ||||| |||||
Db 6 GCGCAGCCAGATAACCGGC 24

RESULT 24
US-10-719-900-276673
; Sequence 276673, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
```

```
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 276673
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-276673

Query Match      67.6%; Score 14.2; DB 60; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGG 19
   ||||| ||||| |||||
Db 4 AGATCATGCCATATTACTG 22

RESULT 25
US-10-933-982-98903
; Sequence 98903, Application US/10933982
; GENERAL INFORMATION:
; APPLICANT: Barts, Jennifer
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
; FILE REFERENCE: 3700
; CURRENT APPLICATION NUMBER: US/10/933,982
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 224976
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 98903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-98903

Query Match      67.6%; Score 14.2; DB 64; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACTGGC 21
   ||||| ||||| |||||
Db 4 CGCATGCCAGATTACTGGC 22

RESULT 26
US-60-232-638-116814/c
; Sequence 116814, Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116814
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YNL237W
US-60-232-638-116814

Query Match      67.6%; Score 14.2; DB 88; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACTGGC 21
   ||||| ||||| |||||
Db 24 CGCATGCAAGATTAAATAGC 6
```



```
; CURRENT APPLICATION NUMBER: US/60/585,352
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: TBD
; PRIOR FILING DATE: TBD
; NUMBER OF SEQ ID NOS: 116211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55437
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-60-585-352-55437

Query Match      67.6%; Score 14.2; DB 124; Length 50;
Best Local Similarity 76.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGGC 21
Db 31 AACCCRTGCTGGATTACTGGC 11

RESULT 33
US-09-953-570A-50875/c
; Sequence 50875, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 50875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-50875

Query Match      66.7%; Score 14; DB 41; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATT 15
Db 22 GCGCATGCCAGATT 9

RESULT 34
US-10-714-333A-748734/c
; Sequence 748734, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 748734
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-714-333A-748734

Query Match      65.7%; Score 13.8; DB 59; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGG 20
Db 17 GCATGCCATCTACTGG 1

RESULT 35
US-10-714-333A-765169
; Sequence 765169, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 765169
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-765169

Query Match      65.7%; Score 13.8; DB 59; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.6e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTAC 17
Db 3 AGCGCAUGUCAGAAUAC 19

RESULT 36
US-09-953-570A-91613
; Sequence 91613, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 91613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-91613

Query Match      65.7%; Score 13.8; DB 41; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGATGCCAGATTACTG 19
Db 1 GCGATGCCAGATTCTCG 17
```

```
RESULT 37
US-09-956-584-124055
; Sequence 124055, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124055
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-956-584-124055

Query Match      65.7%; Score 13.8; DB 42; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGCG 21
Db 3 CAAGCAAGATTACTGCG 19

RESULT 38
US-09-956-584-124056
; Sequence 124056, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-956-584-124056

Query Match      65.7%; Score 13.8; DB 42; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGCG 21
Db 3 CAAGCAAGATTACTGCG 19

RESULT 39
US-09-956-584-124063
; Sequence 124063, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124063
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-956-584-124063

Query Match      65.7%; Score 13.8; DB 42; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGCG 21
Db 5 CAAGCAAGATTACTGCG 21

RESULT 40
US-10-719-900-480794
; Sequence 480794, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 480794
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-480794

Query Match      65.7%; Score 13.8; DB 60; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGG 20
Db 7 GCATGCCAGATCACTGG 23

Search completed: November 24, 2004, 03:15:11
Job time : 1381.58 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 17:30:18 ; Search time 26.2697 Seconds
(without alignments)
338.188 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21

Sequence: 1 agcgcagccagattactggc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 892029 seqs, 211525902 residues

Total number of hits satisfying chosen parameters: 1282072

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Pending Patents NA, New: *

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq: *
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq: *
7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq: *
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
c	1	15	71.4	25	6	US-10-956-157-281467		Sequence 281467,
	2	14.8	70.5	25	6	US-10-956-160-158095		Sequence 158095,
	3	14.8	70.5	25	6	US-10-956-160-158096		Sequence 158096,
	4	13.8	65.7	25	6	US-10-956-157-209367		Sequence 209367,
	5	13.8	65.7	25	6	US-10-956-160-164697		Sequence 164697,
	6	13.6	64.8	25	6	US-10-956-157-288293		Sequence 288293,
	7	13.6	64.8	25	6	US-10-956-160-119577		Sequence 119577,
	8	13.2	62.9	25	6	US-10-956-157-1150549		Sequence 1150549,
	9	13.2	62.9	25	6	US-10-956-160-44697		Sequence 44697, A
	10	13.2	62.9	25	6	US-10-956-160-179056		Sequence 179056,
	11	13	61.9	25	6	US-10-956-160-109185		Sequence 109185,
	12	12.8	61.0	25	6	US-10-956-157-85795		Sequence 85795, A
	13	12.8	61.0	25	6	US-10-956-157-85796		Sequence 85796, A
	14	12.8	61.0	25	6	US-10-956-157-85797		Sequence 85797, A
	15	12.8	61.0	25	6	US-10-956-157-85802		Sequence 85802, A
	16	12.8	61.0	25	6	US-10-956-157-85805		Sequence 85805, A
	17	12.8	61.0	25	6	US-10-956-157-161273		Sequence 161273,
	18	12.8	61.0	25	6	US-10-956-157-171287		Sequence 171287,
	19	12.8	61.0	25	6	US-10-956-157-210009		Sequence 210009,
	20	12.8	61.0	25	6	US-10-956-157-237787		Sequence 237787,
	21	12.8	61.0	25	6	US-10-956-160-16692		Sequence 16692, A
	22	12.8	61.0	25	6	US-10-956-160-77247		Sequence 77247, A
	23	12.8	61.0	25	6	US-10-956-160-96989		Sequence 96989, A
	24	12.8	61.0	25	6	US-10-956-160-159211		Sequence 159211,
	25	12.8	61.0	25	6	US-10-956-160-180069		Sequence 180069,

26	12.6	60.0	25	6	US-10-956-157-123326		Sequence 123326,
27	12.6	60.0	25	6	US-10-956-157-206484		Sequence 206484,
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c	29	59.0	25	6	US-10-956-157-306098		Sequence 306098,
c	30	59.0	25	6	US-10-956-160-47893		Sequence 47893, A
c	31	59.0	25	6	US-10-956-160-55930		Sequence 55930, A
c	32	59.0	25	6	US-10-956-160-76438		Sequence 76438, A
c	33	59.0	25	6	US-10-956-160-158546		Sequence 158546,
c	34	59.0	25	6	US-10-956-160-167178		Sequence 167178,
c	35	59.0	28	6	US-10-489-273-35		Sequence 35, Appl
36	12.2	58.1	19	6	US-10-758-155-2666		Sequence 2666, Ap
37	12.2	58.1	19	6	US-10-758-155-2667		Sequence 2667, Ap
38	12.2	58.1	19	6	US-10-758-155-2732		Sequence 2732, Ap
39	12.2	58.1	19	6	US-10-758-155-2733		Sequence 2733, Ap
40	12.2	58.1	19	6	US-10-758-155-2738		Sequence 2738, Ap
41	12.2	58.1	19	6	US-10-758-155-2739		Sequence 2739, Ap
42	12.2	58.1	19	6	US-10-844-076-2666		Sequence 2666, Ap
43	12.2	58.1	19	6	US-10-844-076-2667		Sequence 2667, Ap
44	12.2	58.1	19	6	US-10-844-076-2732		Sequence 2732, Ap
45	12.2	58.1	19	6	US-10-844-076-2733		Sequence 2733, Ap
46	12.2	58.1	19	6	US-10-844-076-2738		Sequence 2738, Ap
47	12.2	58.1	19	6	US-10-844-076-2739		Sequence 2739, Ap
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53	12.2	58.1	23	6	US-10-758-155-2589		Sequence 2589, Ap
54	12.2	58.1	23	6	US-10-758-155-2630		Sequence 2630, Ap
55	12.2	58.1	23	6	US-10-758-155-2631		Sequence 2631, Ap
56	12.2	58.1	23	6	US-10-758-155-2636		Sequence 2636, Ap
57	12.2	58.1	23	6	US-10-758-155-2637		Sequence 2637, Ap
58	12.2	58.1	23	6	US-10-758-155-2643		Sequence 2643, Ap
59	12.2	58.1	23	6	US-10-758-155-2643		Sequence 2643, Ap
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62	12.2	58.1	23	6	US-10-844-076-2576		Sequence 2576, Ap
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64	12.2	58.1	23	6	US-10-844-076-2582		Sequence 2582, Ap
65	12.2	58.1	23	6	US-10-844-076-2583		Sequence 2583, Ap
66	12.2	58.1	23	6	US-10-844-076-2588		Sequence 2588, Ap
67	12.2	58.1	23	6	US-10-844-076-2589		Sequence 2589, Ap
68	12.2	58.1	23	6	US-10-844-076-2630		Sequence 2630, Ap
69	12.2	58.1	23	6	US-10-844-076-2631		Sequence 2631, Ap
70	12.2	58.1	23	6	US-10-844-076-2636		Sequence 2636, Ap
71	12.2	58.1	23	6	US-10-844-076-2637		Sequence 2637, Ap
72	12.2	58.1	23	6	US-10-844-076-2642		Sequence 2642, Ap
73	12.2	58.1	23	6	US-10-844-076-2643		Sequence 2643, Ap
74	12.2	58.1	23	6	US-10-844-076-2648		Sequence 2648, Ap
75	12.2	58.1	23	6	US-10-844-076-2649		Sequence 2649, Ap
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c	77	12.2	25	6	US-10-956-160-84311		Sequence 84311, A
c	78	12.2	25	6	US-10-956-160-146866		Sequence 146866,
c	79	12.2	25	6	US-10-956-160-151959		Sequence 151959,
c	80	12.2	25	6	US-10-956-160-158894		Sequence 158894,
c	81	12.2	25	6	US-10-956-160-183781		Sequence 183781,
c	82	12.2	44	6	US-10-861-930-13		Sequence 13, Appl
c	83	12	25	6	US-10-956-157-137663		Sequence 137663,
c	84	12	25	6	US-10-956-157-139568		Sequence 139568,
c	85	12	25	6	US-10-956-157-146425		Sequence 146425,
c	86	12	25	6	US-10-956-157-146578		Sequence 146578,
c	87	12	25	6	US-10-956-157-200742		Sequence 200742,
c	88	12	25	6	US-10-956-157-202625		Sequence 202625,
c	89	12	25	6	US-10-956-157-203787		Sequence 203787,
c	90	12	25	6	US-10-956-157-221776		Sequence 221776,
c	91	12	25	6	US-10-956-157-234899		Sequence 234899,
c	92	12	25	6	US-10-956-157-253573		Sequence 253573,
c	93	12	25	6	US-10-956-157-262123		Sequence 262123,
c	94	12	25	6	US-10-956-157-276584		Sequence 276584,
c	95	12	25	6	US-10-956-157-287655		Sequence 287655,
c	96	12	25	6	US-10-956-157-287752		Sequence 287752,
c	97	12	25	6	US-10-956-157-294027		Sequence 294027,
c	98	12	25	6	US-10-956-157-295281		Sequence 295281,

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c 100	12	57.1	25	6	US-10-956-160-14295	Sequence 14295, A	c 173	11.6	55.2	25	6	US-10-956-160-45807	Sequence 45807, A
c 101	12	57.1	25	6	US-10-956-160-23663	Sequence 23663, A	c 174	11.6	55.2	25	6	US-10-956-160-51729	Sequence 51729, A
c 102	12	57.1	25	6	US-10-956-160-27651	Sequence 27651, A	c 175	11.6	55.2	25	6	US-10-956-160-74424	Sequence 74424, A
c 103	12	57.1	25	6	US-10-956-160-46429	Sequence 46429, A	c 176	11.6	55.2	25	6	US-10-956-160-77410	Sequence 77410, A
c 104	12	57.1	25	6	US-10-956-160-49344	Sequence 49344, A	c 177	11.6	55.2	25	6	US-10-956-160-77411	Sequence 77411, A
c 105	12	57.1	25	6	US-10-956-160-143597	Sequence 143597, A	c 178	11.6	55.2	25	6	US-10-956-160-77484	Sequence 77484, A
c 106	12	57.1	25	6	US-10-956-157-143597	Sequence 143597, A	c 179	11.6	55.2	25	6	US-10-956-160-99187	Sequence 99187, A
c 107	12	57.1	25	6	US-10-956-157-143597	Sequence 143597, A	c 180	11.6	55.2	25	6	US-10-956-160-99188	Sequence 99188, A
c 108	11.8	56.2	25	6	US-10-956-157-131869	Sequence 131869, A	c 181	11.6	55.2	25	6	US-10-956-160-99189	Sequence 99189, A
c 109	11.8	56.2	25	6	US-10-956-157-139316	Sequence 139316, A	c 182	11.6	55.2	25	6	US-10-956-160-99190	Sequence 99190, A
c 110	11.8	56.2	25	6	US-10-956-157-139317	Sequence 139317, A	c 183	11.6	55.2	25	6	US-10-956-160-109584	Sequence 109584, A
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c 113	11.8	56.2	25	6	US-10-956-157-152698	Sequence 152698, A	c 186	11.6	55.2	25	6	US-10-956-160-137239	Sequence 137239, A
c 114	11.8	56.2	25	6	US-10-956-157-153801	Sequence 153801, A	c 187	11.6	55.2	25	6	US-10-956-160-137240	Sequence 137240, A
c 115	11.8	56.2	25	6	US-10-956-157-172027	Sequence 172027, A	c 188	11.6	55.2	25	6	US-10-956-160-137241	Sequence 137241, A
c 116	11.8	56.2	25	6	US-10-956-157-176331	Sequence 176331, A	c 189	11.6	55.2	25	6	US-10-956-160-143201	Sequence 143201, A
c 117	11.8	56.2	25	6	US-10-956-157-187594	Sequence 187594, A	c 190	11.6	55.2	25	6	US-10-956-160-163933	Sequence 163933, A
c 118	11.8	56.2	25	6	US-10-956-157-194089	Sequence 194089, A	c 191	11.6	55.2	25	6	US-10-956-160-168075	Sequence 168075, A
c 119	11.8	56.2	25	6	US-10-956-157-199823	Sequence 199823, A	c 192	11.6	55.2	39	6	US-10-794-381-4	Sequence 4, Appl1
c 120	11.8	56.2	25	6	US-10-956-157-209554	Sequence 209554, A	c 193	11.6	55.2	39	6	US-10-794-381-6	Sequence 6, Appl1
c 121	11.8	56.2	25	6	US-10-956-157-215284	Sequence 215284, A	c 194	11.4	54.3	23	6	US-10-758-155-2626	Sequence 2626, Ap
c 122	11.8	56.2	25	6	US-10-956-157-228761	Sequence 228761, A	c 195	11.4	54.3	23	6	US-10-758-155-2627	Sequence 2627, Ap
c 123	11.8	56.2	25	6	US-10-956-157-228733	Sequence 228733, A	c 196	11.4	54.3	23	6	US-10-758-155-2629	Sequence 2629, Ap
c 124	11.8	56.2	25	6	US-10-956-157-260706	Sequence 260706, A	c 197	11.4	54.3	23	6	US-10-758-155-2632	Sequence 2632, Ap
c 125	11.8	56.2	25	6	US-10-956-157-282908	Sequence 282908, A	c 198	11.4	54.3	23	6	US-10-758-155-2633	Sequence 2633, Ap
c 126	11.8	56.2	25	6	US-10-956-157-285821	Sequence 285821, A	c 199	11.4	54.3	23	6	US-10-758-155-2635	Sequence 2635, Ap
c 127	11.8	56.2	25	6	US-10-956-157-303700	Sequence 303700, A	c 200	11.4	54.3	23	6	US-10-758-155-2638	Sequence 2638, Ap
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c 130	11.8	56.2	25	6	US-10-956-160-27492	Sequence 27492, A	c 203	11.4	54.3	23	6	US-10-844-076-2626	Sequence 2626, Ap
c 131	11.8	56.2	25	6	US-10-956-160-36475	Sequence 36475, A	c 204	11.4	54.3	23	6	US-10-844-076-2627	Sequence 2627, Ap
c 132	11.8	56.2	25	6	US-10-956-160-69812	Sequence 69812, A	c 205	11.4	54.3	23	6	US-10-844-076-2629	Sequence 2629, Ap
c 133	11.8	56.2	25	6	US-10-956-160-84536	Sequence 84536, A	c 206	11.4	54.3	23	6	US-10-844-076-2632	Sequence 2632, Ap
c 134	11.8	56.2	25	6	US-10-956-160-88024	Sequence 88024, A	c 207	11.4	54.3	23	6	US-10-844-076-2633	Sequence 2633, Ap
c 135	11.8	56.2	25	6	US-10-956-160-95371	Sequence 95371, A	c 208	11.4	54.3	23	6	US-10-844-076-2635	Sequence 2635, Ap
c 136	11.8	56.2	25	6	US-10-956-160-114349	Sequence 114349, A	c 209	11.4	54.3	23	6	US-10-844-076-2638	Sequence 2638, Ap
c 137	11.8	56.2	25	6	US-10-956-160-172910	Sequence 172910, A	c 210	11.4	54.3	23	6	US-10-844-076-2639	Sequence 2639, Ap
c 138	11.8	56.2	25	6	US-10-956-160-178450	Sequence 178450, A	c 211	11.4	54.3	23	6	US-10-844-076-2641	Sequence 2641, Ap
c 139	11.8	56.2	25	6	US-10-956-160-188185	Sequence 188185, A	c 212	11.4	54.3	23	6	US-10-956-157-117342	Sequence 117342, A
c 140	11.8	56.2	25	6	US-10-956-160-196221	Sequence 196221, A	c 213	11.4	54.3	25	6	US-10-956-157-117358	Sequence 117358, A
c 141	11.8	56.2	25	6	US-10-956-160-198152	Sequence 198152, A	c 214	11.4	54.3	25	6	US-10-956-157-124450	Sequence 124450, A
c 142	11.8	56.2	25	6	US-10-956-160-198198	Sequence 198198, A	c 215	11.4	54.3	25	6	US-10-956-157-139796	Sequence 139796, A
c 143	11.8	56.2	25	6	US-10-956-160-199131	Sequence 199131, A	c 216	11.4	54.3	25	6	US-10-956-157-143574	Sequence 143574, A
c 144	11.6	55.2	20	6	US-10-831-286A-31266	Sequence 31266, A	c 217	11.4	54.3	25	6	US-10-956-157-147277	Sequence 147277, A
c 145	11.6	55.2	20	6	US-10-831-286A-41161	Sequence 41161, A	c 218	11.4	54.3	25	6	US-10-956-157-147360	Sequence 147360, A
c 146	11.6	55.2	20	6	US-10-831-286A-41771	Sequence 41771, A	c 219	11.4	54.3	25	6	US-10-956-157-160076	Sequence 160076, A
c 147	11.6	55.2	22	6	US-10-982-908-9	Sequence 9, Appl1	c 220	11.4	54.3	25	6	US-10-956-157-161592	Sequence 161592, A
c 148	11.6	55.2	25	6	US-10-956-157-96913	Sequence 96913, A	c 221	11.4	54.3	25	6	US-10-956-157-162125	Sequence 162125, A
c 149	11.6	55.2	25	6	US-10-956-157-96921	Sequence 96921, A	c 222	11.4	54.3	25	6	US-10-956-157-162212	Sequence 162212, A
c 150	11.6	55.2	25	6	US-10-956-157-96922	Sequence 96922, A	c 223	11.4	54.3	25	6	US-10-956-157-162275	Sequence 162275, A
c 151	11.6	55.2	25	6	US-10-956-157-96924	Sequence 96924, A	c 224	11.4	54.3	25	6	US-10-956-157-162757	Sequence 162757, A
c 152	11.6	55.2	25	6	US-10-956-157-96927	Sequence 96927, A	c 225	11.4	54.3	25	6	US-10-956-157-173874	Sequence 173874, A
c 153	11.6	55.2	25	6	US-10-956-157-119257	Sequence 119257, A	c 226	11.4	54.3	25	6	US-10-956-157-181911	Sequence 181911, A
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c 156	11.6	55.2	25	6	US-10-956-157-161796	Sequence 161796, A	c 229	11.4	54.3	25	6	US-10-956-157-224402	Sequence 224402, A
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c 161	11.6	55.2	25	6	US-10-956-157-205338	Sequence 205338, A	c 234	11.4	54.3	25	6	US-10-956-157-276531	Sequence 276531, A
c 162	11.6	55.2	25	6	US-10-956-157-230773	Sequence 230773, A	c 235	11.4	54.3	25	6	US-10-956-157-289404	Sequence 289404, A
c 163	11.6	55.2	25	6	US-10-956-157-244385	Sequence 244385, A	c 236	11.4	54.3	25	6	US-10-956-157-304429	Sequence 304429, A
c 164	11.6	55.2	25	6	US-10-956-157-294343	Sequence 294343, A	c 237	11.4	54.3	25	6	US-10-956-160-30509	Sequence 30509, A
c 165	11.6	55.2	25	6	US-10-956-157-294493	Sequence 294493, A	c 238	11.4	54.3	25	6	US-10-956-160-49063	Sequence 49063, A
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c 167	11.6	55.2	25	6	US-10-956-157-305232	Sequence 305232, A	c 240	11.4	54.3	25	6	US-10-956-160-56053	Sequence 56053, A
c 168	11.6	55.2	25	6	US-10-956-157-305233	Sequence 305233, A	c 241	11.4	54.3	25	6	US-10-956-160-93359	Sequence 93359, A
c 169	11.6	55.2	25	6	US-10-956-157-316420	Sequence 316420, A	c 242	11.4	54.3	25	6	US-10-956-160-103344	Sequence 103344, A
c 170	11.6	55.2	25	6	US-10-956-160-31988	Sequence 31988, A	c 243	11.4	54.3	25	6	US-10-956-160-118549	Sequence 118549, A
c 171	11.6	55.2	25	6	US-10-956-160-40448	Sequence 40448, A	c 244	11.4	54.3	25	6	US-10-956-160-118898	Sequence 118898, A

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c 246	11.4	54.3	25	6	US-10-956-160-124102	Sequence 124102,	c 319	11.2	53.3	25	6	US-10-956-160-122293	Sequence 122293,
c 247	11.4	54.3	25	6	US-10-956-160-141151	Sequence 141151,	c 320	11.2	53.3	25	6	US-10-956-160-146207	Sequence 146207,
248	11.4	54.3	25	6	US-10-956-160-153468	Sequence 153468,	c 321	11.2	53.3	25	6	US-10-956-160-153672	Sequence 153672,
249	11.4	54.3	25	6	US-10-956-160-162898	Sequence 162898,	c 322	11.2	53.3	25	6	US-10-956-160-158902	Sequence 158902,
250	11.4	54.3	25	6	US-10-956-160-180912	Sequence 180912,	c 323	11.2	53.3	25	6	US-10-956-160-163418	Sequence 163418,
251	11.4	54.3	25	6	US-10-956-160-206545	Sequence 206545,	c 324	11.2	53.3	25	6	US-10-956-160-172926	Sequence 172926,
c 252	11.4	54.3	44	5	US-09-749-280C-1766	Sequence 1766, Ap	c 325	11.2	53.3	25	6	US-10-956-160-178493	Sequence 178493,
253	11.2	53.3	17	6	US-10-722-939-562	Sequence 562, App	c 326	11.2	53.3	25	6	US-10-956-160-182311	Sequence 182311,
254	11.2	53.3	19	6	US-10-758-155-2672	Sequence 2672, Ap	c 327	11.2	53.3	25	6	US-10-956-160-201269	Sequence 201269,
255	11.2	53.3	19	6	US-10-758-155-2673	Sequence 2673, Ap	c 328	11.2	53.3	30	1	PCT-US03-40884-120	Sequence 120, App
256	11.2	53.3	19	6	US-10-758-155-2676	Sequence 2676, Ap	c 329	11.2	53.3	30	6	US-10-850-359-804	Sequence 804, App
257	11.2	53.3	19	6	US-10-758-155-2727	Sequence 2727, Ap	c 330	11.2	53.3	31	1	PCT-US04-36459-29	Sequence 29, Appl
258	11.2	53.3	19	6	US-10-844-076-2672	Sequence 2672, Ap	c 331	11.2	53.3	34	6	US-10-980-923-49	Sequence 49, Appl
259	11.2	53.3	19	6	US-10-844-076-2673	Sequence 2673, Ap	c 332	11.2	53.3	50	5	US-09-749-280C-1321	Sequence 1321, Ap
260	11.2	53.3	19	6	US-10-844-076-2726	Sequence 2726, Ap	c 333	11.2	53.3	50	5	US-09-749-280C-7567	Sequence 7567, Ap
261	11.2	53.3	19	6	US-10-844-076-2727	Sequence 2727, Ap	c 334	11.2	53.3	25	6	US-10-831-286A-669	Sequence 669, App
262	11.2	53.3	20	1	PCT-US04-31673-178	Sequence 178, App	c 335	11.2	52.4	20	6	US-10-831-286A-1263	Sequence 1263, Ap
c 263	11.2	53.3	20	1	PCT-US04-31673-260	Sequence 260, App	c 336	11.2	52.4	20	6	US-10-831-286A-12833	Sequence 12833, A
c 264	11.2	53.3	20	6	US-10-983-197-20	Sequence 20, Appl	c 337	11.2	52.4	21	6	US-10-831-286A-19297	Sequence 19297, A
265	11.2	53.3	23	6	US-10-758-155-977	Sequence 97, Appl	c 338	11.2	52.4	21	6	US-10-974-036-57	Sequence 57, Appl
266	11.2	53.3	23	6	US-10-758-155-2624	Sequence 2624, Ap	c 339	11.2	52.4	25	5	US-09-978-191B-240	Sequence 240, App
267	11.2	53.3	23	6	US-10-758-155-2625	Sequence 2625, Ap	c 340	11.2	52.4	25	5	US-09-999-829B-240	Sequence 240, App
268	11.2	53.3	23	6	US-10-844-076-2624	Sequence 2624, Ap	c 341	11.2	52.4	25	6	US-10-949-845-9	Sequence 9, Appl
269	11.2	53.3	23	6	US-10-844-076-2625	Sequence 2625, Ap	c 342	11.2	52.4	25	6	US-10-956-157-75183	Sequence 75183, A
c 270	11.2	53.3	25	6	US-10-956-157-12070	Sequence 12070, A	c 343	11.2	52.4	25	6	US-10-956-157-137600	Sequence 137600,
c 271	11.2	53.3	25	6	US-10-956-157-12071	Sequence 12071, A	c 344	11.2	52.4	25	6	US-10-956-157-138153	Sequence 138153,
c 272	11.2	53.3	25	6	US-10-956-157-23846	Sequence 23846, A	c 345	11.2	52.4	25	6	US-10-956-157-145300	Sequence 145300,
c 273	11.2	53.3	25	6	US-10-956-157-23847	Sequence 23847, A	c 346	11.2	52.4	25	6	US-10-956-157-146111	Sequence 146111,
c 274	11.2	53.3	25	6	US-10-956-157-23848	Sequence 23848, A	c 347	11.2	52.4	25	6	US-10-956-157-147417	Sequence 147417,
c 275	11.2	53.3	25	6	US-10-956-157-23850	Sequence 23850, A	c 348	11.2	52.4	25	6	US-10-956-157-151571	Sequence 151571,
c 276	11.2	53.3	25	6	US-10-956-157-23853	Sequence 23853, A	c 349	11.2	52.4	25	6	US-10-956-157-152484	Sequence 152484,
c 277	11.2	53.3	25	6	US-10-956-157-23854	Sequence 23854, A	c 350	11.2	52.4	25	6	US-10-956-157-153957	Sequence 153957,
c 278	11.2	53.3	25	6	US-10-956-157-23855	Sequence 23855, A	c 351	11.2	52.4	25	6	US-10-956-157-155291	Sequence 155291,
c 279	11.2	53.3	25	6	US-10-956-157-26136	Sequence 26136, A	c 352	11.2	52.4	25	6	US-10-956-157-155829	Sequence 155829,
c 280	11.2	53.3	25	6	US-10-956-157-47065	Sequence 47065, A	c 353	11.2	52.4	25	6	US-10-956-157-174958	Sequence 174958,
c 281	11.2	53.3	25	6	US-10-956-157-47069	Sequence 47069, A	c 354	11.2	52.4	25	6	US-10-956-157-175192	Sequence 175192,
c 282	11.2	53.3	25	6	US-10-956-157-47070	Sequence 47070, A	c 355	11.2	52.4	25	6	US-10-956-157-177162	Sequence 177162,
c 283	11.2	53.3	25	6	US-10-956-157-96925	Sequence 96925, A	c 356	11.2	52.4	25	6	US-10-956-157-193285	Sequence 193285,
c 284	11.2	53.3	25	6	US-10-956-157-148052	Sequence 148052, A	c 357	11.2	52.4	25	6	US-10-956-157-200982	Sequence 200982,
c 285	11.2	53.3	25	6	US-10-956-157-148625	Sequence 148625, A	c 358	11.2	52.4	25	6	US-10-956-157-201074	Sequence 201074,
c 286	11.2	53.3	25	6	US-10-956-157-160202	Sequence 160202, A	c 359	11.2	52.4	25	6	US-10-956-157-203344	Sequence 203344,
c 287	11.2	53.3	25	6	US-10-956-157-162383	Sequence 162383, A	c 360	11.2	52.4	25	6	US-10-956-157-205007	Sequence 205007,
c 288	11.2	53.3	25	6	US-10-956-157-163977	Sequence 163977, A	c 361	11.2	52.4	25	6	US-10-956-157-207341	Sequence 207341,
c 289	11.2	53.3	25	6	US-10-956-157-168316	Sequence 168316, A	c 362	11.2	52.4	25	6	US-10-956-157-208841	Sequence 208841,
c 290	11.2	53.3	25	6	US-10-956-157-178927	Sequence 178927, A	c 363	11.2	52.4	25	6	US-10-956-157-214398	Sequence 214398,
c 291	11.2	53.3	25	6	US-10-956-157-192006	Sequence 192006, A	c 364	11.2	52.4	25	6	US-10-956-157-214773	Sequence 214773,
c 292	11.2	53.3	25	6	US-10-956-157-196092	Sequence 196092, A	c 365	11.2	52.4	25	6	US-10-956-157-231676	Sequence 231676,
c 293	11.2	53.3	25	6	US-10-956-157-200732	Sequence 200732, A	c 366	11.2	52.4	25	6	US-10-956-157-257984	Sequence 257984,
c 294	11.2	53.3	25	6	US-10-956-157-201272	Sequence 201272, A	c 367	11.2	52.4	25	6	US-10-956-157-262762	Sequence 262762,
c 295	11.2	53.3	25	6	US-10-956-157-201626	Sequence 201626, A	c 368	11.2	52.4	25	6	US-10-956-157-269827	Sequence 269827,
c 296	11.2	53.3	25	6	US-10-956-157-203928	Sequence 203928, A	c 369	11.2	52.4	25	6	US-10-956-157-270897	Sequence 270897,
c 297	11.2	53.3	25	6	US-10-956-157-216988	Sequence 216988, A	c 370	11.2	52.4	25	6	US-10-956-157-277319	Sequence 277319,
c 298	11.2	53.3	25	6	US-10-956-157-225156	Sequence 225156, A	c 371	11.2	52.4	25	6	US-10-956-157-280569	Sequence 280569,
c 299	11.2	53.3	25	6	US-10-956-157-246877	Sequence 246877, A	c 372	11.2	52.4	25	6	US-10-956-157-280941	Sequence 280941,
c 300	11.2	53.3	25	6	US-10-956-157-253324	Sequence 253324, A	c 373	11.2	52.4	25	6	US-10-956-157-284400	Sequence 284400,
c 301	11.2	53.3	25	6	US-10-956-157-253325	Sequence 253325, A	c 374	11.2	52.4	25	6	US-10-956-157-297394	Sequence 297394,
c 302	11.2	53.3	25	6	US-10-956-157-258788	Sequence 258788, A	c 375	11.2	52.4	25	6	US-10-956-157-303659	Sequence 303659,
c 303	11.2	53.3	25	6	US-10-956-157-274693	Sequence 274693, A	c 376	11.2	52.4	25	6	US-10-956-157-308988	Sequence 308988,
c 304	11.2	53.3	25	6	US-10-956-157-279272	Sequence 279272, A	c 377	11.2	52.4	25	6	US-10-956-160-15623	Sequence 15623, A
c 305	11.2	53.3	25	6	US-10-956-157-295387	Sequence 295387, A	c 378	11.2	52.4	25	6	US-10-956-160-30099	Sequence 30099, A
c 306	11.2	53.3	25	6	US-10-956-157-311027	Sequence 311027, A	c 379	11.2	52.4	25	6	US-10-956-160-32887	Sequence 32887, A
c 307	11.2	53.3	25	6	US-10-956-157-312846	Sequence 312846, A	c 380	11.2	52.4	25	6	US-10-956-160-50447	Sequence 50447, A
c 308	11.2	53.3	25	6	US-10-956-160-8137	Sequence 8137, A	c 381	11.2	52.4	25	6	US-10-956-160-51728	Sequence 51728, A
c 309	11.2	53.3	25	6	US-10-956-160-21192	Sequence 21192, A	c 382	11.2	52.4	25	6	US-10-956-160-84133	Sequence 84133, A
c 310	11.2	53.3	25	6	US-10-956-160-65734	Sequence 65734, A	c 383	11.2	52.4	25	6	US-10-956-160-93380	Sequence 93380, A
c 311	11.2	53.3	25	6	US-10-956-160-79165	Sequence 79165, A	c 384	11.2	52.4	25	6	US-10-956-160-94808	Sequence 94808, A
c 312	11.2	53.3	25	6	US-10-956-160-81718	Sequence 81718, A	c 385	11.2	52.4	25	6	US-10-956-160-96740	Sequence 96740, A
c 313	11.2	53.3	25	6	US-10-956-160-83552	Sequence 83552, A	c 386	11.2	52.4	25	6	US-10-956-160-97797	Sequence 97797, A
c 314	11.2	53.3	25	6	US-10-956-160-90277	Sequence 90277, A	c 387	11.2	52.4	25	6	US-10-956-160-97798	Sequence 97798, A
c 315	11.2	53.3	25	6	US-10-956-160-94263	Sequence 94263, A	c 388	11.2	52.4	25	6	US-10-956-160-98480	Sequence 98480, A
c 316	11.2	53.3	25	6	US-10-956-160-102330	Sequence 102330, A	c 389	11.2	52.4	25	6	US-10-956-160-98604	Sequence 98604, A
c 317	11.2	53.3	25	6	US-10-956-160-114535	Sequence 114535, A	c 390	11.2	52.4	25	6	US-10-956-160-98605	Sequence 98605, A

C 391	11	52.4	25	6	US-10-956-160-98606	Sequence 98606, A	464	10.8	51.4	25	6	US-10-956-157-193252	Sequence 193252,
C 392	11	52.4	25	6	US-10-956-160-98607	Sequence 98607, A	465	10.8	51.4	25	6	US-10-956-157-194420	Sequence 194420,
C 393	11	52.4	25	6	US-10-956-160-98608	Sequence 98608, A	466	10.8	51.4	25	6	US-10-956-157-196259	Sequence 196259,
C 394	11	52.4	25	6	US-10-956-160-101751	Sequence 101751, A	467	10.8	51.4	25	6	US-10-956-157-201288	Sequence 201288,
C 395	11	52.4	25	6	US-10-956-160-102229	Sequence 102229, A	468	10.8	51.4	25	6	US-10-956-157-205552	Sequence 205552,
C 396	11	52.4	25	6	US-10-956-160-104627	Sequence 104627, A	469	10.8	51.4	25	6	US-10-956-157-214056	Sequence 214056,
C 397	11	52.4	25	6	US-10-956-160-107005	Sequence 107005, A	470	10.8	51.4	25	6	US-10-956-157-217138	Sequence 217138,
C 398	11	52.4	25	6	US-10-956-160-117634	Sequence 117634, A	471	10.8	51.4	25	6	US-10-956-157-217634	Sequence 217634,
C 399	11	52.4	25	6	US-10-956-160-119178	Sequence 119178, A	472	10.8	51.4	25	6	US-10-956-157-224207	Sequence 224207,
C 400	11	52.4	25	6	US-10-956-160-120220	Sequence 120220, A	473	10.8	51.4	25	6	US-10-956-157-227296	Sequence 227296,
C 401	11	52.4	25	6	US-10-956-160-122819	Sequence 122819, A	474	10.8	51.4	25	6	US-10-956-157-240209	Sequence 240209,
C 402	11	52.4	25	6	US-10-956-160-126186	Sequence 126186, A	475	10.8	51.4	25	6	US-10-956-157-241988	Sequence 241988,
C 403	11	52.4	25	6	US-10-956-160-154980	Sequence 154980, A	476	10.8	51.4	25	6	US-10-956-157-250072	Sequence 250072,
C 404	11	52.4	25	6	US-10-956-160-159142	Sequence 159142, A	477	10.8	51.4	25	6	US-10-956-157-253502	Sequence 253502,
C 405	11	52.4	25	6	US-10-956-160-160524	Sequence 160524, A	478	10.8	51.4	25	6	US-10-956-157-256536	Sequence 256536,
C 406	11	52.4	25	6	US-10-956-160-162313	Sequence 162313, A	479	10.8	51.4	25	6	US-10-956-157-258672	Sequence 258672,
C 407	11	52.4	25	6	US-10-956-160-176908	Sequence 176908, A	480	10.8	51.4	25	6	US-10-956-157-270531	Sequence 270531,
C 408	11	52.4	25	6	US-10-956-160-183950	Sequence 183950, A	481	10.8	51.4	25	6	US-10-956-157-272169	Sequence 272169,
C 409	11	52.4	25	6	US-10-956-160-193871	Sequence 193871, A	482	10.8	51.4	25	6	US-10-956-157-272170	Sequence 272170,
C 410	11	52.4	25	6	US-10-956-160-196415	Sequence 196415, A	483	10.8	51.4	25	6	US-10-956-157-272170	Sequence 272170,
C 411	11	52.4	25	6	US-10-956-160-199284	Sequence 199284, A	484	10.8	51.4	25	6	US-10-956-157-275233	Sequence 275233,
C 412	11	52.4	25	6	US-10-977-537-9	Sequence 9, Appl	485	10.8	51.4	25	6	US-10-956-157-303152	Sequence 303152,
C 413	11	52.4	30	6	US-10-831-286A-25841	Sequence 25841, A	486	10.8	51.4	25	6	US-10-956-157-303718	Sequence 303718,
C 414	11	52.4	38	6	US-10-951-303-4562	Sequence 4562, Ap	487	10.8	51.4	25	6	US-10-956-157-303961	Sequence 303961,
C 415	11	52.4	46	6	US-10-949-845-11	Sequence 11, Appl	488	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 416	11	52.4	46	6	US-10-977-537-11	Sequence 11, Appl	489	10.8	51.4	25	6	US-10-956-160-16722	Sequence 16722, A
C 417	11	52.4	50	5	US-09-978-191B-344	Sequence 344, App	490	10.8	51.4	25	6	US-10-956-160-17376	Sequence 21736, A
C 418	11	52.4	50	5	US-09-999-829B-344	Sequence 344, App	491	10.8	51.4	25	6	US-10-956-160-43070	Sequence 43070, A
C 419	11	52.4	50	5	US-09-749-280C-5306	Sequence 5306, Ap	492	10.8	51.4	25	6	US-10-956-160-51153	Sequence 51153, A
C 420	11	52.4	50	5	US-09-749-280C-5341	Sequence 5341, Ap	493	10.8	51.4	25	6	US-10-956-160-56193	Sequence 56193, A
C 421	11	52.4	50	5	US-09-749-280C-5342	Sequence 5342, Ap	494	10.8	51.4	25	6	US-10-956-160-56193	Sequence 56193, A
C 422	10.8	51.4	20	6	US-10-866-013-23	Sequence 23, Appl	495	10.8	51.4	25	6	US-10-956-160-57203	Sequence 57203, A
C 423	10.8	51.4	20	6	US-10-831-286A-26110	Sequence 26110, A	496	10.8	51.4	25	6	US-10-956-160-65414	Sequence 65414, A
C 424	10.8	51.4	20	6	US-10-831-286A-26751	Sequence 26751, A	497	10.8	51.4	25	6	US-10-956-160-65414	Sequence 65414, A
C 425	10.8	51.4	20	6	US-10-831-286A-26839	Sequence 26839, A	498	10.8	51.4	25	6	US-10-956-160-76430	Sequence 76430, A
C 426	10.8	51.4	20	6	US-10-831-286A-26849	Sequence 26849, A	499	10.8	51.4	25	6	US-10-956-160-85344	Sequence 85344, A
C 427	10.8	51.4	20	6	US-10-831-286A-27400	Sequence 27400, A	500	10.8	51.4	25	6	US-10-956-160-85795	Sequence 85795, A
C 428	10.8	51.4	20	6	US-10-831-286A-43362	Sequence 43362, A	501	10.8	51.4	25	6	US-10-956-160-86054	Sequence 86054, A
C 429	10.8	51.4	21	6	US-10-475-021A-10	Sequence 10, Appl	502	10.8	51.4	25	6	US-10-956-160-88746	Sequence 88746, A
C 430	10.8	51.4	25	6	US-10-956-157-12053	Sequence 12053, A	503	10.8	51.4	25	6	US-10-956-160-102131	Sequence 102131, A
C 431	10.8	51.4	25	6	US-10-956-157-36136	Sequence 36136, A	504	10.8	51.4	25	6	US-10-956-160-120377	Sequence 120377, A
C 432	10.8	51.4	25	6	US-10-956-157-36137	Sequence 36137, A	505	10.8	51.4	25	6	US-10-956-160-126066	Sequence 126066, A
C 433	10.8	51.4	25	6	US-10-956-157-36140	Sequence 36140, A	506	10.8	51.4	25	6	US-10-956-160-141593	Sequence 141593, A
C 434	10.8	51.4	25	6	US-10-956-157-36145	Sequence 36145, A	507	10.8	51.4	25	6	US-10-956-160-142129	Sequence 142129, A
C 435	10.8	51.4	25	6	US-10-956-157-36149	Sequence 36149, A	508	10.8	51.4	25	6	US-10-956-160-146713	Sequence 146713, A
C 436	10.8	51.4	25	6	US-10-956-157-48971	Sequence 48971, A	509	10.8	51.4	25	6	US-10-956-160-148410	Sequence 148410, A
C 437	10.8	51.4	25	6	US-10-956-157-57473	Sequence 57473, A	510	10.8	51.4	25	6	US-10-956-160-150908	Sequence 150908, A
C 438	10.8	51.4	25	6	US-10-956-157-85669	Sequence 85669, A	511	10.8	51.4	25	6	US-10-956-160-153316	Sequence 153316, A
C 439	10.8	51.4	25	6	US-10-956-157-85670	Sequence 85670, A	512	10.8	51.4	25	6	US-10-956-160-157938	Sequence 157938, A
C 440	10.8	51.4	25	6	US-10-956-157-85671	Sequence 85671, A	513	10.8	51.4	25	6	US-10-956-160-158135	Sequence 158135, A
C 441	10.8	51.4	25	6	US-10-956-157-118986	Sequence 118986, A	514	10.8	51.4	25	6	US-10-956-160-163029	Sequence 163029, A
C 442	10.8	51.4	25	6	US-10-956-157-118987	Sequence 118987, A	515	10.8	51.4	25	6	US-10-956-160-167945	Sequence 167945, A
C 443	10.8	51.4	25	6	US-10-956-157-118989	Sequence 118989, A	516	10.8	51.4	25	6	US-10-956-160-169286	Sequence 169286, A
C 444	10.8	51.4	25	6	US-10-956-157-118993	Sequence 118993, A	517	10.8	51.4	25	6	US-10-956-160-180507	Sequence 180507, A
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C 450	10.8	51.4	25	6	US-10-956-157-135681	Sequence 135681, A	523	10.8	51.4	25	6	US-10-956-160-196233	Sequence 196233, A
C 451	10.8	51.4	25	6	US-10-956-157-136376	Sequence 136376, A	524	10.8	51.4	25	6	US-10-956-160-197948	Sequence 197948, A
C 452	10.8	51.4	25	6	US-10-956-157-145876	Sequence 145876, A	525	10.8	51.4	25	6	US-10-956-160-198670	Sequence 198670, A
C 453	10.8	51.4	25	6	US-10-956-157-150696	Sequence 150696, A	526	10.8	51.4	26	6	US-10-956-160-208119	Sequence 208119, A
C 454	10.8	51.4	25	6	US-10-956-157-151852	Sequence 151852, A	527	10.8	51.4	30	6	US-10-343-436-57	Sequence 57, Appl
C 455	10.8	51.4	25	6	US-10-956-157-154184	Sequence 154184, A	528	10.8	51.4	31	6	US-10-723-518-84	Sequence 84, Appl
C 456	10.8	51.4	25	6	US-10-956-157-154489	Sequence 154489, A	529	10.8	51.4	31	6	US-10-722-939-180	Sequence 180, App
C 457	10.8	51.4	25	6	US-10-956-157-159152	Sequence 159152, A	530	10.8	51.4	34	6	US-10-722-939-182	Sequence 182, App
C 458	10.8	51.4	25	6	US-10-956-157-161595	Sequence 161595, A	531	10.8	51.4	35	6	US-10-635-265B-19	Sequence 19, Appl
C 459	10.8	51.4	25	6	US-10-956-157-165543	Sequence 165543, A	532	10.8	51.4	35	6	US-10-511-341-173	Sequence 173, App
C 460	10.8	51.4	25	6	US-10-956-157-166073	Sequence 166073, A	533	10.8	51.4	38	5	US-10-511-341-174	Sequence 174, App
C 461	10.8	51.4	25	6	US-10-956-157-175084	Sequence 175084, A	534	10.8	51.4	39	6	US-09-610-313B-42	Sequence 42, Appl
C 462	10.8	51.4	25	6	US-10-956-157-185652	Sequence 185652, A	535	10.8	51.4	39	6	US-10-842-032-37	Sequence 37, Appl
C 463	10.8	51.4	25	6	US-10-956-157-192676	Sequence 192676, A	536	10.8	51.4	50	5	US-09-749-280C-6889	Sequence 6889, Ap

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538	10.6	50.5	19	6	US-10-758-155-2264	Sequence 2264, Ap	c 611	10.6	50.5	21	6	US-10-758-155-2508	Sequence 2508, Ap
539	10.6	50.5	19	6	US-10-758-155-2265	Sequence 2265, Ap	c 612	10.6	50.5	21	6	US-10-758-155-2509	Sequence 2509, Ap
540	10.6	50.5	19	6	US-10-758-155-2662	Sequence 2662, Ap	c 613	10.6	50.5	21	6	US-10-844-076-2275	Sequence 2275, Ap
541	10.6	50.5	19	6	US-10-758-155-2663	Sequence 2663, Ap	c 614	10.6	50.5	21	6	US-10-844-076-2278	Sequence 2278, Ap
542	10.6	50.5	19	6	US-10-758-155-2664	Sequence 2664, Ap	c 615	10.6	50.5	21	6	US-10-844-076-2373	Sequence 2373, Ap
543	10.6	50.5	19	6	US-10-758-155-2665	Sequence 2665, Ap	c 616	10.6	50.5	21	6	US-10-844-076-2374	Sequence 2374, Ap
544	10.6	50.5	19	6	US-10-758-155-2728	Sequence 2728, Ap	c 617	10.6	50.5	21	6	US-10-844-076-2385	Sequence 2385, Ap
545	10.6	50.5	19	6	US-10-758-155-2729	Sequence 2729, Ap	c 618	10.6	50.5	21	6	US-10-844-076-2386	Sequence 2386, Ap
546	10.6	50.5	19	6	US-10-758-155-2730	Sequence 2730, Ap	c 619	10.6	50.5	21	6	US-10-844-076-2449	Sequence 2449, Ap
547	10.6	50.5	19	6	US-10-758-155-2731	Sequence 2731, Ap	c 620	10.6	50.5	21	6	US-10-844-076-2451	Sequence 2451, Ap
548	10.6	50.5	19	6	US-10-758-155-2734	Sequence 2734, Ap	c 621	10.6	50.5	21	6	US-10-844-076-2453	Sequence 2453, Ap
549	10.6	50.5	19	6	US-10-758-155-2735	Sequence 2735, Ap	c 622	10.6	50.5	21	6	US-10-844-076-2455	Sequence 2455, Ap
550	10.6	50.5	19	6	US-10-758-155-2736	Sequence 2736, Ap	c 623	10.6	50.5	21	6	US-10-844-076-2496	Sequence 2496, Ap
551	10.6	50.5	19	6	US-10-758-155-2737	Sequence 2737, Ap	c 624	10.6	50.5	21	6	US-10-844-076-2497	Sequence 2497, Ap
552	10.6	50.5	19	6	US-10-844-076-2244	Sequence 2244, Ap	c 625	10.6	50.5	21	6	US-10-844-076-2500	Sequence 2500, Ap
553	10.6	50.5	19	6	US-10-844-076-2264	Sequence 2264, Ap	c 626	10.6	50.5	21	6	US-10-844-076-2501	Sequence 2501, Ap
554	10.6	50.5	19	6	US-10-844-076-2265	Sequence 2265, Ap	c 627	10.6	50.5	21	6	US-10-844-076-2504	Sequence 2504, Ap
555	10.6	50.5	19	6	US-10-844-076-2266	Sequence 2266, Ap	c 628	10.6	50.5	21	6	US-10-844-076-2505	Sequence 2505, Ap
556	10.6	50.5	19	6	US-10-844-076-2663	Sequence 2663, Ap	c 629	10.6	50.5	21	6	US-10-844-076-2508	Sequence 2508, Ap
557	10.6	50.5	19	6	US-10-844-076-2664	Sequence 2664, Ap	c 630	10.6	50.5	21	6	US-10-844-076-2509	Sequence 2509, Ap
558	10.6	50.5	19	6	US-10-844-076-2665	Sequence 2665, Ap	c 631	10.6	50.5	21	8	US-60-522-459-10675	Sequence 10675, A
559	10.6	50.5	19	6	US-10-844-076-2728	Sequence 2728, Ap	c 632	10.6	50.5	23	6	US-10-758-155-2572	Sequence 2572, Ap
560	10.6	50.5	19	6	US-10-844-076-2729	Sequence 2729, Ap	c 633	10.6	50.5	23	6	US-10-758-155-2573	Sequence 2573, Ap
561	10.6	50.5	19	6	US-10-844-076-2730	Sequence 2730, Ap	c 634	10.6	50.5	23	6	US-10-758-155-2574	Sequence 2574, Ap
562	10.6	50.5	19	6	US-10-844-076-2731	Sequence 2731, Ap	c 635	10.6	50.5	23	6	US-10-758-155-2575	Sequence 2575, Ap
563	10.6	50.5	19	6	US-10-844-076-2734	Sequence 2734, Ap	c 636	10.6	50.5	23	6	US-10-758-155-2578	Sequence 2578, Ap
564	10.6	50.5	19	6	US-10-844-076-2735	Sequence 2735, Ap	c 637	10.6	50.5	23	6	US-10-758-155-2579	Sequence 2579, Ap
565	10.6	50.5	19	6	US-10-844-076-2736	Sequence 2736, Ap	c 638	10.6	50.5	23	6	US-10-758-155-2580	Sequence 2580, Ap
566	10.6	50.5	19	6	US-10-844-076-2737	Sequence 2737, Ap	c 639	10.6	50.5	23	6	US-10-758-155-2581	Sequence 2581, Ap
567	10.6	50.5	19	6	US-10-883-218-142	Sequence 142, App	c 640	10.6	50.5	23	6	US-10-758-155-2584	Sequence 2584, Ap
c 568	10.6	50.5	19	6	US-10-883-218-144	Sequence 544, App	c 641	10.6	50.5	23	6	US-10-758-155-2585	Sequence 2585, Ap
569	10.6	50.5	19	8	PCT-US04-3622B-799	Sequence 6349, App	c 642	10.6	50.5	23	6	US-10-758-155-2586	Sequence 2586, Ap
570	10.6	50.5	20	1	PCT-US04-36220-150	Sequence 150, App	c 643	10.6	50.5	23	6	US-10-758-155-2587	Sequence 2587, Ap
c 571	10.6	50.5	20	1	PCT-US04-36220-250	Sequence 250, App	c 644	10.6	50.5	23	6	US-10-758-155-2628	Sequence 2628, Ap
c 572	10.6	50.5	20	6	US-10-832-622B-458	Sequence 458, App	c 645	10.6	50.5	23	6	US-10-758-155-2634	Sequence 2634, Ap
c 573	10.6	50.5	20	6	US-10-832-622B-799	Sequence 799, App	c 646	10.6	50.5	23	6	US-10-758-155-2640	Sequence 2640, Ap
c 574	10.6	50.5	20	6	US-10-831-286A-1718	Sequence 1718, Ap	c 647	10.6	50.5	23	6	US-10-758-155-2644	Sequence 2644, Ap
575	10.6	50.5	20	6	US-10-831-286A-1809	Sequence 2809, Ap	c 648	10.6	50.5	23	6	US-10-758-155-2645	Sequence 2645, Ap
576	10.6	50.5	20	6	US-10-831-286A-1841	Sequence 2841, Ap	c 649	10.6	50.5	23	6	US-10-758-155-2646	Sequence 2646, Ap
577	10.6	50.5	20	6	US-10-831-286A-1842	Sequence 2842, Ap	c 650	10.6	50.5	23	6	US-10-758-155-2647	Sequence 2647, Ap
c 578	10.6	50.5	20	6	US-10-831-286A-1808	Sequence 1808, Ap	c 651	10.6	50.5	23	6	US-10-844-076-2572	Sequence 2572, Ap
c 579	10.6	50.5	20	6	US-10-831-286A-13083	Sequence 13083, A	c 652	10.6	50.5	23	6	US-10-844-076-2573	Sequence 2573, Ap
c 580	10.6	50.5	20	6	US-10-831-286A-15681	Sequence 15681, A	c 653	10.6	50.5	23	6	US-10-844-076-2574	Sequence 2574, Ap
c 581	10.6	50.5	20	6	US-10-831-286A-15901	Sequence 15901, A	c 654	10.6	50.5	23	6	US-10-844-076-2575	Sequence 2575, Ap
c 582	10.6	50.5	20	6	US-10-831-286A-18066	Sequence 18066, A	c 655	10.6	50.5	23	6	US-10-844-076-2578	Sequence 2578, Ap
c 583	10.6	50.5	20	6	US-10-831-286A-19336	Sequence 19336, A	c 656	10.6	50.5	23	6	US-10-844-076-2579	Sequence 2579, Ap
c 584	10.6	50.5	20	6	US-10-831-286A-19685	Sequence 19685, A	c 657	10.6	50.5	23	6	US-10-844-076-2580	Sequence 2580, Ap
c 585	10.6	50.5	20	6	US-10-831-286A-21033	Sequence 21033, A	c 658	10.6	50.5	23	6	US-10-844-076-2581	Sequence 2581, Ap
c 586	10.6	50.5	20	6	US-10-831-286A-23026	Sequence 23026, A	c 659	10.6	50.5	23	6	US-10-844-076-2584	Sequence 2584, Ap
c 587	10.6	50.5	20	6	US-10-831-286A-25726	Sequence 25726, A	c 660	10.6	50.5	23	6	US-10-844-076-2585	Sequence 2585, Ap
c 588	10.6	50.5	20	6	US-10-831-286A-28548	Sequence 28548, A	c 661	10.6	50.5	23	6	US-10-844-076-2586	Sequence 2586, Ap
c 589	10.6	50.5	20	6	US-10-831-286A-28949	Sequence 28949, A	c 662	10.6	50.5	23	6	US-10-844-076-2587	Sequence 2587, Ap
c 590	10.6	50.5	20	6	US-10-831-286A-33684	Sequence 33684, A	c 663	10.6	50.5	23	6	US-10-844-076-2628	Sequence 2628, Ap
c 591	10.6	50.5	20	6	US-10-831-286A-36335	Sequence 36335, A	c 664	10.6	50.5	23	6	US-10-844-076-2634	Sequence 2634, Ap
c 592	10.6	50.5	20	6	US-10-831-286A-39705	Sequence 39705, A	c 665	10.6	50.5	23	6	US-10-844-076-2640	Sequence 2640, Ap
c 593	10.6	50.5	20	6	US-10-980-002-150	Sequence 150, App	c 666	10.6	50.5	23	6	US-10-844-076-2644	Sequence 2644, Ap
c 594	10.6	50.5	20	6	US-10-980-002-250	Sequence 250, App	c 667	10.6	50.5	23	6	US-10-844-076-2645	Sequence 2645, Ap
c 595	10.6	50.5	21	6	US-10-758-155-2275	Sequence 2275, Ap	c 668	10.6	50.5	23	6	US-10-844-076-2646	Sequence 2646, Ap
c 596	10.6	50.5	21	6	US-10-758-155-2278	Sequence 2278, Ap	c 669	10.6	50.5	23	6	US-10-844-076-2647	Sequence 2647, Ap
c 597	10.6	50.5	21	6	US-10-758-155-2373	Sequence 2373, Ap	c 670	10.6	50.5	25	6	US-10-956-157-12877	Sequence 12877, A
c 598	10.6	50.5	21	6	US-10-758-155-2374	Sequence 2374, Ap	c 671	10.6	50.5	25	6	US-10-956-157-13409	Sequence 13409, A
c 599	10.6	50.5	21	6	US-10-758-155-2386	Sequence 2386, Ap	c 672	10.6	50.5	25	6	US-10-956-157-13412	Sequence 13412, A
c 600	10.6	50.5	21	6	US-10-758-155-2386	Sequence 2386, Ap	c 673	10.6	50.5	25	6	US-10-956-157-13420	Sequence 13420, A
c 601	10.6	50.5	21	6	US-10-758-155-2449	Sequence 2449, Ap	c 674	10.6	50.5	25	6	US-10-956-157-28654	Sequence 28654, A
c 602	10.6	50.5	21	6	US-10-758-155-2451	Sequence 2451, Ap	c 675	10.6	50.5	25	6	US-10-956-157-28657	Sequence 28657, A
c 603	10.6	50.5	21	6	US-10-758-155-2453	Sequence 2453, Ap	c 676	10.6	50.5	25	6	US-10-956-157-28663	Sequence 28663, A
c 604	10.6	50.5	21	6	US-10-758-155-2455	Sequence 2455, Ap	c 677	10.6	50.5	25	6	US-10-956-157-47923	Sequence 47923, A
c 605	10.6	50.5	21	6	US-10-758-155-2496	Sequence 2496, Ap	c 678	10.6	50.5	25	6	US-10-956-157-47924	Sequence 47924, A
c 606	10.6	50.5	21	6	US-10-758-155-2497	Sequence 2497, Ap	c 679	10.6	50.5	25	6	US-10-956-157-47926	Sequence 47926, A
c 607	10.6	50.5	21	6	US-10-758-155-2500	Sequence 2500, Ap	c 680	10.6	50.5	25	6	US-10-956-157-47930	Sequence 47930, A
c 608	10.6	50.5	21	6	US-10-758-155-2501	Sequence 2501, Ap	c 681	10.6	50.5	25	6	US-10-956-157-47934	Sequence 47934, A
c 609	10.6	50.5	21	6	US-10-758-155-2504	Sequence 2504, Ap	c 682	10.6	50.5	25	6	US-10-956-157-70289	Sequence 70289, A

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684	10.6	50.5	25	6	US-10-956-157-87786	Sequence 87786, A	757	10.6	50.5	25	6	US-10-956-160-44931	Sequence 44931, A
685	10.6	50.5	25	6	US-10-956-157-110900	Sequence 110900, A	c 758	10.6	50.5	25	6	US-10-956-160-48439	Sequence 48439, A
686	10.6	50.5	25	6	US-10-956-157-123848	Sequence 123848, A	c 759	10.6	50.5	25	6	US-10-956-160-48473	Sequence 48473, A
687	10.6	50.5	25	6	US-10-956-157-124026	Sequence 124026, A	c 760	10.6	50.5	25	6	US-10-956-160-49958	Sequence 49958, A
688	10.6	50.5	25	6	US-10-956-157-132216	Sequence 132216, A	c 761	10.6	50.5	25	6	US-10-956-160-53597	Sequence 53597, A
689	10.6	50.5	25	6	US-10-956-157-137378	Sequence 137378, A	c 762	10.6	50.5	25	6	US-10-956-160-53597	Sequence 53597, A
690	10.6	50.5	25	6	US-10-956-157-137607	Sequence 137607, A	c 763	10.6	50.5	25	6	US-10-956-160-57918	Sequence 57918, A
691	10.6	50.5	25	6	US-10-956-157-143108	Sequence 143108, A	c 764	10.6	50.5	25	6	US-10-956-160-57914	Sequence 57914, A
692	10.6	50.5	25	6	US-10-956-157-145092	Sequence 145092, A	c 765	10.6	50.5	25	6	US-10-956-160-61413	Sequence 61413, A
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694	10.6	50.5	25	6	US-10-956-157-158730	Sequence 158730, A	c 767	10.6	50.5	25	6	US-10-956-160-65934	Sequence 65934, A
695	10.6	50.5	25	6	US-10-956-157-159262	Sequence 159262, A	c 768	10.6	50.5	25	6	US-10-956-160-68626	Sequence 68626, A
696	10.6	50.5	25	6	US-10-956-157-160511	Sequence 160511, A	c 769	10.6	50.5	25	6	US-10-956-160-68627	Sequence 68627, A
697	10.6	50.5	25	6	US-10-956-157-162472	Sequence 162472, A	c 770	10.6	50.5	25	6	US-10-956-160-68628	Sequence 68628, A
698	10.6	50.5	25	6	US-10-956-157-166249	Sequence 166249, A	c 771	10.6	50.5	25	6	US-10-956-160-72202	Sequence 72202, A
699	10.6	50.5	25	6	US-10-956-157-168650	Sequence 168650, A	c 772	10.6	50.5	25	6	US-10-956-160-81656	Sequence 81656, A
700	10.6	50.5	25	6	US-10-956-157-170232	Sequence 170232, A	c 773	10.6	50.5	25	6	US-10-956-160-87637	Sequence 87637, A
701	10.6	50.5	25	6	US-10-956-157-172957	Sequence 172957, A	c 774	10.6	50.5	25	6	US-10-956-160-88908	Sequence 88908, A
702	10.6	50.5	25	6	US-10-956-157-175563	Sequence 175563, A	c 775	10.6	50.5	25	6	US-10-956-160-95702	Sequence 95702, A
703	10.6	50.5	25	6	US-10-956-157-175857	Sequence 175857, A	c 776	10.6	50.5	25	6	US-10-956-160-100228	Sequence 100228, A
704	10.6	50.5	25	6	US-10-956-157-177494	Sequence 177494, A	c 777	10.6	50.5	25	6	US-10-956-160-100228	Sequence 100228, A
705	10.6	50.5	25	6	US-10-956-157-178675	Sequence 178675, A	c 778	10.6	50.5	25	6	US-10-956-160-101026	Sequence 101026, A
706	10.6	50.5	25	6	US-10-956-157-178796	Sequence 178796, A	c 779	10.6	50.5	25	6	US-10-956-160-102057	Sequence 102057, A
707	10.6	50.5	25	6	US-10-956-157-188344	Sequence 188344, A	c 780	10.6	50.5	25	6	US-10-956-160-102057	Sequence 102057, A
708	10.6	50.5	25	6	US-10-956-157-192392	Sequence 192392, A	c 781	10.6	50.5	25	6	US-10-956-160-106949	Sequence 106949, A
709	10.6	50.5	25	6	US-10-956-157-193555	Sequence 193555, A	c 782	10.6	50.5	25	6	US-10-956-160-119693	Sequence 119693, A
710	10.6	50.5	25	6	US-10-956-157-196952	Sequence 196952, A	c 783	10.6	50.5	25	6	US-10-956-160-127931	Sequence 127931, A
711	10.6	50.5	25	6	US-10-956-157-197133	Sequence 197133, A	c 784	10.6	50.5	25	6	US-10-956-160-133352	Sequence 133352, A
712	10.6	50.5	25	6	US-10-956-157-197606	Sequence 197606, A	c 785	10.6	50.5	25	6	US-10-956-160-137086	Sequence 137086, A
713	10.6	50.5	25	6	US-10-956-157-199492	Sequence 199492, A	c 786	10.6	50.5	25	6	US-10-956-160-138103	Sequence 138103, A
714	10.6	50.5	25	6	US-10-956-157-199497	Sequence 199497, A	c 787	10.6	50.5	25	6	US-10-956-160-138350	Sequence 138350, A
715	10.6	50.5	25	6	US-10-956-157-200173	Sequence 200173, A	c 788	10.6	50.5	25	6	US-10-956-160-138558	Sequence 138558, A
716	10.6	50.5	25	6	US-10-956-157-201523	Sequence 201523, A	c 789	10.6	50.5	25	6	US-10-956-160-140100	Sequence 140100, A
717	10.6	50.5	25	6	US-10-956-157-202585	Sequence 202585, A	c 790	10.6	50.5	25	6	US-10-956-160-141731	Sequence 141731, A
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ALIGNMENTS

RESULT 1
US-10-956-157-281467/c
; Sequence 281467, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 281467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-281467
Query Match 71.4%; Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACT 18
Db 23 GCATGCCAGATTACT 9

RESULT 2
US-10-956-160-158095
; Sequence 158095, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158095
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-158095
Query Match 70.5%; Score 14.8; DB 6; Length 25;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACTG 19
Db 2 GAGCGTGCAGATTACTG 19

RESULT 3
US-10-956-160-158096
; Sequence 158096, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-158096
Query Match 70.5%; Score 14.8; DB 6; Length 25;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACTG 19
Db 2 GAGCGTGCAGATTACTG 19

RESULT 4
US-10-956-157-209367/c
; Sequence 209367, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209367
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-209367
Query Match 65.7%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGG 20
Db 25 GCATGCCAGATTACTGG 9

RESULT 5
US-10-956-160-164697
; Sequence 164697, Application US/10956160
```



```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 164697
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-10-956-160-164697

Query Match      65.7%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGGC 21
   |||||
Db 9 CAAGCCAGATTGCTGGC 25

RESULT 6
US-10-956-157-288293/c
; Sequence 288293, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 288293
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-288293

Query Match      64.8%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGGC 21
   |||||
Db 21 GTGCATGCCAGACAGCTGGC 2

RESULT 7
US-10-956-160-119577
; Sequence 119577, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 119577
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-10-956-160-119577

Query Match      64.8%; Score 13.6; DB 6; Length 25;
```

```
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGG 20
   |||||
Db 2 AGCGCATGCTGGATTGTGG 21

RESULT 8
US-10-956-157-150549/c
; Sequence 150549, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 150549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-150549

Query Match      62.9%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21
   |||||
Db 24 GCATGCCAGACAGCTGGC 7

RESULT 9
US-10-956-160-44697/c
; Sequence 44697, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 44697
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-10-956-160-44697

Query Match      62.9%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21
   |||||
Db 23 GCAGGCCAAATTAATGGC 6

RESULT 10
US-10-956-160-179056
; Sequence 179056, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
```

```

; CURRENT APPLICATION NUMBER: US/10/956,160
;
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-179056

```

Query Match 62.9%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. NO. 5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21
||| ||| ||| ||| ||| |||
db 2 GCCTGACAGGGTTACTGGC 19

```

RESULT 11
US-10-956-160-109185
; Sequence 109185, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: wyeth
; APPLICANT: Mounste, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: MODELS OF INFLAMMA
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 109185.
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-109185

```

```
Query Match      61.9%; Score 13; DB 6; Length 25;
Best Local Similarity 76.2%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

Qy 1 AGCGCATGCCAGATTACTGGC 21
||| ||| | | | | |
3 AGCAGATGACTGCTCCTGGC 23

```

RESULT 12
US-10-956-157-85795
; Sequence 85795, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAY
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 1010
; CURRENT APPLICATION NUMBER: US/10/956,
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85795
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-85795

```

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy
d**b**

4 GCATGCCAGATTACTG 19
8 GTATTCCAGATTACTG 23

RESULT 13

```

US-10-956-157-85796
? Sequence 85796, Application US/10956157
? GENERAL INFORMATION:
? APPLICANT: Wyeth
? APPLICANT: Mounds, William
? TITLE OF INVENTION: NUCLEIC ACID ARRAY
? TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
? FILE REFERENCE: 031896-043000 (AM 1010)
? CURRENT APPLICATION NUMBER: US/10/956,
? CURRENT FILING DATE: 2004-10-04
? NUMBER OF SEQ ID NOS: 319805
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 85796
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Probe Sequence
US-10-956-157-85796

```

```
Query Match          61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
Db 10 GTATTCCAGATTACTG 25

RESULT 14

```

RES001 14
US-10-956-157-85797
; Sequence 85797, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAY
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 1010
; CURRENT APPLICATION NUMBER: US/10/956,
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85797
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-85797

```

```
Query Match      61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
pb 9 GTATTCCAGATTACTG 24

PERMITTEE: 15

```
RES001 15
US-10-956-157-85802
? Sequence 85802, Application US/10956157
? GENERAL INFORMATION:
? APPLICANT: Wyeth
? APPLICANT: Wyeth
? APPLICANT: Mounts, William
? TITLE OF INVENTION: NUCLEIC ACID ARRAY
? TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
? FILE REFERENCE: 031896-043000 (AM 1010)
? CURRENT APPLICATION NUMBER: US/10/956,
? CURRENT FILING DATE: 2004-10-04
? NUMBER OF SEQ ID NOS: 319805
? SOFTWARE: Patent version 3.2
? SEQ ID NO 85802
? LENGTH: 25
```

; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-85802

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
Db 7 GTATTCAGATTACTG 22

RESULT 16

US-10-956-157-85805
; Sequence 85805, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 85805

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-85805

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
Db 6 GTATTCAGATTACTG 21

RESULT 17

US-10-956-157-161273

; Sequence 161273, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 161273

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-161273

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
Db 10 GTATTCAGATTACTG 25

RESULT 18

US-10-956-157-171287

; Sequence 171287, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 171287

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-171287

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171287
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-171287

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGGC 21
| | | | | | | | | |
Db 4 ATGCCAGTTACTGGC 19

RESULT 19

US-10-956-157-210009/c

; Sequence 210009, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 210009

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-210009

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGG 20
| | | | | | | | | |
Db 22 CATGCCATAATACTGG 7

RESULT 20

US-10-956-157-237787

; Sequence 237787, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 237787

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-237787

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;

```
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GCATGCCAGATTACTG 19
Db 4 GTATCCAGATTACTG 19

RESULT 21
US-10-956-160-16692
; Sequence 16692, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-16692

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 ATGCCAGATTACTGCG 21
Db 3 ATGACAGACTACTGCG 18

RESULT 22
US-10-956-160-77247/c
; Sequence 77247, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77247
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-77247

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CATGCCAGATTACTGG 20
Db 25 CATGCCACATAACTGG 10

RESULT 23
US-10-956-160-96989/c
; Sequence 96989, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
```

```
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96989
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-96989
```

```
Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 CATGCCAGATTACTGG 20
Db 23 CATGCCACATAACTGG 8
```

```
RESULT 24
US-10-956-160-159211/c
; Sequence 159211, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-159211
```

```
Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 CATGCCAGATTACTGG 20
Db 19 CATGCCACATAACTGG 4
```

```
RESULT 25
US-10-956-160-180069
; Sequence 180069, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180069
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-180069
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Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 5 CATGCCAGATTACTGG 20
Db 3 CTGGCAGATTACTGG 18
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RESULT 26
US-10-956-157-123326
; Sequence 123326, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-123326
Query Match 60.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGATGCCAGATTACTG 19
Db 6 AGTGTCTCCAGATTATTG 24

RESULT 27
US-10-956-157-206484
; Sequence 206484, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-206484
Query Match 60.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCAGATGCCAGATTACTGG 20
Db 1 GCCCTTGTCCAGATTCTCG 19

RESULT 28
US-10-956-157-301261/c
; Sequence 301261, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301261
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Probe Sequence
US-10-956-157-301261
Query Match 60.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACTGGC 21
Db 25 CTCCTGGCGGATTACTGGC 7

RESULT 29
US-10-956-157-306098/c
; Sequence 306098, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 306098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-306098
Query Match 59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GCCAGATTACTGGC 21
Db 20 GCCAGATTACTGGC 7

RESULT 30
US-10-956-160-47893/c
; Sequence 47893, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-47893
Query Match 59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GCCAGATTACTGGC 21
Db 22 GCCAGATTACTGGC 9

RESULT 31
US-10-956-160-55930
; Sequence 55930, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55930
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-55930

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 ATGCCAGATTACTG 19
Db      11 ATGCCTGATTACTG 24

RESULT 32
US-10-956-160-76438/c
; Sequence 76438, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-76438

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 TGCCAGATTACTGG 20
Db      24 TGCCAGATTACTGG 11

RESULT 33
US-10-956-160-158546
; Sequence 158546, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-158546

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 GCGCATGCCAGATT 15
Db      2 GAGCATGCCAGATT 15

RESULT 34
US-10-956-160-167178/c
; Sequence 167178, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167178
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-167178

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 GCGCATGACTGGC 21
Db      20 GCGAGTACTGGC 7

RESULT 35
US-10-489-273-35
; Sequence 35, Application US/10489273
; GENERAL INFORMATION:
; APPLICANT: Turner, Arthur Keith
; APPLICANT: Greenwood, Judith
; APPLICANT: Stephens, Jonathan Clive
; APPLICANT: Beavis, Juliet Claire
; APPLICANT: Darsley, Michael James
; TITLE OF INVENTION: Attenuated Bacteria Useful in Vaccines
; FILE REFERENCE: 117-499 / N83542B
; CURRENT APPLICATION NUMBER: US/10/489,273
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: PCT/GB02/04164
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: GB 0121998.9
; PRIOR FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-489-273-35

Query Match          59.0%; Score 12.4; DB 6; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCGCATGCCAGATT 15
Db      2 GCGCATGCCAGATT 15

RESULT 36
US-10-758-155-2666
; Sequence 2666, Application US/10758155
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
; US-10-758-155-2732

Query Match          58.1%; Score 12.2; DB 6; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGGC 21
Db 3 CAUGCUGGAUUGCUGGC 19

RESULT 39
US-10-758-155-2733
; Sequence 2733, Application US/10758155
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBH02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2733
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
; US-10-758-155-2733

Query Match          58.1%; Score 12.2; DB 6; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGGC 21
Db 3 CAUGCUGGAUUGCUGGC 19

RESULT 40
US-10-758-155-2738
; Sequence 2738, Application US/10758155
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
```

```
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBH02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2738
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
; US-10-758-155-2738

Query Match          58.1%; Score 12.2; DB 6; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGGC 21
Db 2 CAUGCUGGAUUGCUGGC 18

Search completed: November 24, 2004, 03:20:46
Job time : 35.2697 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 112.708 Seconds
(without alignments)
978.085 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21
Sequence: 1 agcgcagccagattactgac 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : N_Geneseq_23Sep04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	21	100.0	21	6	AD43736
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4	13.8	65.7	21	10	ADE29100
5	13.6	64.8	44	2	AAT65036
6	13.2	62.9	19	4	AAT65036
7	13.2	62.9	20	10	ADP81091
8	13.2	62.9	21	2	AXX83448
9	13.2	62.9	22	6	AXN83493
10	13.2	62.9	32	6	ABQ87925
11	13.2	62.9	32	6	ABQ87925
12	13.2	62.9	32	6	ABQ87926
13	13	61.9	18	2	AZ41030
14	13	61.9	18	2	AZ22124
15	13	61.9	18	10	AAD60500
16	13	61.9	20	12	ADP81733
17	13	61.9	20	12	ADP81699
18	13	61.9	32	4	AC93092
19	13	61.9	32	4	AC93091
20	13	61.9	32	12	ADI80472
21	13	61.9	32	12	ADI80471

c	22	12.8	61.0	21	4	AAH62283	Aah62283 NRIP1 pol
	23	12.8	61.0	23	6	ABSS7999	Abss7999 PCR prime
	24	12.8	61.0	24	5	AAI4408	Aai4408 Human bas
c	25	12.8	61.0	24	6	ABQ05495	Abq05495 Oligonucl
c	26	12.8	61.0	24	6	ABQ11823	Abq11823 Oligonucl
c	27	12.8	61.0	24	6	ABQ00780	Abq00780 Oligonucl
	28	12.8	61.0	24	6	ABQ05536	Abq05536 Oligonucl
	29	12.8	61.0	24	6	ABQ11857	Abq11857 Oligonucl
c	30	12.8	61.0	24	9	AAI62586	Aai62586 Human A2
c	31	12.8	61.0	25	6	ABQ13359	Abq13359 Oligonucl
c	32	12.8	61.0	25	6	ABQ13393	Abq13393 Oligonucl
c	33	12.8	61.0	28	2	AAQ46940	Aaq46940 Human bFG
	34	12.8	61.0	28	2	AAQ59860	Aat59860 Sense pri
	35	12.8	61.0	33	4	AAH48106	Aah48106 Ribulose
	36	12.8	61.0	41	4	AAH48109	Aah48109 Ribulose
	37	12.8	61.0	49	2	AAAF82407	Aaf82407 Thermophi
c	38	12.6	60.0	19	4	AAAF82407	Aaf82407 Thermophi
	39	12.6	60.0	20	2	AAAX94343	Aax94343 PCR prime
	40	12.6	60.0	21	2	AAZ21594	Aaz21594 PCR prime
	41	12.6	60.0	21	6	ABL42959	AbL42959 Human chr
	42	12.6	60.0	25	5	AAI61787	Aai61787 Soybean 2
c	43	12.6	60.0	34	3	AAAI95696	Aaa95696 Bacillus
	44	12.6	60.0	38	2	AAQ46917	Aaq46917 PCR prime
	45	12.6	60.0	41	6	ABZ44895	Abz44895 Human cyt
	46	12.6	60.0	41	6	ABZ50445	Abz50445 Human cyt
c	47	12.6	60.0	46	6	ABA90115	Aba90115 Oestrogen
c	48	12.6	60.0	46	6	ABA90172	Aba90172 Oestrogen
c	49	12.6	60.0	46	6	ABA90169	Aba90169 Oestrogen
c	50	12.6	60.0	46	6	ABA90092	Aba90092 Oestrogen
c	51	12.6	60.0	46	6	ABA90091	Aba90091 Oestrogen
c	52	12.6	60.0	46	6	ABA90097	Aba90097 Oestrogen
c	53	12.6	60.0	46	6	ABA90098	Aba90098 Oestrogen
c	54	12.6	60.0	46	6	ABA90094	Aba90094 Oestrogen
c	55	12.6	60.0	46	6	ABA90170	Aba90170 Oestrogen
c	56	12.6	60.0	46	6	ABA90171	Aba90171 Oestrogen
c	57	12.6	60.0	46	6	ABQ87878	Abq87878 Human ESR
c	58	12.6	60.0	46	6	ABQ87880	Abq87880 Human ESR
c	59	12.6	60.0	46	6	ABQ87881	Abq87881 Human ESR
c	60	12.6	60.0	46	6	ABQ87879	Abq87879 Human ESR
c	61	12.6	60.0	46	6	ABQ87801	Abq87801 Human ESR
c	62	12.6	60.0	46	6	ABQ87807	Abq87807 Human ESR
c	63	12.6	60.0	46	6	ABQ87824	Abq87824 Human ESR
c	64	12.6	60.0	46	6	ABQ87803	Abq87803 Human ESR
c	65	12.6	60.0	46	6	ABQ87806	Abq87806 Human ESR
c	66	12.6	60.0	46	6	ABQ87800	Abq87800 Human ESR
c	67	12.6	60.0	46	8	ABX33914	Abx33914 Human ESR
c	68	12.6	60.0	46	8	ABX33842	Abx33842 Human ESR
c	69	12.6	60.0	46	8	ABX33915	Abx33915 Human ESR
c	70	12.6	60.0	46	8	ABX33837	Abx33837 Human ESR
c	71	12.6	60.0	46	8	ABX33843	Abx33843 Human ESR
c	72	12.6	60.0	46	8	ABX33916	Abx33916 Human ESR
c	73	12.6	60.0	46	8	ABX33839	Abx33839 Human ESR
c	74	12.6	60.0	46	8	ABX33836	Abx33836 Human ESR
c	75	12.6	60.0	46	8	ABX33860	Abx33860 Human ESR
c	76	12.6	60.0	46	8	ABX33917	Abx33917 Human ESR
c	77	12.4	59.0	20	12	ADJ58593	Adj58593 Class A C
	78	12.4	59.0	21	6	AAI67796	Aai67796 E. coli O
	79	12.4	59.0	23	9	ACF35777	Acf35777 Mouse MMP
c	80	12.4	59.0	25	9	ACI96905	AcI96905 Human mic
	81	12.4	59.0	25	9	ACK05636	Ack05636 Human mic
	82	12.4	59.0	28	8	ACC79451	Acc79451 EAS1 del
c	83	12.4	59.0	42	2	AAT31709	Aat31709 Respirato
c	84	12.4	59.0	42	2	AAT31710	Aat31710 Respirato
c	85	12.4	59.0	42	2	AAZ30538	Aaz30538 RSV G pro
c	86	12.4	59.0	42	2	AAZ30537	Aaz30537 RSV G pro
c	87	12.4	59.0	42	5	AAF90137	Aaf90137 Nucleotid
c	88	12.4	59.0	42	5	AAF90138	Aaf90138 Nucleotid
	89	12.4	59.0	45	2	AAQ44969	Aaq44969 FIV gag g
	90	12.4	59.0	48	6	ABZ48115	Abz48115 Human ATP
	91	12.4	59.0	48	6	ABZ48115	Abz48115 Human ATP
c	92	12.2	58.1	19	2	AAQ86259	Aaq86259 Verocytot
c	93	12.2	58.1	19	2	AAQ86259	Aaq86259 Verocytot
c	94	12.2	58.1	19	3	AAA94562	Aaa94562 Oligonucl

c 95	12.2	58.1	20	2	AAZ02084	Aaz02084 PCR prime	c 168	11.8	56.2	20	12	ADK96648	Adk96648 Primer of
c 96	12.2	58.1	20	6	ABL44022	AbL44022 Human chr	169	11.8	56.2	21	4	AAE97043	Aaf97043 Human gen
c 97	12.2	58.1	20	10	ADH93713	Adh93713 Human gen	c 170	11.8	56.2	21	4	AAE97599	Aaf97599 Human gen
c 98	12.2	58.1	22	6	AAK99354	Aak99354 Antisense	c 171	11.8	56.2	21	12	ADN00683	Adn00683 reca PCR
c 99	12.2	58.1	22	6	AAK51433	Aak51433 Starfish	c 172	11.8	56.2	22	6	ABL44143	AbL44143 Human chr
c 100	12.2	58.1	25	3	AAAL4076	AaAl4076 Human SPR	c 173	11.8	56.2	25	9	ACK26950	Ack26950 Human mic
c 101	12.2	58.1	25	9	AAI62155	AaI62155 Soybean 3	c 174	11.8	56.2	25	9	ACK03103	Ack03103 Human mic
c 102	12.2	58.1	25	9	ACK15960	Ack15960 Human mic	c 175	11.8	56.2	25	9	ACI23522	AcI23522 Human mic
c 103	12.2	58.1	25	9	ACK19535	Ack19535 Human mic	c 176	11.8	56.2	25	9	ACI81477	AcI81477 Human mic
c 104	12.2	58.1	26	8	ABZ20585	Abz20585 A thalian	c 177	11.8	56.2	30	2	AAQ04634	AaQ04634 TCRV9PST
c 105	12.2	58.1	26	10	AD444635	Adf44635 Human ICO	c 178	11.8	56.2	30	2	AAQ25301	AaQ25301 T-cell re
c 106	12.2	58.1	27	6	AAQ25095	AaQ25095 DR-A enha	c 179	11.8	56.2	31	12	ADQ79971	Adm79971 Synthetic
c 107	12.2	58.1	27	6	ABA03313	AbA03313 Streptomy	c 180	11.8	56.2	38	12	ADM36298	Adm36298 Modified
c 108	12.2	58.1	27	6	ABA03313	AbA03313 Streptomy	c 181	11.8	56.2	39	2	AAQ75898	AaQ75898 CDR-graft
c 109	12.2	58.1	27	10	ADF44634	Adf44634 Human ICO	c 182	11.8	56.2	20	2	AAQ41033	AaQ41033 Human gen
c 110	12.2	58.1	30	2	AAQ36789	AaQ36789 Mycobacte	c 183	11.6	55.2	20	2	AAQ93394	AaQ93394 PCR prime
c 111	12.2	58.1	31	6	ABA03319	AbA03319 Streptomy	c 184	11.6	55.2	22	2	AAQ93394	AaQ93394 PCR prime
c 112	12.2	58.1	32	6	ABQ87932	AbQ87932 Enterohae	c 185	11.6	55.2	22	3	AAA95571	AaA95571 TCR Valph
c 113	12.2	58.1	32	6	ABQ87946	AbQ87946 Enterohae	c 186	11.6	55.2	22	12	ADK67740	Adk67740 Murine fa
c 114	12.2	58.1	34	6	ABK87179	AbK87179 A. pernix	c 187	11.6	55.2	23	6	ABAO4844	AbA04844 Human PCR
c 115	12.2	58.1	34	6	ABS52447	AbS52447 Thermophi	c 188	11.6	55.2	23	8	ACC71766	Acc71766 PCR prime
c 116	12.2	58.1	42	2	AAQ90107	AaQ90107 Ha-ras fr	c 189	11.6	55.2	24	2	AAK86555	AaK86555 Primer re
c 117	12.2	58.1	44	2	AAE65037	Aat65037 Aspergill	c 190	11.6	55.2	25	6	ABV81964	AbV81964 Human HTP
c 118	12.2	58.1	44	2	AAQ02757	AaQ02757 Oligonucl	c 191	11.6	55.2	25	6	ABV81965	AbV81965 Human HTP
c 119	12.2	58.1	44	10	ABZ57904	Abz57904 RNA secon	c 192	11.6	55.2	25	9	ACI93929	AcI93929 Human mic
c 120	12.2	58.1	50	4	AAI77361	AaI77361 Human sil	c 193	11.6	55.2	25	9	ACI93929	AcI93929 Human mic
c 121	12.2	58.1	20	5	AAQ09105	AaQ09105 Human MEK	c 194	11.6	55.2	30	2	AAQ84732	AaQ84732 Primer to
c 122	12.2	57.1	20	6	ABL45362	AbL45362 Human chr	c 195	11.6	55.2	30	2	AAQ84732	AaQ84732 Primer to
c 123	12.2	57.1	20	6	ABT93220	AbT93220 Capture o	c 196	11.6	55.2	30	2	AAZ07618	AaZ07618 HCV NS1/E
c 124	12.2	57.1	20	12	ADU25471	AdJ25471 Human end	c 197	11.6	55.2	30	2	AAZ00428	AaZ00428 Hepatitis
c 125	12.2	57.1	23	8	AAQ49636	AaQ49636 Human EPO	c 198	11.6	55.2	30	2	AAZ26763	AaZ26763 PCR prime
c 126	12.2	57.1	24	6	ACC57383	Acc57383 Human KRA	c 199	11.6	55.2	30	2	ADF66097	Adf66097 Hepatitis
c 127	12.2	57.1	24	6	ABT83010	Abi83010 Capture o	c 200	11.6	55.2	30	2	ADF66102	Adf66102 Hepatitis
c 128	12.2	57.1	24	6	ABT83011	Abi83011 Capture o	c 201	11.6	55.2	30	3	AAZ55031	AaZ55031 Neisseria
c 129	12.2	57.1	24	6	ABT92277	Abi92277 Capture o	c 202	11.6	55.2	31	2	AAZ66766	AaZ66766 Human DF3
c 130	12.2	57.1	24	6	ABT92276	Abi92276 Capture o	c 203	11.6	55.2	31	3	AAZ35908	AaZ35908 Human gen
c 131	12.2	57.1	25	6	ABV81963	Abv81963 Human HTP	c 204	11.6	55.2	31	6	AAI37984	AaI37984 Human imm
c 132	12.2	57.1	25	6	ABV81963	Abv81963 Human HTP	c 205	11.6	55.2	31	10	ADF69474	Adf69474 Tapesia y
c 133	12.2	57.1	25	6	ABV81959	Abv81959 Human HTP	c 206	11.6	55.2	33	2	AAZ34638	AaZ34638 Primer fo
c 134	12.2	57.1	25	6	ABV81961	Abv81961 Human HTP	c 207	11.6	55.2	33	6	ABZ22187	AbZ22187 Human glu
c 135	12.2	57.1	25	6	ABV81961	Abv81961 Human HTP	c 208	11.6	55.2	33	9	ACC84746	Acc84746 E. coli p
c 136	12.2	57.1	25	6	ABV81958	Abv81958 Human HTP	c 209	11.6	55.2	36	2	AAQ99619	AaQ99619 Human Ah
c 137	12.2	57.1	25	9	ACI26693	AcI26693 Human mic	c 210	11.6	55.2	37	2	AAV16041	AaV16041 PCR prime
c 138	12.2	57.1	25	12	ADG76734	AdG76734 Human olf	c 211	11.6	55.2	37	3	AAZ43300	AaZ43300 Murine ty
c 139	12.2	57.1	27	10	ABZ84571	AbZ84571 Toxicolog	c 212	11.6	55.2	37	3	AAZ43300	AaZ43300 Murine ty
c 140	12.2	57.1	28	4	AAE75355	AaE75355 Pestiviru	c 213	11.6	55.2	37	8	ACD53443	AcD53443 HBV G-cle
c 141	12.2	57.1	29	3	AAQ04125	AaQ04125 Polymorph	c 214	11.6	55.2	37	12	ADM61953	Adm61953 Hepatitis
c 142	12.2	57.1	29	3	AAZ54569	AaZ54569 Neisseria	c 215	11.6	55.2	45	6	ABK86059	AbK86059 Protein C
c 143	12.2	57.1	29	3	AAZ54761	AaZ54761 Neisseria	c 216	11.6	55.2	46	4	AAH93855	AaH93855 Human pro
c 144	12.2	57.1	29	3	AAZ54803	AaZ54803 Neisseria	c 217	11.6	55.2	46	4	AAH93859	AaH93859 Human pro
c 145	12.2	57.1	29	3	AAZ81314	AaZ81314 N. mening	c 218	11.6	55.2	46	4	AAZ63948	AaZ63948 Human pro
c 146	12.2	57.1	29	3	AAZ21599	AaZ21599 Neisseria	c 219	11.6	55.2	46	4	AAZ63952	AaZ63952 Human pro
c 147	12.2	57.1	30	2	AAZ99188	AaZ99188 N. mening	c 220	11.6	55.2	46	5	ACA59760	AcA59760 Prostate
c 148	12.2	57.1	30	5	AAZ89117	AaZ89117 Neisseria	c 221	11.6	55.2	46	5	ACA59756	AcA59756 Prostate
c 149	12.2	57.1	33	4	AAH48797	AaH48797 Erythro	c 222	11.6	55.2	46	6	ABL95319	AbL95319 Human cod
c 150	12.2	57.1	34	4	AAH91676	AaH91676 Human inf	c 223	11.6	55.2	46	6	ABL95323	AbL95323 Human cod
c 151	12.2	57.1	37	6	AAH96699	AaH96699 Human Chk	c 224	11.6	55.2	46	6	ABA90113	AbA90113 Oestrogen
c 152	12.2	57.1	37	6	AAH59224	AaH59224 Human CUC	c 225	11.6	55.2	46	6	ABA90125	AbA90125 Oestrogen
c 153	12.2	57.1	37	6	ABK59203	AbK59203 Human CUC	c 226	11.6	55.2	46	6	ABA90125	AbA90125 Oestrogen
c 154	12.2	57.1	37	8	ACD53542	AcD53542 HBV G-cle	c 227	11.6	55.2	46	6	ABA90174	AbA90174 Oestrogen
c 155	12.2	57.1	37	8	ACD53452	AcD53452 HBV G-cle	c 228	11.6	55.2	46	6	ABA90133	AbA90133 Oestrogen
c 156	12.2	57.1	37	12	ADM62001	Adm62001 Hepatitis	c 229	11.6	55.2	46	6	ABA90099	AbA90099 Oestrogen
c 157	12.2	57.1	37	12	ADM61962	Adm61962 Hepatitis	c 230	11.6	55.2	46	6	ABA90104	AbA90104 Oestrogen
c 158	12.2	57.1	38	2	AAZ48796	AaZ48796 Erythro	c 231	11.6	55.2	46	6	ABQ87822	AbQ87822 Human ESR
c 159	12.2	57.1	40	2	AAZ08558	AaZ08558 Oligonucl	c 232	11.6	55.2	46	6	ABQ87808	AbQ87808 Human ESR
c 160	12.2	57.1	40	2	AAZ08557	AaZ08557 Oligonucl	c 233	11.6	55.2	46	6	ABQ87811	AbQ87811 Human ESR
c 161	12.2	57.1	41	6	ABZ47661	AbZ47661 Human ATP	c 234	11.6	55.2	46	6	ABQ87842	AbQ87842 Human ESR
c 162	12.2	57.1	41	6	ABZ45066	AbZ45066 Human ATP	c 235	11.6	55.2	46	6	ABQ87883	AbQ87883 Human ESR
c 163	12.2	57.1	43	2	AAV19848	AaV19848 Primer fo	c 236	11.6	55.2	46	6	ABQ87834	AbQ87834 Human ESR
c 164	12.2	57.1	44	10	ADD25977	AdD25977 Human ery	c 237	11.6	55.2	46	8	ABQ87813	AbQ87813 Human ESR
c 165	12.2	57.1	44	10	ADD25979	AdD25979 Human ery	c 238	11.6	55.2	46	8	ACC95483	Acc95483 Prostate
c 166	11.8	56.2	18	2	AAQ09583	AaQ09583 Human bla	c 239	11.6	55.2	46	8	ACC95487	Acc95487 Prostate
c 167	11.8	56.2	20	4	AAF83480	AaF83480 Human ADA	c 240	11.6	55.2	46	8	ABX33844	AbX33844 Human ESR

C 241	11.6	55.2	46	8	ABX33870	Human ESR	Abx33870	C 314	11.4	54.3	37	12	ADM61959	Hepatitis
C 242	11.6	55.2	46	8	ABX33878	Human ESR	Abx33878	C 315	11.4	54.3	37	12	ADM61992	Hepatitis
C 243	11.6	55.2	46	8	ABX33847	Human ESR	Abx33847	C 316	11.4	54.3	37	12	ADM61994	Hepatitis
C 244	11.6	55.2	46	8	ABX33849	Human ESR	Abx33849	C 317	11.4	54.3	38	10	ADG79103	Schizophr
C 245	11.6	55.2	46	8	ABX33858	Human ESR	Abx33858	C 318	11.4	54.3	39	6	ABS61225	Human pol
C 246	11.6	55.2	46	10	ADB14061	Human pro	Adb14061	C 319	11.4	54.3	39	12	ADL65077	Human sin
C 247	11.6	55.2	46	10	ADB14065	Human mat	Adb14065	C 320	11.4	54.3	39	12	ADL65224	Human sin
C 248	11.6	55.2	46	10	ADG26481	Human pro	Adg26481	C 321	11.4	54.3	40	2	AAV85690	LRPS exon
C 249	11.6	55.2	46	10	ADG26477	Human pro	Adg26477	C 322	11.4	54.3	40	6	ABN88696	E2F aptam
C 250	11.6	55.2	47	2	AAQ25091	DR-A enha	Aaq25091	C 323	11.4	54.3	40	6	ABT11996	E coli ex
C 251	11.6	55.2	50	6	ABK86058	Protein C	Abk86058	C 324	11.4	54.3	40	12	ADG25842	Human OAT
C 252	11.6	55.2	50	6	ABZ06497	Human leu	Abz06497	C 325	11.4	54.3	41	9	ACC42022	Human SCN
C 253	11.6	55.2	50	6	ABZ06887	Human leu	Abz06887	C 326	11.4	54.3	41	9	ACC42022	Human SCN
C 254	11.4	54.3	17	2	AAQ07263	S-region	Aaq07263	C 327	11.4	54.3	43	10	ADE15723	E. coli t
C 255	11.4	54.3	20	2	AAT18880	TCL-1 gen	Aat18880	C 328	11.4	54.3	44	4	AAAL28558	Human SNP
C 256	11.4	54.3	20	4	AAH45015	PCR prime	Aah45015	C 329	11.4	54.3	45	2	AAV01772	C. tracho
C 257	11.4	54.3	20	6	ABK99735	Human RAI	Abk99735	C 330	11.4	54.3	45	6	ABZ22133	Thioredox
C 258	11.4	54.3	20	6	ABQ62344	Human syn	Abq62344	C 331	11.4	54.3	45	2	AAAT15858	Thermosta
C 259	11.4	54.3	20	12	ADO51318	Human UBE	Ado51318	C 332	11.4	54.3	47	3	AAZ67307	Human map
C 260	11.4	54.3	20	12	ADP81720	Human MAG	Adp81720	C 333	11.4	54.3	47	12	ADO18168	Primer of
C 261	11.4	54.3	20	12	ADP81750	Human mel	Adp81750	C 334	11.4	54.3	48	6	ABN85198	Mutagenic
C 262	11.4	54.3	21	9	ADA113899	Short int	Ada113899	C 335	11.4	54.3	50	2	AAAX86588	PCR prime
C 263	11.4	54.3	22	5	ABSL11698	Human odo	Absl11698	C 336	11.2	53.3	50	3	AAZ61244	Primer Ac
C 264	11.4	54.3	22	6	ABK95513	Novel G-p	Abk95513	C 337	11.2	53.3	50	3	AAZ61244	Primer Ac
C 265	11.4	54.3	22	6	ABK95513	Novel G-p	Abk95513	C 338	11.2	53.3	50	3	AAZ61244	Primer Ac
C 266	11.4	54.3	22	11	ADL98011	Human olf	Adl98011	C 339	11.2	53.3	17	12	ADO79982	CENPCL ex
C 267	11.4	54.3	22	12	ADH42719	Novel hum	Adh42719	C 340	11.2	53.3	19	3	AAAX86588	PCR prime
C 268	11.4	54.3	22	12	ADQ07020	Novel siR	Adq07020	C 341	11.2	53.3	19	3	AAAX86588	PCR prime
C 269	11.4	54.3	23	4	AAH23021	VEGPR-2 g	Aah23021	C 342	11.2	53.3	19	6	ABSA1922	Vascular
C 270	11.4	54.3	23	10	ABX90512	Human VEG	Abx90512	C 343	11.2	53.3	19	6	ABSA1922	Vascular
C 271	11.4	54.3	24	2	AAT59862	Sense pri	Aat59862	C 344	11.2	53.3	20	4	AAAD02844	A. thalia
C 272	11.4	54.3	24	6	ABQ06153	Oligonucl	Abq06153	C 345	11.2	53.3	20	6	AAAD1799	Human RBC
C 273	11.4	54.3	24	6	ABQ01111	Oligonucl	Abq01111	C 346	11.2	53.3	20	6	ABIS15151	Capture o
C 274	11.4	54.3	24	6	ABQ06194	Oligonucl	Abq06194	C 347	11.2	53.3	20	12	ADJ156706	Rat hypot
C 275	11.4	54.3	24	6	ABT191269	Capture o	Abt191269	C 348	11.2	53.3	20	12	ADJ84977	Nucleic a
C 276	11.4	54.3	24	6	ABT191268	Capture o	Abt191268	C 349	11.2	53.3	20	12	ADN30412	Human Not
C 277	11.4	54.3	25	2	AAAT61970	Primer co	Aaat61970	C 350	11.2	53.3	21	4	AAAF97527	Human gen
C 278	11.4	54.3	25	9	ACI19934	Human mic	Act19934	C 351	11.2	53.3	21	4	AAAF97527	Human gen
C 279	11.4	54.3	25	9	ACI19934	Human mic	Act19934	C 352	11.2	53.3	21	6	AAAD23667	SNP speci
C 280	11.4	54.3	25	10	ADE34184	Plastid t	Ade34184	C 353	11.2	53.3	21	6	AAAD23667	Nicotiana
C 281	11.4	54.3	26	2	AAQ89943	Listeria	Aaq89943	C 354	11.2	53.3	21	10	ADH72752	PCR prime
C 282	11.4	54.3	27	2	AAQ47090	Lymphotox	Aaq47090	C 355	11.2	53.3	21	12	ADK96397	Primer of
C 283	11.4	54.3	27	2	AAAT73380	Primer ol	Aaat73380	C 356	11.2	53.3	21	12	ADK96397	Primer of
C 284	11.4	54.3	27	2	AAV21946	Nuclease	Aav21946	C 357	11.2	53.3	21	12	ADK96397	Primer of
C 285	11.4	54.3	27	12	ADM98067	Mouse try	Adm98067	C 358	11.2	53.3	21	12	ADK96397	Primer of
C 286	11.4	54.3	27	12	ADM96248	Mouse try	Adm96248	C 359	11.2	53.3	22	10	ADD89851	Human cAM
C 287	11.4	54.3	28	2	AAZ76390	Human tum	Aaz76390	C 360	11.2	53.3	22	12	ADK94910	Primer of
C 288	11.4	54.3	28	2	AAV55606	Primer fo	Aav55606	C 361	11.2	53.3	23	2	AAT89558	Bloom's s
C 289	11.4	54.3	28	2	AAV55606	Primer fo	Aav55606	C 362	11.2	53.3	23	2	AAT89558	Bloom's s
C 290	11.4	54.3	28	3	AAAX33983	Low adeno	Aax33983	C 363	11.2	53.3	23	10	ADD89840	Human cAM
C 291	11.4	54.3	28	3	AAAF20105	Human tum	Aaf20105	C 364	11.2	53.3	24	6	ABQ04658	Human inf
C 292	11.4	54.3	28	4	AAAC62135	PCR prime	Aac62135	C 365	11.2	53.3	24	6	ABQ00342	Oligonucl
C 293	11.4	54.3	28	10	ABZ95799	Human tum	Abz95799	C 366	11.2	53.3	24	6	ABQ07006	Oligonucl
C 294	11.4	54.3	28	11	ABD19539	Human tum	Abd19539	C 367	11.2	53.3	24	6	ABQ10986	Oligonucl
C 295	11.4	54.3	29	2	AAZ20234	Brassica	Aaz20234	C 368	11.2	53.3	24	6	ABQ01521	Oligonucl
C 296	11.4	54.3	29	2	AAZ20241	Mustard r	Aaz20241	C 369	11.2	53.3	24	6	ABQ04699	Oligonucl
C 297	11.4	54.3	29	9	ADA27217	PCR prime	Ada27217	C 370	11.2	53.3	24	6	ABQ04699	Oligonucl
C 298	11.4	54.3	30	2	AAQ45374	Primer to	Aaq45374	C 371	11.2	53.3	24	6	ABQ06965	Oligonucl
C 299	11.4	54.3	32	3	AAZ890592	Human TRF	Aaz890592	C 372	11.2	53.3	24	6	ABQ06965	Oligonucl
C 300	11.4	54.3	33	3	AAZ88636	Human TRF	Aaz88636	C 373	11.2	53.3	24	6	ABQ06965	Oligonucl
C 301	11.4	54.3	33	3	AAAC60124	Oligomer	Aac60124	C 374	11.2	53.3	24	10	ACC57628	Mouse MAP
C 302	11.4	54.3	33	3	AAAC60125	Oligomer	Aac60125	C 375	11.2	53.3	25	2	AAV15566	Sequence
C 303	11.4	54.3	33	3	AAAO7456	PCR prime	Aaa07456	C 376	11.2	53.3	25	6	ABQ12522	Oligonucl
C 304	11.4	54.3	33	3	AAZ48628	Light cha	Aaz48628	C 377	11.2	53.3	25	6	ABQ12522	Oligonucl
C 305	11.4	54.3	33	3	AAAL12363	Feline hu	Aaal12363	C 378	11.2	53.3	25	9	ABQ12563	Oligonucl
C 306	11.4	54.3	33	5	AAAC83238	Anti-EGFR	Aac83238	C 379	11.2	53.3	25	9	ABQ12563	Oligonucl
C 307	11.4	54.3	33	6	ABK11443	Mouse DNA	Abk11443	C 380	11.2	53.3	25	9	ABQ12563	Oligonucl
C 308	11.4	54.3	34	2	AAT15853	Thermosta	Aat15853	C 381	11.2	53.3	25	9	ACK22648	Human mic
C 309	11.4	54.3	35	10	ADE50872	Human TRP	Ade50872	C 382	11.2	53.3	25	9	ACK22648	Human mic
C 310	11.4	54.3	35	12	ADL65324	Lactobaci	Adl65324	C 383	11.2	53.3	25	9	ACK22648	Human mic
C 311	11.4	54.3	37	8	ACD53535	HBV G-cle	Acd53535	C 384	11.2	53.3	25	9	ACK22648	Human mic
C 312	11.4	54.3	37	8	ACD53533	HBV G-cle	Acd53533	C 385	11.2	53.3	25	9	ACK22648	Human mic
C 313	11.4	54.3	37	8	ACD53449	HBV G-cle	Acd53449	C 386	11.2	53.3	25	10	ABQ84410	DPPI0 PCR

387	11.2	53.3	26	2	AA0707447	Aax07447 Rhodother	C 460	11	52.4	21	9	ADA13906	Adal13906 Short int
388	11.2	53.3	26	6	ABT04218	Abt04218 Human G-p	C 461	11	52.4	21	9	ADA13902	Adal13902 Short int
389	11.2	53.3	26	8	ABZ69360	Abz69360 Bacteriop	C 462	11	52.4	21	9	ADA13905	Adal13905 Short int
390	11.2	53.3	26	8	ABZ69364	Abz69364 Bacteriop	C 463	11	52.4	21	9	ADA13900	Adal13900 Short int
391	11.2	53.3	26	12	ADH30968	Adh30968 Human G-p	C 464	11	52.4	21	9	ADA13903	Adal13903 Short int
392	11.2	53.3	29	3	AAZ88270	Aaz88270 Sec B nuc	C 465	11	52.4	21	9	ADA13898	Adal13898 Short int
393	11.2	53.3	30	2	AAQ49367	Aaq49367 PCR prime	C 466	11	52.4	21	9	ADA13907	Adal13907 Short int
394	11.2	53.3	30	6	ABX67560	Abx67560 Novel Hel	C 467	11	52.4	21	9	ADA13904	Adal13904 Short int
395	11.2	53.3	30	10	ADE15918	Ade15918 Non-antib	C 468	11	52.4	21	10	ADB88626	Adb88626 Frizzled-
396	11.2	53.3	31	8	AAU53243	Aau53243 PCR prime	C 469	11	52.4	21	12	ADK97255	Adk97255 Primer of
397	11.2	53.3	31	10	AAU53243	Aau53243 PCR prime	C 470	11	52.4	22	2	AAQ05279	Aaq05279 Sequence
398	11.2	53.3	31	12	AAU53243	Aau53243 PCR prime	C 471	11	52.4	22	2	AAQ05279	Aaq05279 Sequence
399	11.2	53.3	31	12	ADL08094	Adl08094 Human SNP	C 472	11	52.4	22	3	AAU5326	Aau5326 Hepatitis
400	11.2	53.3	32	9	ACF57397	Act57397 Pichia pa	C 473	11	52.4	22	6	ABQ94026	Abq94026 NOV13 for
401	11.2	53.3	33	6	AAK92923	Aak92923 Coryneb	C 474	11	52.4	22	6	ADL17602	Adl17602 Forward P
402	11.2	53.3	33	6	AAK92923	Aak92923 Coryneb	C 475	11	52.4	22	6	ADL17602	Adl17602 Forward P
403	11.2	53.3	34	2	AAU59674	Aau59674 Mutagenic	C 476	11	52.4	22	12	ADN42690	Adn42690 Human NOV
404	11.2	53.3	34	2	AAU59674	Aau59674 Mutagenic	C 477	11	52.4	22	12	ADN42690	Adn42690 Human NOV
405	11.2	53.3	34	2	AAU59674	Aau59674 Mutagenic	C 478	11	52.4	22	12	ADN42690	Adn42690 Human NOV
406	11.2	53.3	34	3	AAA14935	Aaa14935 PCR prime	C 479	11	52.4	22	4	AAF28015	Aaf28015 Human TR1
407	11.2	53.3	36	6	AAU46831	Aau46831 Sheep alp	C 480	11	52.4	24	4	AAF28015	Aaf28015 Human TR1
408	11.2	53.3	36	6	AAU46831	Aau46831 Sheep alp	C 481	11	52.4	24	4	AAF28015	Aaf28015 Human TR1
409	11.2	53.3	36	6	AAU46831	Aau46831 Sheep alp	C 482	11	52.4	24	4	AAF28015	Aaf28015 Human TR1
410	11.2	53.3	36	10	ADE15912	Ade15912 Non-antib	C 483	11	52.4	24	4	AAF28015	Aaf28015 Human TR1
411	11.2	53.3	36	12	ADM93359	Adm93359 Chimeric	C 484	11	52.4	24	4	AAF28015	Aaf28015 Human TR1
412	11.2	53.3	38	10	ADG78987	Adg78987 Schizophr	C 485	11	52.4	24	9	ACH66209	Ach66209 Human tum
413	11.2	53.3	40	2	AAU96608	Aau96608 Cycloitol-	C 486	11	52.4	24	9	ACH66209	Ach66209 Human tum
414	11.2	53.3	41	3	AAU53863	Aau53863 Primer GD	C 487	11	52.4	25	2	AAU53863	Aau53863 Primer GD
415	11.2	53.3	41	4	AAU48110	Aau48110 Ribulose	C 488	11	52.4	25	2	AAU53863	Aau53863 Primer GD
416	11.2	53.3	41	6	ABZ60083	Abz60083 Human DNA	C 489	11	52.4	25	2	AAU53863	Aau53863 Primer GD
417	11.2	53.3	41	6	ABZ44750	Abz44750 Human ATP	C 490	11	52.4	25	3	AAU53863	Aau53863 Primer GD
418	11.2	53.3	41	6	ABZ44750	Abz44750 Human ATP	C 491	11	52.4	25	3	AAU53863	Aau53863 Primer GD
419	11.2	53.3	41	12	ADM95046	Adm95046 Nitrosomo	C 492	11	52.4	25	5	AAU53863	Aau53863 Primer GD
420	11.2	53.3	44	10	ACU79660	Acc79660 Camel ant	C 493	11	52.4	25	5	AAU53863	Aau53863 Primer GD
421	11.2	53.3	45	12	ADH27909	Adh27909 Human chr	C 494	11	52.4	25	8	ACA63661	Act63661 Novel hum
422	11.2	53.3	46	6	ABA90154	Abz90154 Oestrogen	C 495	11	52.4	25	8	ACA63661	Act63661 Novel hum
423	11.2	53.3	46	6	ABA90154	Abz90154 Oestrogen	C 496	11	52.4	25	8	ACA63661	Act63661 Novel hum
424	11.2	53.3	46	6	ABQ87863	Abq87863 Human ESR	C 497	11	52.4	25	8	ACA63661	Act63661 Novel hum
425	11.2	53.3	46	6	ABQ87863	Abq87863 Human ESR	C 498	11	52.4	25	8	ACA63661	Act63661 Novel hum
426	11.2	53.3	46	8	ABX33859	Abx33859 Human ESR	C 499	11	52.4	25	9	ACK19865	Act19865 Human mic
427	11.2	53.3	46	8	ABX33859	Abx33859 Human ESR	C 500	11	52.4	25	9	ACK19865	Act19865 Human mic
428	11.2	53.3	47	3	AAU68191	Aau68191 Human map	C 501	11	52.4	25	9	ACK19865	Act19865 Human mic
429	11.2	53.3	47	3	AAU68191	Aau68191 Human map	C 502	11	52.4	25	9	ACK19865	Act19865 Human mic
430	11.2	53.3	47	8	ABZ25341	Abz25341 PCR prime	C 503	11	52.4	25	9	ACK19865	Act19865 Human mic
431	11.2	53.3	47	8	ABZ25341	Abz25341 PCR prime	C 504	11	52.4	25	9	ACK19865	Act19865 Human mic
432	11.2	53.3	49	3	AAU99358	Aau99358 Human ser	C 505	11	52.4	25	9	ACK19865	Act19865 Human mic
433	11.2	53.3	50	4	AAU28113	Aau28113 Human SNP	C 506	11	52.4	25	9	ACK19865	Act19865 Human mic
434	11.2	53.3	50	4	AAU28113	Aau28113 Human SNP	C 507	11	52.4	25	9	ACK19865	Act19865 Human mic
435	11.2	53.3	50	6	ABZ07111	Abz07111 Human leu	C 508	11	52.4	25	10	ADB73746	Adb73746 Human PRO
436	11.2	53.3	50	6	ABZ04227	Abz04227 Human leu	C 509	11	52.4	25	10	ADB73746	Adb73746 Human PRO
437	11.2	53.3	50	6	ABZ01152	Abz01152 Human leu	C 510	11	52.4	25	10	ADB73746	Adb73746 Human PRO
438	11.2	53.3	50	6	ABZ05786	Abz05786 Human leu	C 511	11	52.4	25	10	ADB73746	Adb73746 Human PRO
439	11.2	53.3	50	6	ABZ06721	Abz06721 Human leu	C 512	11	52.4	25	10	ADB73746	Adb73746 Human PRO
440	11.2	53.3	50	6	ABZ07240	Abz07240 Human leu	C 513	11	52.4	25	10	ADB73746	Adb73746 Human PRO
441	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 514	11	52.4	25	10	ADB73746	Adb73746 Human PRO
442	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 515	11	52.4	25	10	ADB73746	Adb73746 Human PRO
443	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 516	11	52.4	25	10	ADB73746	Adb73746 Human PRO
444	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 517	11	52.4	25	10	ADB73746	Adb73746 Human PRO
445	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 518	11	52.4	25	10	ADB73746	Adb73746 Human PRO
446	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 519	11	52.4	25	10	ADB73746	Adb73746 Human PRO
447	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 520	11	52.4	25	10	ADB73746	Adb73746 Human PRO
448	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 521	11	52.4	25	10	ADB73746	Adb73746 Human PRO
449	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 522	11	52.4	25	10	ADB73746	Adb73746 Human PRO
450	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 523	11	52.4	25	10	ADB73746	Adb73746 Human PRO
451	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 524	11	52.4	25	10	ADB73746	Adb73746 Human PRO
452	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 525	11	52.4	25	10	ADB73746	Adb73746 Human PRO
453	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 526	11	52.4	25	10	ADB73746	Adb73746 Human PRO
454	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 527	11	52.4	25	10	ADB73746	Adb73746 Human PRO
455	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 528	11	52.4	25	10	ADB73746	Adb73746 Human PRO
456	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 529	11	52.4	25	10	ADB73746	Adb73746 Human PRO
457	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 530	11	52.4	25	10	ADB73746	Adb73746 Human PRO
458	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 531	11	52.4	25	10	ADB73746	Adb73746 Human PRO
459	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 532	11	52.4	25	12	ADB48574	Adb48574 Human PRO

C 533	11	52.4	25	12	AD89675	Ad89675 Human PRO	C 606	11	52.4	36	8	ACD56094	Ad56094 HBV enzym
C 534	11	52.4	25	12	AD61315	Ad61315 Human PRO	C 607	11	52.4	36	10	AD606506	Ad606506 Vector pg
C 535	11	52.4	25	12	AD64007	Ad64007 Human PRO	C 608	11	52.4	36	10	AD606505	Ad606505 Vector pg
C 536	11	52.4	25	12	AD64580	Ad64580 Human PRO	C 609	11	52.4	36	12	ADJ63897	AdJ63897 Plant lip
C 537	11	52.4	25	12	AD62419	Ad62419 Human PRO	C 610	11	52.4	36	12	ADJ63897	AdJ63897 Plant lip
C 538	11	52.4	25	12	AD64063	Ad64063 Human PRO	C 611	11	52.4	37	3	ADQ49147	AdQ49147 PDGF rece
C 539	11	52.4	25	12	AD62357	Ad62357 Human PRO	C 612	11	52.4	37	3	ADQ49147	AdQ49147 PDGF rece
C 540	11	52.4	25	12	AD63358	Ad63358 Human PRO	C 613	11	52.4	37	4	AAH96740	AAH96740 Human Chk
C 541	11	52.4	25	12	AD62702	Ad62702 Human PRO	C 614	11	52.4	37	4	AAH96771	AAH96771 Human Chk
C 542	11	52.4	25	12	AD62702	Ad62702 Human PRO	C 615	11	52.4	37	4	ABK05536	ABK05536 Human NOG
C 543	11	52.4	25	12	AD64125	Ad64125 Human PRO	C 616	11	52.4	37	4	ABK05562	ABK05562 Human NOG
C 544	11	52.4	25	12	AD63293	Ad63293 Human PRO	C 617	11	52.4	37	4	ABL47776	ABL47776 Human GRI
C 545	11	52.4	25	12	AD62530	Ad62530 Human PRO	C 618	11	52.4	37	6	ABK20763	ABK20763 Human ERG
C 546	11	52.4	25	12	AD62640	Ad62640 Human PRO	C 619	11	52.4	37	6	ABK20828	ABK20828 Human ERG
C 547	11	52.4	25	12	AD63419	Ad63419 Human PRO	C 620	11	52.4	37	6	ABK59194	ABK59194 Human CLC
C 548	11	52.4	25	12	AD64647	Ad64647 Human PRO	C 621	11	52.4	37	6	ABK59214	ABK59214 Human CLC
C 549	11	52.4	25	12	AD65041	Ad65041 Human PRO	C 622	11	52.4	37	6	ABK59220	ABK59220 Human CLC
C 550	11	52.4	25	12	AD64978	Ad64978 Human PRO	C 623	11	52.4	37	8	ACD53445	ACD53445 HBV G-cle
C 551	11	52.4	25	12	AD65166	Ad65166 Human PRO	C 624	11	52.4	37	8	ACC70729	ACC70729 Yeast PCR
C 552	11	52.4	25	12	AD64916	Ad64916 Human PRO	C 625	11	52.4	37	11	ADM55096	ADM55096 G-cleaver
C 553	11	52.4	25	12	AD64854	Ad64854 Human PRO	C 626	11	52.4	37	12	ADM64057	ADM64057 Hepatitis
C 554	11	52.4	25	12	AD65103	Ad65103 Human PRO	C 627	11	52.4	37	12	ADM61955	ADM61955 Hepatitis
C 555	11	52.4	25	12	AD65898	Ad65898 Human PRO	C 628	11	52.4	38	2	AAT66699	AAT66699 Primer cy
C 556	11	52.4	25	12	AD62437	Ad62437 Human PRO	C 629	11	52.4	38	2	AAH96669	AAH96669 Probe use
C 557	11	52.4	25	12	ADH2546	AdH2546 Human neu	C 630	11	52.4	39	4	AAH96669	AAH96669 Probe use
C 558	11	52.4	25	12	ADL0707	AdL0707 Human PRO	C 631	11	52.4	40	2	AAV36565	AAV36565 Human bra
C 559	11	52.4	25	12	ADL0707	AdL0707 Human PRO	C 632	11	52.4	40	2	AAV36565	AAV36565 Self-clea
C 560	11	52.4	25	12	AD04912	Ad04912 Human ade	C 633	11	52.4	41	4	AAV36565	AAV36565 Self-clea
C 561	11	52.4	25	12	ADP1649	AdP1649 Renal cel	C 634	11	52.4	41	4	AAV36565	AAV36565 Self-clea
C 562	11	52.4	26	3	AA55838	AA55838 Histone d	C 635	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 563	11	52.4	26	3	AAH4312	AAH43120 Antisense	C 636	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 564	11	52.4	26	4	AAH4312	AAH43120 Antisense	C 637	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 565	11	52.4	26	4	AAH4312	AAH43120 Antisense	C 638	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 566	11	52.4	26	4	AAH4312	AAH43120 Antisense	C 639	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 567	11	52.4	26	4	AAH4312	AAH43120 Antisense	C 640	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 568	11	52.4	26	4	AAH4312	AAH43120 Antisense	C 641	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 569	11	52.4	26	4	AAH4312	AAH43120 Antisense	C 642	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 570	11	52.4	27	2	AAH4312	AAH43120 Antisense	C 643	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 571	11	52.4	27	2	AAH4312	AAH43120 Antisense	C 644	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 572	11	52.4	27	6	ABK15325	ABK15325 PCR prime	C 645	11	52.4	41	6	AAV36565	AAV36565 Self-clea
C 573	11	52.4	27	12	ADN06126	AdN06126 Cricetulu	C 646	11	52.4	41	10	ACC42768	ACC42768 Histone H
C 574	11	52.4	28	2	AAH51027	AAH51027 5' primer	C 647	11	52.4	41	10	ACC42768	ACC42768 Histone H
C 575	11	52.4	28	2	AAH51028	AAH51028 5' primer	C 648	11	52.4	41	10	ACC42768	ACC42768 Histone H
C 576	11	52.4	28	2	AAH51028	AAH51028 5' primer	C 649	11	52.4	41	10	ACC42768	ACC42768 Histone H
C 577	11	52.4	28	3	AAH51116	AAH51116 PCR prime	C 650	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 578	11	52.4	28	3	AAH51116	AAH51116 PCR prime	C 651	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 579	11	52.4	28	4	AAH51116	AAH51116 PCR prime	C 652	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 580	11	52.4	28	4	AAH51116	AAH51116 PCR prime	C 653	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 581	11	52.4	28	6	AAH51116	AAH51116 PCR prime	C 654	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 582	11	52.4	28	10	ACF03379	ACF03379 Mycoplasma	C 655	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 583	11	52.4	28	12	ADJ76691	AdJ76691 OAS2 reve	C 656	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 584	11	52.4	29	2	AAH09775	AAH09775 Human mar	C 657	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 585	11	52.4	29	2	AAH09775	AAH09775 Human mar	C 658	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 586	11	52.4	29	3	AAH04584	AAH04584 Polymorph	C 659	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 587	11	52.4	30	2	AAH28031	AAH28031 Primer T4	C 660	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 588	11	52.4	30	6	ABK89309	ABK89309 N-acetyl	C 661	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 589	11	52.4	30	6	ABK89309	ABK89309 N-acetyl	C 662	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 590	11	52.4	30	8	ABK89309	ABK89309 N-acetyl	C 663	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 591	11	52.4	30	10	AD02111	Ad02111 Taqman pr	C 664	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 592	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 665	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 593	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 666	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 594	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 667	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 595	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 668	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 596	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 669	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 597	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 670	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 598	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 671	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 599	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 672	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 600	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 673	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 601	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 674	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 602	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 675	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 603	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 676	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 604	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 677	11	52.4	41	6	ABA90117	ABA90117 Oestrogen
C 605	11	52.4	31	3	AAH78876	AAH78876 Human gen	C 678	11	52.4	41	6	ABA90117	ABA90117 Oestrogen

c 679	11	52.4	46	8	ABX33862	Abx33862 Human ESR	752	11	52.4	50	12	ADG51765	Adg51765 Human PRO
c 680	11	52.4	46	8	ABX33912	Abx33912 Human ESR	753	11	52.4	50	12	ADG49269	Adg49269 Human PRO
c 681	11	52.4	46	8	ABX33913	Abx33913 Human ESR	754	11	52.4	50	12	ADG48645	Adg48645 Human PRO
c 682	11	52.4	46	8	ABX33848	Abx33848 Human ESR	755	11	52.4	50	12	ADG51141	Adg51141 Human PRO
c 683	11	52.4	46	8	ABX33874	Abx33874 Human ESR	756	11	52.4	50	12	ADG59085	Adg59085 Human PRO
c 684	11	52.4	48	3	AAA30308	Aaa30308 M. tuberc	757	11	52.4	50	12	ADG62541	Adg62541 Human PRO
c 685	11	52.4	48	6	ABQ94452	Abq94452 Tumour su	758	11	52.4	50	12	ADH25566	Adh25566 Human neu
c 686	11	52.4	49	6	ABQ75061	Abq75061 Vector co	759	11	52.4	50	12	ADML7343	Adml7343 Human PRO
c 687	11	52.4	50	2	AAT02969	Aat02969 Interleuk	760	11	52.4	50	12	ADL07177	Adl07177 Human PRO
c 688	11	52.4	50	2	AA234184	Aa234184 Human PRO	761	10.8	51.4	16	2	AAT43995	Aat43995 Octopine
c 689	11	52.4	50	3	AA58480	Aac58480 Human PRO	c 762	10.8	51.4	16	2	AAV64339	Aav64339 A. tumefa
c 690	11	52.4	50	3	AA78806	Aac78806 Human PRO	c 763	10.8	51.4	17	8	ABT38386	Abt38386 Tumour su
c 691	11	52.4	50	3	AA77646	Aaa77646 Human PRO	764	10.8	51.4	17	10	ADI50569	Adi50569 Human tum
c 692	11	52.4	50	4	AAL32133	Aal32133 Human SNP	c 765	10.8	51.4	17	10	ADI48125	Adi48125 Human tum
c 693	11	52.4	50	4	AAL32134	Aal32134 Human SNP	c 766	10.8	51.4	17	11	ADMA43630	Adm43630 Signature
c 694	11	52.4	50	4	AAL32098	Aal32098 Human SNP	767	10.8	51.4	18	8	ABX79721	Abx79721 EST polym
c 695	11	52.4	50	4	AAH90486	Aah90486 Human SNP	c 768	10.8	51.4	18	8	ADF48806	Adf48806 Vibrio pa
c 696	11	52.4	50	6	AB202787	Ab202787 Human leu	769	10.8	51.4	19	10	ADC84328	Adc84328 Human pap
c 697	11	52.4	50	6	AB204399	Ab204399 Human leu	770	10.8	51.4	19	10	ADF44230	Adf44230 HPV CP806
c 698	11	52.4	50	6	AB201657	Ab201657 Human leu	c 771	10.8	51.4	19	12	ADQ60771	Adq60771 Anti-AKT3
c 699	11	52.4	50	6	AB204224	Ab204224 Human leu	772	10.8	51.4	20	2	AAx79128	Aax79128 Primer At
c 700	11	52.4	50	8	ACA63752	Aca63752 Novel hum	773	10.8	51.4	20	6	ABQ92652	Abq92652 Human leu
c 701	11	52.4	50	8	ACA71916	Aca71916 Human PRO	774	10.8	51.4	20	6	ABZ30709	Abz30709 Candida a
c 702	11	52.4	50	8	ABX92556	Abx92556 Human PRO	775	10.8	51.4	20	6	ABN89725	Abn89725 Human ABC
c 703	11	52.4	50	8	ACA66297	Aca66297 Human sec	c 776	10.8	51.4	20	6	ABN89727	Abn89727 Human ABC
c 704	11	52.4	50	9	ADA24883	Ada24883 Secreted	c 777	10.8	51.4	20	12	ADH10876	Adh10876 Human cat
c 705	11	52.4	50	9	ACD29898	Acd29898 Novel hum	778	10.8	51.4	20	12	ADH10803	Adh10803 Human cat
c 706	11	52.4	50	9	ADA12544	Ada12544 Human sec	c 779	10.8	51.4	20	12	ADI1686	Adi1686 Human pro
c 707	11	52.4	50	9	ACD29313	Acd29313 Novel hum	c 780	10.8	51.4	20	12	ADI181745	Adi181745 Human pro
c 708	11	52.4	50	10	ADB73850	Adb73850 Human PRO	781	10.8	51.4	20	12	ADJ86940	Adj86940 Nucleic a
c 709	11	52.4	50	10	ADB76566	Adb76566 Human PRO	c 782	10.8	51.4	20	12	ADK95978	Adk95978 Primer of
c 710	11	52.4	50	10	ADC43992	Adc43992 Human PRO	c 783	10.8	51.4	20	12	ADK94362	Adk94362 Forward p
c 711	11	52.4	50	10	ADC61752	Adc61752 Human PRO	c 784	10.8	51.4	20	12	ADM11814	Adm11814 Endotheli
c 712	11	52.4	50	10	ADC63716	Adc63716 Human PRO	785	10.8	51.4	20	12	ADM11352	Adm11352 Endotheli
c 713	11	52.4	50	10	ADC66816	Adc66816 Human PRO	c 786	10.8	51.4	20	12	ADN01281	Adn01281 Endotheli
c 714	11	52.4	50	10	ADC68940	Adc68940 Human PRO	c 787	10.8	51.4	20	12	ADP68662	Adp68662 Human PPA
c 715	11	52.4	50	10	ADC63000	Adc63000 Human PRO	788	10.8	51.4	21	2	AXA83448	Aax83448 ZAM retro
c 716	11	52.4	50	10	ADC68065	Adc68065 Human PRO	c 789	10.8	51.4	21	4	APF96690	Aaf96690 Human gen
c 717	11	52.4	50	10	ADC41385	Adc41385 Human PRO	c 790	10.8	51.4	21	6	ABA04885	Abao4885 TT virus
c 718	11	52.4	50	10	ADC67440	Adc67440 Human PRO	c 791	10.8	51.4	21	10	ABV75972	Abv75972 Mouse GLU
c 719	11	52.4	50	10	ADC62376	Adc62376 Human PRO	792	10.8	51.4	21	10	ADL07578	Adl07578 R. picket
c 720	11	52.4	50	10	ADC42009	Adc42009 Human PRO	c 793	10.8	51.4	21	11	ADJ12916	Adj12916 Human DNA
c 721	11	52.4	50	10	ADE49378	Ade49378 Human PRO	c 794	10.8	51.4	21	11	ADJ13508	Adj13508 Human DNA
c 722	11	52.4	50	10	ADE35432	Ade35432 Human PRO	c 795	10.8	51.4	21	11	ADM65359	Adm65359 NRY polym
c 723	11	52.4	50	10	ADE16546	Ade16546 Human PRO	c 796	10.8	51.4	22	2	AAQ92322	Aaq92322 Mango thi
c 724	11	52.4	50	10	ADB73161	Adb73161 Human PRO	797	10.8	51.4	22	2	AAQ09940	Aaq09940 Human bla
c 725	11	52.4	50	10	ADD72519	Add72519 Human PRO	c 798	10.8	51.4	22	3	AAV15247	Aav15247 Thioester
c 726	11	52.4	50	10	ABE17170	Abel7170 Human PRO	799	10.8	51.4	22	3	AA666728	Aa666728 Dog genom
c 727	11	52.4	50	10	ADF47184	Adf47184 Human PRO	800	10.8	51.4	22	8	ABZ76438	Abz76438 IBV S-1 g
c 728	11	52.4	50	10	ADG33407	Adg33407 Human DNA	c 801	10.8	51.4	23	8	AAZ55207	Aaz55207 HIV-1 tar
c 729	11	52.4	50	10	ADG52941	Adg52941 Human PRO	c 802	10.8	51.4	24	2	AAT43545	Aat43545 Primer 72
c 730	11	52.4	50	10	ADG60261	Adg60261 Human PRO	803	10.8	51.4	24	2	AAV81937	Aav81937 Caenorhab
c 731	11	52.4	50	10	ADL61021	Adl61021 Human PRO	c 804	10.8	51.4	24	3	AAAL12813	Aaal12813 PCR prime
c 732	11	52.4	50	10	ACD42717	Acd42717 Secreted	805	10.8	51.4	24	6	ADJ26335	Adj26335 ace2e18b
c 733	11	52.4	50	12	ADE48678	Ade48678 Human PRO	806	10.8	51.4	24	11	ADL95470	Adl95470 Angiotens
c 734	11	52.4	50	12	ADE89779	Ade89779 Human PRO	807	10.8	51.4	24	12	ADQ90193	Adq90193 Chlamydia
c 735	11	52.4	50	12	ADP61419	Adp61419 Human PRO	808	10.8	51.4	25	4	AAZ21338	Aaz21338 Shigella
c 736	11	52.4	50	12	ADP40111	Adp40111 Human PRO	809	10.8	51.4	25	4	AAF79599	Aaf79599 Human Akt
c 737	11	52.4	50	12	ADP45907	Adp45907 Human PRO	c 810	10.8	51.4	25	4	AAH40525	Aah40525 SNP speci
c 738	11	52.4	50	12	ADP24303	Adp24303 Human PRO	c 811	10.8	51.4	25	5	AAI62117	Aai62117 Soybean 3
c 739	11	52.4	50	12	ADP40735	Adp40735 Human PRO	812	10.8	51.4	25	9	ACI85321	Act85321 Human mic
c 740	11	52.4	50	12	ADP23679	Adp23679 Human PRO	813	10.8	51.4	25	9	ACK185320	Act185320 Human mic
c 741	11	52.4	50	12	ADP33662	Adp33662 Human PRO	814	10.8	51.4	25	9	ACK05637	Act05637 Human mic
c 742	11	52.4	50	12	ADP27129	Adp27129 Human PRO	c 815	10.8	51.4	25	9	ACI65687	Act65687 Human mic
c 743	11	52.4	50	12	ADP27765	Adp27765 Human PRO	815	10.8	51.4	25	9	ACI47560	Act47560 Human mic
c 744	11	52.4	50	12	ADP41359	Adp41359 Human PRO	c 817	10.8	51.4	25	9	ACI96904	Act96904 Human mic
c 745	11	52.4	50	12	ADP33038	Adp33038 Human PRO	818	10.8	51.4	25	9	ACK12303	Act12303 Human mic
c 746	11	52.4	50	12	ADP25404	Adp25404 Human PRO	c 819	10.8	51.4	25	9	ACK181476	Act181476 Human mic
c 747	11	52.4	50	12	ADP26505	Adp26505 Human PRO	c 820	10.8	51.4	25	9	ACH52970	Act52970 DNA targe
c 748	11	52.4	50	12	ADP34294	Adp34294 Human PRO	c 821	10.8	51.4	25	10	ADC26465	Adc26465 NOV prote
c 749	11	52.4	50	12	ADP46531	Adp46531 Human PRO	c 822	10.8	51.4	26	2	AAQ63946	Aaq63946 Probe for
c 750	11	52.4	50	12	ADG50517	Adg50517 Human PRO	c 823	10.8	51.4	26	3	AAZ91983	Aaz91983 Mahogany
c 751	11	52.4	50	12	ADG49893	Adg49893 Human PRO	c 824	10.8	51.4	26	6	ABL49982	AbL49982 Rice OSSA

C 825	10.8	51.4	27	4	AH21598	Aah21598 Human hyp	C 898	10.8	51.4	50	4	AA28112	Aal28112 Human SNP
C 826	10.8	51.4	27	8	ABZ68363	Abz68363 Primer Te	C 899	10.8	51.4	50	4	AAI78425	Aai78425 Human gill
C 827	10.8	51.4	27	8	ABT16214	Abt16214 NOVX rela	C 900	10.8	51.4	50	6	ABZ01191	Abz01191 Human leu
C 828	10.8	51.4	27	10	ADC26483	Adc26483 NOV prote	C 901	10.8	51.4	50	6	ABZ03490	Abz03490 Human leu
C 829	10.8	51.4	27	10	ADC51654	Adc51654 5' PCR pr	C 902	10.8	51.4	50	10	ADG33470	Adg33470 Human DNA
C 830	10.8	51.4	27	12	ADO41905	Ado41905 Novel hum	C 903	10.6	50.5	17	2	AAT53604	Aat53604 Rat ICAM
C 831	10.8	51.4	27	12	ADP69073	Adp69073 Human NOV	C 904	10.6	50.5	17	6	ABV79960	Abv79960 Human HTP
C 832	10.8	51.4	28	2	AX15329	Ax15329 Oligonucl	C 905	10.6	50.5	17	6	ABV79961	Abv79961 Human HTP
C 833	10.8	51.4	28	3	AZ37290	Az37290 PCR prime	C 906	10.6	50.5	17	10	ADF62571	Adf62571 Human PCC
C 834	10.8	51.4	28	3	AA10286	Aa10286 Lambda ph	C 907	10.6	50.5	18	3	AAA66931	Aa66931 Dog genom
C 835	10.8	51.4	28	4	AAF26450	Aaf26450 HIV-1 pol	C 908	10.6	50.5	18	4	AAH74505	Aah74505 PCR prime
C 836	10.8	51.4	28	6	ABL60690	Ab160690 S. enteri	C 909	10.6	50.5	18	4	ADP71078	Adp71078 Mutant hu
C 837	10.8	51.4	28	6	ABK96401	Abk96401 PCR prime	C 910	10.6	50.5	19	3	AAZ37296	Aaz37296 PCR prime
C 838	10.8	51.4	29	3	AA16765	Aa16765 Human sec	C 911	10.6	50.5	19	6	ASG97804	Asg97804 Murine SA
C 839	10.8	51.4	29	10	ADC22115	Adc22115 Group II	C 912	10.6	50.5	19	12	ADM16144	Adm16144 Murine SA
C 840	10.8	51.4	30	2	AAV4583	Aav4583 Primer 40	C 913	10.6	50.5	20	2	AAQ93439	Aaq93439 Equine cl
C 841	10.8	51.4	30	6	ABX68919	Abx68919 Novel Hel	C 914	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 842	10.8	51.4	30	12	ADM11826	Adm11826 Composite	C 915	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 843	10.8	51.4	30	12	ADP08008	Adp08008 Human RAD	C 916	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 844	10.8	51.4	31	2	AAV67583	Aav67583 Nucleotid	C 917	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 845	10.8	51.4	31	2	AAK06354	Aak06354 Human bia	C 918	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 846	10.8	51.4	31	2	AAK06287	Aak06287 Human bia	C 919	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 847	10.8	51.4	31	3	AAZ45640	Aaz45640 PCR prime	C 920	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 848	10.8	51.4	31	3	AAZ79211	Aaz79211 Human gen	C 921	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 849	10.8	51.4	31	3	AAA79033	Aaa79033 Human gen	C 922	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 850	10.8	51.4	31	12	ADO79546	Ado79546 KIAA0783	C 923	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 851	10.8	51.4	31	12	ADO79547	Ado79547 KIAA0783	C 924	10.6	50.5	20	2	AAQ93440	Aaq93440 Equine cl
C 852	10.8	51.4	32	2	AAK87128	Aak87128 Platelet	C 925	10.6	50.5	20	3	AAQ93440	Aaq93440 Equine cl
C 853	10.8	51.4	32	6	ABK53072	Abk53072 Tobacco s	C 926	10.6	50.5	20	3	AAQ93440	Aaq93440 Equine cl
C 854	10.8	51.4	33	2	AAQ46735	Aaq46735 HIV ampli	C 927	10.6	50.5	20	3	AAQ93440	Aaq93440 Equine cl
C 855	10.8	51.4	33	2	AAQ44311	Aaq44311 HTLV-1 am	C 928	10.6	50.5	20	4	AAH24675	Aah24675 Nucleotid
C 856	10.8	51.4	33	2	AAQ89511	Aaq89511 Human imm	C 929	10.6	50.5	20	4	AAH24675	Aah24675 Nucleotid
C 857	10.8	51.4	33	5	AB197660	Ab197660 Endogenou	C 930	10.6	50.5	20	4	AAH24675	Aah24675 Nucleotid
C 858	10.8	51.4	33	6	ABQ76004	Abq76004 Human ger	C 931	10.6	50.5	20	5	AAQ93440	Aaq93440 Equine cl
C 859	10.8	51.4	34	12	ADJ93351	Adj93351 Bpntase 3	C 932	10.6	50.5	20	5	AAQ93440	Aaq93440 Equine cl
C 860	10.8	51.4	35	10	ADF50493	Adf50493 Mutagenic	C 933	10.6	50.5	20	6	ABN86460	Abn86460 E. coli h
C 861	10.8	51.4	35	10	ADF50494	Adf50494 Mutagenic	C 934	10.6	50.5	20	6	ABN86460	Abn86460 E. coli h
C 862	10.8	51.4	35	10	ADF76038	Adf76038 RNA PCR p	C 935	10.6	50.5	20	6	ABX10634	Abx10634 Synthetic
C 863	10.8	51.4	35	10	ADF75958	Adf75958 DNA PCR p	C 936	10.6	50.5	20	8	ACC49979	Acc49979 AGGF prim
C 864	10.8	51.4	36	2	AAQ74610	Aaq74610 Primer fo	C 937	10.6	50.5	20	8	ABZ81582	Abz81582 PKA regul
C 865	10.8	51.4	36	6	ABL49295	Ab149295 Human lun	C 938	10.6	50.5	20	9	ACC84110	Acc84110 Thermoasc
C 866	10.8	51.4	36	6	ABQ92481	Abq92481 Human lun	C 939	10.6	50.5	20	9	ACC84110	Acc84110 Thermoasc
C 867	10.8	51.4	36	9	ADA28534	Ada28534 Lung tumo	C 940	10.6	50.5	20	10	ADB99384	Adb99384 Human PCR
C 868	10.8	51.4	36	10	ADH37098	Adh37098 Lung cano	C 941	10.6	50.5	20	10	ADF87378	Adf87378 Single nu
C 869	10.8	51.4	36	12	ADM56901	Adm56901 Human lun	C 942	10.6	50.5	20	10	ACA88968	Acca88968 Selection
C 870	10.8	51.4	37	2	AAQ74519	Aaq74519 Primer fo	C 943	10.6	50.5	20	12	ADH63406	Adh63406 Human glu
C 871	10.8	51.4	37	2	AAV72392	Aav72392 A. nidula	C 944	10.6	50.5	20	12	ADH64222	Adh64222 Human glu
C 872	10.8	51.4	38	2	AAK86025	Aak86025 PCR prime	C 945	10.6	50.5	20	12	ADH63695	Adh63695 Human glu
C 873	10.8	51.4	38	3	AAA12834	Aaa12834 Bacterial	C 946	10.6	50.5	20	12	ADH63695	Adh63695 Human glu
C 874	10.8	51.4	38	6	ABL39950	Ab139950 HIV type	C 947	10.6	50.5	20	12	ADK80252	Adk80252 Primer of
C 875	10.8	51.4	38	9	ACD28028	Ac28028 Human pol	C 948	10.6	50.5	20	12	ADJ25370	Adj25370 Human end
C 876	10.8	51.4	38	10	ADG79067	Adg79067 Schizophr	C 949	10.6	50.5	20	12	ADJ25202	Adj25202 Human end
C 877	10.8	51.4	38	12	ADM73776	Adm73776 HIV-1 typ	C 950	10.6	50.5	20	12	ADK80244	Adk80244 Chimeric
C 878	10.8	51.4	40	2	AAK76461	Aak76461 Human BRC	C 951	10.6	50.5	20	12	ADK80308	Adk80308 Chimeric
C 879	10.8	51.4	40	10	ADH11095	Adh11095 E.coli AT	C 952	10.6	50.5	20	12	ADK80210	Adk80210 Chimeric
C 880	10.8	51.4	41	2	AAV81512	Aav81512 Oligonucl	C 953	10.6	50.5	20	12	ADK80644	Adk80644 Chimeric
C 881	10.8	51.4	41	3	AAK73029	Aak73029 Transglut	C 954	10.6	50.5	20	12	ADK80644	Adk80644 Chimeric
C 882	10.8	51.4	41	3	AAQ76007	Abq76007 Human ger	C 955	10.6	50.5	20	12	ADO51568	Ado51568 Human ser
C 883	10.8	51.4	41	6	ABQ76006	Abq76006 Human ger	C 956	10.6	50.5	20	12	ADO51534	Ado51534 Human ser
C 884	10.8	51.4	41	6	ABT14775	Abt14775 Human Bcl	C 957	10.6	50.5	21	2	AAK730378	Aak730378 Kvl. 2-HA
C 885	10.8	51.4	41	8	AAK78454	Aak78454 Primer 1.	C 958	10.6	50.5	21	2	AAV40864	Aav40864 Primer fo
C 886	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 959	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 887	10.8	51.4	45	2	AAK28661	Aak28661 Amplifica	C 960	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 888	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 961	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 889	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 962	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 890	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 963	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 891	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 964	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 892	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 965	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 893	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 966	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 894	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 967	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 895	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 968	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 896	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 969	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo
C 897	10.8	51.4	45	2	AAK30006	Aak30006 Amplifica	C 970	10.6	50.5	21	2	AAV40868	Aav40868 Primer fo


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c 971 10.6 50.5 21 12 ADI59763
c 972 10.6 50.5 21 12 ADK71066
c 973 10.6 50.5 21 12 ADP83662
c 974 10.6 50.5 21 12 ADP83662
c 975 10.6 50.5 21 12 ADQ28803
c 976 10.6 50.5 22 4 AAC84332
c 977 10.6 50.5 22 8 AAO06060
c 978 10.6 50.5 22 8 ABX72432
c 979 10.6 50.5 22 10 ADJ95231
c 980 10.6 50.5 22 12 ADN63211
c 981 10.6 50.5 22 12 ADP11050
c 982 10.6 50.5 23 10 ADF31891
c 983 10.6 50.5 23 12 ADI30523
c 984 10.6 50.5 23 12 ADI59981
c 985 10.6 50.5 23 12 ADI59872
c 986 10.6 50.5 23 12 ADI59978
c 987 10.6 50.5 24 2 AAQ13972
c 988 10.6 50.5 24 6 ABQ11011
c 989 10.6 50.5 24 6 ABQ04724
c 990 10.6 50.5 24 6 ABQ04765
c 991 10.6 50.5 24 6 ABQ11052
c 992 10.6 50.5 24 6 ABQ00368
c 993 10.6 50.5 24 6 AB185441
c 994 10.6 50.5 24 6 AB184436
c 995 10.6 50.5 24 6 AB185440
c 996 10.6 50.5 24 6 AB184437
c 997 10.6 50.5 24 10 ADE85981
c 998 10.6 50.5 25 2 AAT04462
c 999 10.6 50.5 25 3 AAZ91935
c1000 10.6 50.5 25 4 AAH39127
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ALIGNMENTS

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RESULT 1
AAD43284
ID AAD43284 standard; DNA; 21 BP.
AC AAD43284;
XX
XX
XX
XX 14-NOV-2002 (first entry)
XX
XX DNA used to illustrate the methods of the invention.
XX
XX Amplification; target nucleic acid; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX misc_binding 8..12
XX /tag= a
XX /bound_moiety= "Nucleotides 21-17"
XX
XX misc_binding 17..21
XX /tag= b
XX /bound_moiety= "Nucleotides 12-8"
XX
XX EP1236805-A1.
XX
XX 04-SEP-2002.
XX
XX 27-FEB-2002; 2002EP-00004483.
XX
XX 02-MAR-2001; 2001EP-00105172.
XX
XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Jaeger S;
XX
XX WPI; 2002-610695/66.
XX
XX Amplification of a target nucleic acid region using a specific control
```

```
PT sequence.
XX
XX Disclosure; Page 16; 28pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
XX acid region in a sample using a specific control sequence. The invention
XX is also directed to a method of determination of a target nucleic acid
XX using a special control nucleic acid. Nucleic acids of the invention are
XX used as a control in a reaction for amplifying target nucleic acids and
XX as a control in a hybridisation reaction for determination of target
XX nucleic acids. The present sequence is a DNA used to illustrate the
XX methods of the invention
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21; DB 6; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.85;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AGCGCATGCCAGATTACTGGC 21
XX Db 1 AGCGCATGCCAGATTACTGGC 21
XX
XX RESULT 2
XX AAD43736
XX ID AAD43736 standard; DNA; 21 BP.
XX AC AAD43736;
XX
XX 14-NOV-2002 (first entry)
XX
XX DNA sequence to illustrate the method of the invention.
XX
XX Amplification; target nucleic acid; control nucleic acid; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX misc_binding 8..12
XX /tag= a
XX /bound_moiety= "Nucleotides 21-17"
XX
XX misc_binding 17..21
XX /tag= b
XX /bound_moiety= "Nucleotides 12-8"
XX
XX EP1236804-A1.
XX
XX 04-SEP-2002.
XX
XX 02-MAR-2001; 2001EP-00105172.
XX
XX 02-MAR-2001; 2001EP-00105172.
XX
XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Jaeger S;
XX
XX WPI; 2002-610694/66.
XX
XX Amplification of a target nucleic acid region using control sequences.
XX
XX Disclosure; Page 15; 29pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
XX acid region. The method is useful for amplification of a nucleic acid
XX molecule using control nucleic acid sequences. The control nucleic acid
XX sequences are at least in part parallel-complementary to the sequence of
XX the target nucleic acid. The present sequence is a DNA used to illustrate
XX the method of the invention
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
```


Query Match 100.0%; Score 21; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.85;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCGCATGCCAGATTACTGGC 21
 DB 1 AGCGCATGCCAGATTACTGGC 21

RESULT 3
 ADE29100/c
 ID ADE29100 standard; RNA; 21 BP.
 XX
 AC ADE29100;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE SNUOPTIN antisense silencing RNA - SEQ ID 86.
 XX
 KW anti-HIV; SID; selected interacting domain; HIV; gene therapy; siRNA;
 KW silencing RNA; HIV-1 integrase; LEDGF; MCM7; HBO1; Snurportin; VBPI;
 KW Transportin-SR; EIF3S3; ss; SNUOPTIN.
 XX
 OS Unidentified.
 XX
 PN WO2003046176-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-EP013868.
 XX
 PR 26-NOV-2001; 2001US-0333346P.
 XX
 PR 31-MAY-2002; 2002US-0385132P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P, Rain J, Benarous R, Emiliani S, Berlioz-Torrent C;
 PI Blot G;
 XX
 DR WPI; 2003-505199/47.
 XX
 PT New complex between two interacting proteins, useful for screening
 PT molecules that inhibit human immunodeficiency virus or for preparing a
 PT medicament for treating HIV-1.
 XX
 PS Example 8; SEQ ID NO 86; 102pp; English.
 XX
 CC The invention relates to a novel complex between two interacting proteins
 CC listed within the specification. The complex of the invention
 CC demonstrates anti-HIV activity whilst the SID (selected interacting
 CC domains) and polypeptides may be useful for screening molecules that
 CC inhibit human immunodeficiency virus (HIV), as well as during gene
 CC therapy procedures. The siRNAs (silencing RNAs) targeted against cellular
 CC proteins interacting with HIV-1 integrase, LEDGF, MCM7, HBO1, Snurportin,
 CC VBPI, Transportin-SR and EIF3S3, are useful in preparing a medicament for
 CC treating HIV-1. The current sequence is that of the siRNA of the
 CC invention.
 XX
 SQ Sequence 21 BP; 3 A; 5 C; 6 G; 2 T; 5 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 10; Length 21;
 Best Local Similarity 88.2%; Pred. No. 3.8e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CATGCCAGATTACTGGC 21
 DB 18 CATGCCAGAGACTGGC 2

RESULT 4
 ADE29099
 ID ADE29099 standard; RNA; 21 BP.

XX ADE29099;
 XX 29-JAN-2004 (first entry)
 XX SNUOPTIN sense silencing RNA - SEQ ID 85.
 XX
 XX anti-HIV; SID; selected interacting domain; HIV; gene therapy; siRNA;
 XX silencing RNA; HIV-1 integrase; LEDGF; MCM7; HBO1; Snurportin; VBPI;
 XX Transportin-SR; EIF3S3; ss; SNUOPTIN.
 XX
 OS Unidentified.
 XX
 PN WO2003046176-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-EP013868.
 XX
 PR 26-NOV-2001; 2001US-0333346P.
 XX
 PR 31-MAY-2002; 2002US-0385132P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P, Rain J, Benarous R, Emiliani S, Berlioz-Torrent C;
 PI Blot G;
 XX
 DR WPI; 2003-505199/47.
 XX
 PT New complex between two interacting proteins, useful for screening
 PT molecules that inhibit human immunodeficiency virus or for preparing a
 PT medicament for treating HIV-1.
 XX
 PS Example 8; SEQ ID NO 85; 102pp; English.
 XX
 CC The invention relates to a novel complex between two interacting proteins
 CC listed within the specification. The complex of the invention
 CC demonstrates anti-HIV activity whilst the SID (selected interacting
 CC domains) and polypeptides may be useful for screening molecules that
 CC inhibit human immunodeficiency virus (HIV), as well as during gene
 CC therapy procedures. The siRNAs (silencing RNAs) targeted against cellular
 CC proteins interacting with HIV-1 integrase, LEDGF, MCM7, HBO1, Snurportin,
 CC VBPI, Transportin-SR and EIF3S3, are useful in preparing a medicament for
 CC treating HIV-1. The current sequence is that of the siRNA of the
 CC invention.
 XX
 SQ Sequence 21 BP; 5 A; 6 C; 5 G; 2 T; 3 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 10; Length 21;
 Best Local Similarity 76.5%; Pred. No. 3.8e+03;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 CATGCCAGATTACTGGC 21
 DB 2 CAUGCCAGAGACUGGC 18

RESULT 5
 AAT65036
 ID AAT65036 standard; DNA; 44 BP.
 XX
 AC AAT65036;
 XX
 DT 19-JUN-1997 (first entry)
 XX
 DE Aspergillus oryzae alpha-glucosidase gene PCR sense primer.
 XX
 KW Fungus; fungal; enhancer element; terminator; recombinant protein;
 KW polymerase chain reaction; amplification primer; ss.
 XX
 OS Synthetic.
 XX
 PN JP09009968-A.

XX 14-JAN-1997.
PD
XX
XX 29-JUN-1995; 95JP-00163579.
XX
XX 29-JUN-1995; 95JP-00163579.
XX
XX (OZEK-) OZEKI KK.
PA (KOKU-) KOKUZEI CHO CHORHAN.
XX
XX WPI; 1997-126425/12.
DR
XX
XX Fungal DNA enhancer element - used to transform other host fungus e.g
PT Aspergillus oryzae, to produce large quantities of a gene product.
XX
XX Example 11; Page 12; 25pp; Japanese.
XX
XX The promoter region of the alpha-glucosidase (agda) gene of Aspergillus
CC oryzae contains two novel enhancer elements: one (designated "enhancer-
CC B") corresponds to the consensus sequence CGGNATTGA and the other
CC (designated "enhancer-C") is of sequence CCAATCAGCGT. By inserting at
CC least one of the enhancer elements into a promoter region which is
CC functional in fungi, the activity of the promoter is enhanced. Using such
CC improved promoters, a gene of interest can be expressed efficiently in
CC transformed fungi. An oligonucleotide primer of the present sequence was
CC used in the construction of a high expression plasmid which contained an
CC enhanced promoter
XX
XX Sequence 44 BP; 10 A; 12 C; 13 G; 9 T; 0 U; 0 Other;
SQ
Query Match 64.8%; Score 13.6; DB 2; Length 44;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGCGCATGCCAGATTACTGG 20
||| ||||| ||||| |||||
Db 3 AGAGCATGCCATATGACTAG 22

RESULT 6
AAF58409
ID AAF58409 standard; DNA; 19 BP.
XX
XX AAF58409;
AC
XX
XX 25-APR-2001 (first entry)
DT
XX
XX Murine mOCILrP1 clone PCR primer OCILm47.
DE
XX
XX Osteopathic; mononuclear osteoclast precursor formation inhibition;
KW calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;
KW osteoclast differentiation; bone resorption; primary hyperparathyroidism;
KW Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;
KW humoral hypercalcaemia; cancer; PCR primer; ss.
XX
XX Mus musculus.
OS
XX
XX WO200105964-A1.
PN
XX
XX 25-JAN-2001.
PD
XX
XX 19-JUL-2000; 2000WO-AU000864.
PF
XX
XX 19-JUL-1999; 99AU-00001675.
PR
XX
XX (SVIN-) ST VINCENTS INST MEDICAL RES.
PA
XX
XX Zhou H, Kartsogiannis V, Hu Y, Gillespie MT, Ng KW;
PI WPI; 2001-103148/11.
XX
XX Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed
PT on an osteoblast cell surface and used for treating excessive bone

PT resorption in conditions such as osteoporosis and Paget's disease.
XX Claim 35; Page 17; 131pp; English.
XX
XX The present invention relates to osteoclast inhibitory lectin coding
CC sequences and proteins (OCIL; see AAF58407). OCIL is a type II membrane
CC protein which is expressed on osteoblast cell surfaces. OCIL inhibits
CC osteoclast differentiation from haematopoietic cell precursors. OCIL is
CC useful for treating a condition with excessive bone resorption, including
CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
CC conditions where cancer has metastasised to the bone
XX
XX Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 62.9%; Score 13.2; DB 4; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CGCATGCCAGATTACTGG 20
||| ||||| ||||| |||||
Db 2 CCCATGCCAGATTGCTTG 19

RESULT 7
ADF91091/c
ID ADF91091 standard; DNA; 20 BP.
XX
XX ADF91091;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Microorganism detection PCR primer, SEQ ID 174.
DE
XX
XX Detection; microorganism; PCR; primer; bacterium; fungus; protozoan;
KW virus; diarrhoea; food poisoning; ss.
XX
XX Escherichia coli.
OS
XX
XX JP2003164282-A.
PN
XX
XX 10-JUN-2003.
PD
XX
XX 29-NOV-2001; 2001JP-00365153.
PF
XX
XX 29-NOV-2001; 2001JP-00365153.
PR
XX
XX (RAKA-) RAKAN KK.
PA (GIFU-) GIFU DAIGAKUCHO.
PA
XX
XX WPI; 2003-793230/75.
XX
XX Rapid, sensitive detection of specific or unspecified microbes causing
PT diarrhea and food poisoning, using primers which target universal and
PT specific genes, and amplifying by PCR under heat cycle conditions
PT suitable for many detections.
XX
XX Claim 1; SEQ ID NO 174; 69pp; Japanese.
PS
XX
XX The present invention relates to a method for detecting microorganisms
CC using primers (ADF90918-ADF91145). The method is used for detecting
CC microorganisms (bacteria, fungi, protozoa, viruses) which cause diarrhoea
CC symptoms, and pathogenic microbes of food poisoning. The method can be
CC used to detect unspecified microbes, or specific pathogens, or for the
CC simultaneous detection of many kinds of microorganism.
XX
XX Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 62.9%; Score 13.2; DB 10; Length 20;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 GCATGCCAGATTACTGGC 21

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Db      | ||| ||||| |||||
        18 GAATGTCAGATACTGGC 1

RESULT 8
AAx83448/c
ID  AAx83448 standard; DNA; 21 BP.
XX
AC  AAx83448;
XX
DT  27-AUG-2003 (revised)
DT  14-SEP-1999 (first entry)
XX
DE  ZAM retroelement genome PCR primer o2.
XX
KW  Genome; retroelement; retrovirus; ZAM; gag; pol; env; LTR; vector;
KW  long terminal repeat; gene therapy; primer; PCR; amplification; ss.
XX
OS  Synthetic.
OS  Drosophila melanogaster.
XX
FN  FR2772045-A1.
XX
PD  11-JUN-1999.
XX
PF  10-DEC-1997; 97FR-00015655.
XX
PR  10-DEC-1997; 97FR-00015655.
XX
PA  (UYAU-) UNIV AUVERGNE.
XX
PI  Leblanc P, Vaury C;
XX
PT  WPI; 1999-359998/31.
XX
PT  New Drosophila ZAM retroelement nucleic acid - useful in gene transfer or
XX  gene therapy.
XX
PS  Example 1; Page 11; 55pp; French.
XX
CC  Primers AAX83446-X83447 were used to PCR amplify the complete genomic DNA
CC  sequence of a novel retroelement ZAM (AAX83445) found in Drosophila
CC  melanogaster. Similarly to other retroelements and retroviruses, ZAM
CC  contains 3 genes (gag, pol and env) and long terminal repeats (LTR's) at
CC  either end of the genome. Vectors containing the sequence can be used for
CC  gene transfer or gene therapy. (Updated on 27-AUG-2003 to correct OS
CC  field.)
XX
SQ  Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match      62.9%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTGGC 21
Db      20 GAATGCCAGTTAACTGGC 3

RESULT 9
ABN83493/c
ID  ABN83493 standard; DNA; 22 BP.
XX
AC  ABN83493;
XX
DT  30-AUG-2002 (first entry)
XX
DE  Escherichia coli O157:H7 PCR primer stx2R.
XX
KW  PCR; primer; bacterium strain typing; enterohaemorrhagic; ss.
XX
OS  Escherichia coli O157:H7.
XX

Query Match      62.9%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTGGC 21
Db      20 GAATGCCAGTTAACTGGC 3

RESULT 10
ABQ87925/c
ID  ABQ87925 standard; DNA; 32 BP.
XX
AC  ABQ87925;
XX
DT  10-SEP-2002 (first entry)
XX
DE  Enterohaemorrhagic Escherichia coli detection PCR primer SEQ ID NO 24.
XX
KW  Enterohaemorrhagic Escherichia coli; EHEC; slt; Shigella-like toxin; eae;
KW  hlyA; detection; food; PCR; primer; ss.
XX
OS  Escherichia coli.
XX
FN  WO200253771-A2.
XX
PD  11-JUL-2002.
XX
PF  15-OCT-2001; 2001WO-EP011901.
XX
PR  08-JAN-2001; 2001DE-01000493.
XX
PA  (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
PI  Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
XX
DR  WPI; 2002-528864/56.
XX
PT  Detecting enterohaemorrhagic Escherichia coli, from the presence of
PT  sequences from the Shigella-like toxin locus and at least one of eae and

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PN      WO200236827-A1.
XX
PD      10-MAY-2002.
XX
PF      01-NOV-2001; 2001WO-US044963.
XX
PR      01-NOV-2000; 2000US-0244973P.
XX
PA      (GEHO) GEN HOSPITAL CORP.
XX
XX      Kudva I, Calderwood SB, Ausubel FW;
XX      WPI; 2002-519260/55.
XX
PT      Typing the strain of bacterial isolate, by providing genomic DNA from the
PT      isolate, performing polymerization on DNA using primers comprising
PT      restriction nuclease site, thus producing amplicon having restriction
PT      site.
XX
PS      Example 2; Page 43; 87pp; English.
XX
CC      The present invention relates to a method for typing the strain of a
CC      bacterial isolate (I). The method involves providing genomic DNA (GDNA)
CC      from (I), performing PCR on GDNA using a first and second primer to
CC      amplify GDNA comprising a restriction nuclease restriction site, thus
CC      producing an amplicon having the restriction site, and characterising the
CC      amplicon and thus typing the strain of (I). To illustrate the method a
CC      genomic sequence, comprising O-islands, from enterohaemorrhagic
CC      Escherichia coli O157:H7 was used. The present sequence is a PCR primer
CC      used to amplify a virulence gene from E. coli O157:H7
XX
SQ      Sequence 22 BP; 4 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match      62.9%; Score 13.2; DB 6; Length 22;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTGGC 21
Db      20 GAATGTCAGATACTGGC 3

RESULT 10
ABQ87925/c
ID  ABQ87925 standard; DNA; 32 BP.
XX
AC  ABQ87925;
XX
DT  10-SEP-2002 (first entry)
XX
DE  Enterohaemorrhagic Escherichia coli detection PCR primer SEQ ID NO 24.
XX
KW  Enterohaemorrhagic Escherichia coli; EHEC; slt; Shigella-like toxin; eae;
KW  hlyA; detection; food; PCR; primer; ss.
XX
OS  Escherichia coli.
XX
FN  WO200253771-A2.
XX
PD  11-JUL-2002.
XX
PF  15-OCT-2001; 2001WO-EP011901.
XX
PR  08-JAN-2001; 2001DE-01000493.
XX
PA  (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
PI  Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
XX
DR  WPI; 2002-528864/56.
XX
PT  Detecting enterohaemorrhagic Escherichia coli, from the presence of
PT  sequences from the Shigella-like toxin locus and at least one of eae and

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PT hlyA loci.
 XX Claim 3; Page 18; 86pp; German.
 PS
 CC The invention relates to detection (M1) of enterohaemorrhagic Escherichia
 CC coli (EHEC) in a sample from the presence of nucleic acid sequences from
 CC the slt (Shigella-like toxin) locus and the eae and/or hlyA loci. (M1) is
 CC useful for detecting of EHEC e.g. in foods. The method provides secure
 CC detection of EHEC (including differentiation from other types of E.
 CC coli), with minimal interference from other sample components such as
 CC inhibitors of the polymerase chain reaction, DNA of non-pathogenic
 CC bacteria or the quenching phenomenon. The present sequence is that of one
 CC of the PCR primers of the invention (ABQ87902-ABQ87999)
 XX
 SQ Sequence 32 BP; 4 A; 8 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 6; Length 32;
 Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GCATGCCAGATTACTGGC 21
 DB 26 GAATGTCAGATAACTGGC 9
 RESULT 11
 ABQ87940
 ID ABQ87940 standard; DNA; 32 BP.
 XX AC
 XX ABQ87940;
 DT 10-SEP-2002 (first entry)
 DE Enterohaemorrhagic Escherichia coli detection PCR primer SEQ ID NO 39.
 XX
 KW Enterohaemorrhagic Escherichia coli; EHEC; slt; Shigella-like toxin; eae;
 KW hlyA; detection; food; PCR; primer; ss.
 XX Escherichia coli.
 XX WO200253771-A2.
 FN 11-JUL-2002.
 PD
 XX
 XX 15-OCT-2001; 2001WO-EP011901.
 PF
 XX 08-JAN-2001; 2001DE-01000493.
 PR
 XX (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 PA Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
 PI WPI; 2002-528864/56.
 XX
 XX Detecting enterohaemorrhagic Escherichia coli, from the presence of
 PT sequences from the Shigella-like toxin locus and at least one of eae and
 PT hlyA loci.
 PS Claim 3; Page 19; 86pp; German.
 XX
 CC The invention relates to detection (M1) of enterohaemorrhagic Escherichia
 CC coli (EHEC) in a sample from the presence of nucleic acid sequences from
 CC the slt (Shigella-like toxin) locus and the eae and/or hlyA loci. (M1) is
 CC useful for detecting of EHEC e.g. in foods. The method provides secure
 CC detection of EHEC (including differentiation from other types of E.
 CC coli), with minimal interference from other sample components such as
 CC inhibitors of the polymerase chain reaction, DNA of non-pathogenic
 CC bacteria or the quenching phenomenon. The present sequence is that of one
 CC of the PCR primers of the invention (ABQ87902-ABQ87999)
 XX
 SQ Sequence 32 BP; 11 A; 9 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 6; Length 32;
 Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GCATGCCAGATTACTGGC 21
 DB 7 GAATGTCAGATAACTGGC 24
 RESULT 12
 ABQ87926/c
 ID ABQ87926 standard; DNA; 32 BP.
 XX AC
 XX ABQ87926;
 DT 10-SEP-2002 (first entry)
 DE Enterohaemorrhagic Escherichia coli detection PCR primer SEQ ID NO 25.
 XX
 KW Enterohaemorrhagic Escherichia coli; EHEC; slt; Shigella-like toxin; eae;
 KW hlyA; detection; food; PCR; primer; ss.
 XX Escherichia coli.
 XX WO200253771-A2.
 FN 11-JUL-2002.
 PD
 XX
 XX 15-OCT-2001; 2001WO-EP011901.
 PF
 XX 08-JAN-2001; 2001DE-01000493.
 PR
 XX (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 PA Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
 PI WPI; 2002-528864/56.
 XX
 XX Detecting enterohaemorrhagic Escherichia coli, from the presence of
 PT sequences from the Shigella-like toxin locus and at least one of eae and
 PT hlyA loci.
 PS Claim 3; Page 18; 86pp; German.
 XX
 CC The invention relates to detection (M1) of enterohaemorrhagic Escherichia
 CC coli (EHEC) in a sample from the presence of nucleic acid sequences from
 CC the slt (Shigella-like toxin) locus and the eae and/or hlyA loci. (M1) is
 CC useful for detecting of EHEC e.g. in foods. The method provides secure
 CC detection of EHEC (including differentiation from other types of E.
 CC coli), with minimal interference from other sample components such as
 CC inhibitors of the polymerase chain reaction, DNA of non-pathogenic
 CC bacteria or the quenching phenomenon. The present sequence is that of one
 CC of the PCR primers of the invention (ABQ87902-ABQ87999)
 XX
 SQ Sequence 32 BP; 4 A; 8 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 6; Length 32;
 Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GCATGCCAGATTACTGGC 21
 DB 26 GAATGTCAGATAACTGGC 9
 RESULT 13
 AAZ41030/c
 ID AAZ41030 standard; DNA; 18 BP.
 XX AC
 XX AAZ41030;
 DT 26-JAN-2000 (first entry)
 DE Cellular inhibitor of apoptosis-2 phosphorothioate antisense oligo #22.

XX Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.

XX Synthetic.
 OS Homo sapiens.

XX WO9953101-A1.

XX 21-OCT-1999.

XX 13-APR-1999; 99WO-US008268.

XX 13-APR-1998; 98US-0081483P.

XX 28-APR-1998; 98US-00067638.

XX (ISIS-) ISIS PHARM INC.

XX Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasnor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX WPI; 1999-620446/53.

XX Identifying compounds which modulate expression of nucleic acids, used to
 PT provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity.

XX Example 21; Page 100; 264pp; English.

XX A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of the
 CC compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria, and
 CC evaluating in silico the binding of the virtual compounds with the tNA
 CC according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONs) that modulate the expression of
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONs with
 CC the tNA according to defined criteria; and (2) a method of defining a set
 CC of compounds that modulate the expression of a tNA sequence via binding
 CC of the compounds with the tNA. The methods can be used for the generation
 CC and identification of synthetic compounds having defined physical,
 CC chemical or bioactive properties. Information gathered from assays of
 CC such compounds is used to identify nucleic acid sequences that are
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.
 CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
 CC AA52701 to AA52706, represent sequences used in the exemplification of
 CC the present invention

XX Sequence 18 BP; 5 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ATGCCAGATTACT 18
 DB 16 ATGCCAGATTACT 4

RESULT 14

AAZ22124/c

ID AAZ22124 standard; DNA; 18 BP.

XX AAZ22124;

XX 26-NOV-1999 (first entry)

DE Human c-IAP-2 mRNA inhibiting antisense oligo ISIS #23433.

XX

KW Cellular Inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;
 KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation; ss.

XX Synthetic.
 OS Homo sapiens.

XX US5958771-A.

XX 28-SEP-1999.

XX 03-DEC-1998; 98US-00205144.

XX 03-DEC-1998; 98US-00205144.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsert LM, Ackermann EJ;
 WPI; 1999-561046/47.

XX Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
 PT useful for e.g. diagnostics, therapeutics, and as research reagents.

XX Example 15; Col 39; 33pp; English.

XX The invention provides antisense compounds of 8-30 nucleotides that
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2 (c-IAP-
 CC 2). The antisense compounds may be used for diagnostics, therapeutics
 CC (for modulating the expression of c-IAP-2), prophylaxis (e.g. to prevent
 CC or delay infection, inflammation, or tumor formation), as research
 CC reagents (e.g. to distinguish between members of a biological pathway)
 CC and in kits. Sequences AAZ22103-142 represent phosphorothioate
 CC oligonucleotides used for antisense inhibition of cellular inhibitor of
 CC apoptosis-2

XX Sequence 18 BP; 5 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACT 18

DB 16 ATGCCAGATTACT 4

RESULT 15

AAD60500/c

ID AAD60500 standard; DNA; 18 BP.

XX AAD60500;

XX 18-DEC-2003 (first entry)

XX Human c-IAP-2 antisense oligonucleotide #ISIS #23473.

XX Human; antisense; cellular inhibitor of apoptosis-2; c-IAP-2; cancer;
 KW hyperproliferative condition; apoptosis inhibitor 2; autoimmune disease;
 KW API-1; hIAP-1; MHC; gene therapy; phosphorothioate; ss.

XX Homo sapiens.

XX Synthetic.

XX Key modified_base 1..18

XX /tag= a

XX /mod_base= OTHER

XX /note= "Phosphorothioate backbone; All cytidine residues
 are 5-methylcytidines"

XX modified_base 1..4

XX /tag= b

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 15..18
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 PN US2003083300-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 16-JUL-2002; 2002US-00197290.
 XX
 PR 23-SEP-1999; 99WO-US022083.
 XX
 PR 04-OCT-2001; 2001US-00857299.
 XX
 PA (BENN/) BENNETT C F.
 PA (ACKE/) ACKERMANN E J.
 PA (COWS/) COWSERT L M.
 XX
 PI Bennett CF, Ackermann EJ, Cowsert LM;
 XX
 DR WPI; 2003-755119/71.
 XX

XX New antisense compound, preferably an oligonucleotide, for inhibiting
 PT expression of human Cellular Inhibitor of Apoptosis-2 in human cells or
 PT tissues, and for treating diseases, such as cancer or an autoimmune
 PT disease.
 PT

XX Example 16; Page 22; 34pp; English.

XX The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding human cellular inhibitor of apoptosis-2 (also known as c-IAP-2,
 CC apoptosis inhibitor 2, API-1, hIAP-1 and MIHC) to inhibit its expression.
 CC Antisense compounds of the invention are used to induce apoptosis in
 CC human cells or tissues to treat diseases or conditions associated with
 CC insufficient apoptosis. They are used to treat diseases or conditions
 CC associated with c-IAP-2 such as hyperproliferative conditions especially
 CC cancer or autoimmune diseases. The invention is also useful in antisense
 CC gene therapy. The present sequence is an antisense oligonucleotide
 CC targetted to human c-IAP-2 DNA
 XX

XX Sequence 18 BP; 5 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACT 18
 Db 16 ATGCCAGATTACT 4
 |||||
 |||||

RESULT 16
 ADP81733/c
 ID ADP81733 standard; DNA; 20 BP.
 XX
 AC ADP81733;
 XX

DT 26-AUG-2004 (first entry)

DE Human melanoma antigen E-D1 DNA target region #4.

XX MAGE-D1; melanoma antigen family D 1;
 KW neurotrophin receptor-interacting MAGE homologue; NRAGE; Dlxin-1;
 KW hyperproliferative disorder; human; melanoma antigen E-D1; ds.
 XX

OS Homo sapiens.

XX US2004110702-A1.

XX 10-JUN-2004.

XX 10-DEC-2002; 2002US-00317278.

XX

PR 10-DEC-2002; 2002US-00317278.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Dean NM, Dobie KW;

XX WPI; 2004-440382/41.

XX New compounds, particularly oligonucleotides targeted to a nucleic acid
 PT encoding melanoma antigen E-D1 (MAGE-D1), useful for treating diseases
 PT associated with MAGE-D1, e.g. hyperproliferative disorders.
 XX

PS Example 15; SEQ ID NO 51; 36pp; English.

XX The invention relates to compounds, compositions and methods for
 CC modulating the expression of melanoma antigen E-D1 (MAGE-D1). MAGE-D1 is
 CC also called as melanoma antigen family D 1, neurotrophin receptor-
 CC interacting MAGE homologue (NRAGE) and Dlxin-1. The composition comprise
 CC antisense oligonucleotides targeted to MAGE-D1. The composition comprise
 CC and methods are useful for treating a disease or condition associated
 CC with MAGE-D1, such as a hyperproliferative disorder. They are also useful
 CC in research and diagnostics for modulating the expression of MAGE-D1. The
 CC present sequence is human MAGE-D1 DNA target region. This sequence is
 CC used to illustrate the method of the invention.
 XX

XX Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGCCAGATTACTG 19

Db 13 TGCCAGATTACTG 1
 |||||
 |||||

RESULT 17

ADP81699

ID ADP81699 standard; DNA; 20 BP.

XX AC ADP81699;

XX 26-AUG-2004 (first entry)

XX Human MAGE-D1 antisense oligonucleotide, ISIS 212943.

XX MAGE-D1; melanoma antigen family D 1;

KW neurotrophin receptor-interacting MAGE homologue; NRAGE; Dlxin-1;

KW hyperproliferative disorder; human; melanoma antigen E-D1; antisense;
 XX phosphorothioate backbone; ss.

OS Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone in which all cytidine
 residues are 5-methylcytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) bases"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) bases"

XX US2004110702-A1.

XX 10-JUN-2004.

XX

PF 10-DEC-2002; 2002US-00317278.
 XX
 PR 10-DEC-2002; 2002US-00317278.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dean NM, Dobie KW;
 XX
 DR WPI; 2004-440382/41.
 XX
 PT New compounds, particularly oligonucleotides targeted to a nucleic acid
 PT encoding melanoma antigen E-D1 (MAGE-D1), useful for treating diseases
 PT associated with MAGE-D1, e.g. hyperproliferative disorders.
 XX
 PS Example 15; SEQ ID NO 17; 36pp; English.
 XX
 CC The invention relates to compounds, compositions and methods for
 CC modulating the expression of melanoma antigen E-D1 (MAGE-D1). MAGE-D1 is
 CC also called as melanoma antigen, family D, 1, neurotrophin receptor-
 CC interacting MAGE homologue (NRAGE) and Dlxin-1. The composition comprise
 CC antisense oligonucleotides targeted to MAGE-D1. The compound, composition
 CC and methods are useful for treating a disease or condition associated
 CC with MAGE-D1, such as a hyperproliferative disorder. They are also useful
 CC in research and diagnostics for modulating the expression of MAGE-D1. The
 CC present sequence is an antisense oligonucleotide targeted to human MAGE-
 CC D1 DNA. This sequence is used to illustrate the method of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 61.9%; Score 13; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 TGCCAGATTACTG 19
 Db 8 TGCCAGATTACTG 20
 RESULT 18
 AAC93092
 ID AAC93092 standard; DNA; 32 BP.
 XX
 AC AAC93092;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE E. coli cerulenin mutagenic primer I197A Antisense.
 XX
 KW Beta-ketoacyl ACP synthase; KAS; cell fatty acid composition;
 KW oilseed crop; cancer; immunosuppressant; anti-parasitic agent;
 KW antibiotic; PCR primer; ss.
 XX
 OS Escherichia coli.
 XX
 PN WO200075343-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 09-JUN-2000; 2000WO-US016151.
 XX
 PR 09-JUN-1999; 99US-0138308P.
 XX
 PA (CALJ) CALGENE LLC.
 XX
 PI Dehesh K, Val D;
 XX
 DR WPI; 2001-061730/07.
 XX
 PT Engineering beta-ketoacyl-ACP synthase useful for altering the fatty acid
 PT composition of a host cell, comprises modifying the sequence encoding KAS
 PT and expressing the modified sequence in the host cell.
 XX
 PS Example 2; Page 22; 145pp; English.

XX The present invention provides a method for obtaining an altered beta-
 CC ketoacyl ACP synthase (KAS) protein. These engineered proteins have
 CC altered substrate specificity and are produced by modifying the coding
 CC sequence and then expressing it in a host cell. The proteins are useful
 CC in the altering of the fatty acid composition of a plant, particularly in
 CC the modification of oilseed crops, and in the identification of molecules
 CC for use in cancer therapy, as immunosuppressants, anti-parasitic agents
 CC and antibiotics
 XX
 SQ Sequence 32 BP; 5 A; 14 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 61.9%; Score 13; DB 4; Length 32;
 Best Local Similarity 76.2%; Pred. No. 1e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AGCGCATGCCAGATTACTGGC 21
 Db 6 AACGCCGCCGGAGTACTGGC 26
 RESULT 19
 AAC93091/C
 ID AAC93091 standard; DNA; 32 BP.
 XX
 AC AAC93091;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE E. coli cerulenin mutagenic primer I197A Sense.
 XX
 KW Beta-ketoacyl ACP synthase; KAS; cell fatty acid composition;
 KW oilseed crop; cancer; immunosuppressant; anti-parasitic agent;
 KW antibiotic; PCR primer; ss.
 XX
 OS Escherichia coli.
 XX
 PN WO200075343-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 09-JUN-2000; 2000WO-US016151.
 XX
 PR 09-JUN-1999; 99US-0138308P.
 XX
 PA (CALJ) CALGENE LLC.
 XX
 PI Dehesh K, Val D;
 XX
 DR WPI; 2001-061730/07.
 XX
 PT Engineering beta-ketoacyl-ACP synthase useful for altering the fatty acid
 PT composition of a host cell, comprises modifying the sequence encoding KAS
 PT and expressing the modified sequence in the host cell.
 XX
 PS Example 2; Page 22; 145pp; English.
 XX
 CC The present invention provides a method for obtaining an altered beta-
 CC ketoacyl ACP synthase (KAS) protein. These engineered proteins have
 CC altered substrate specificity and are produced by modifying the coding
 CC sequence and then expressing it in a host cell. The proteins are useful
 CC in the altering of the fatty acid composition of a plant, particularly in
 CC the modification of oilseed crops, and in the identification of molecules
 CC for use in cancer therapy, as immunosuppressants, anti-parasitic agents
 CC and antibiotics
 XX
 SQ Sequence 32 BP; 6 A; 7 C; 14 G; 5 T; 0 U; 0 Other;
 Query Match 61.9%; Score 13; DB 4; Length 32;
 Best Local Similarity 76.2%; Pred. No. 1e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AGCGCATGCCAGATTACTGGC 21

Db 27 AACGCCCGCGGAGTACTGGC 7
||||| ||| ||| ||| ||| ||| |||

RESULT 20
ADI80472
ID ADI80472 standard; DNA; 32 BP.
XX
AC ADI80472;
XX
DT 22-APR-2004 (first entry)
XX
DE E. coli KAS II PCR site-directed mutagenesis I197A antisense primer.
XX
KW beta-ketoacyl-ACP synthase; KAS; enzyme; acyl-ACP substrate;
KW altered substrate specificity; PCR; site-directed mutagenesis; primer;
KW ss.
XX
OS Escherichia coli.
OS Synthetic.
XX
PN WO2004007744-A2.
XX
PD 22-JAN-2004.
XX
PF 31-JUL-2000; 2000WO-US022359.
XX
PR 31-JUL-2000; 2000WO-US022359.
XX
PA (CALJ) CALGENE LLC.
XX
PI Kaytayoon D, Val D;
XX
DR WPI; 2004-122971/12.
XX
PT Obtaining engineered approximately-beta-ketoacyl-ACP synthase (KAS), useful
PT for preparing constructs to direct expression in a host cell comprising
PT modifying a gene sequence encoding a first KAS protein to produce a
PT modified KAS gene sequence.
XX
PS Example 2; SEQ ID NO 16; 40pp; English.

CC The present invention describes a method for obtaining an engineered beta
CC -ketoacyl-ACP synthase (KAS) having an altered substrate specificity with
CC respect to the acyl-ACP substrates utilised by the KAS. Also described:
CC (1) an amino acid sequence encoding a KAS protein, where the sequence has
CC at least one substitution, insertion or deletion of at least one amino
CC acid residue selected from residue 105-120, 130-140, 190-205 and 340-400
CC and the protein has an altered substrate specificity; (2) a nucleic acid
CC construct comprising an operably linked components in the 5' to 3',
CC direction of transcription: (a) a transcriptional initiation region; and
CC (b) a polynucleotide sequence encoding a KAS having an altered substrate
CC specificity; and (3) a method for altering the fatty acid composition of
CC a host cell. The method is useful for obtaining an engineered KAS having
CC an altered substrate specificity with respect to the acyl-ACP substrates
CC utilised by the KAS. The engineered nucleic acid sequences are useful in
CC the preparation of constructs to direct expression in a host cell. It can
CC also be used in the preparation of plant expression constructs to alter
CC the fatty acid composition of a plant cell. The DNA constructs can be
CC used for transcription or translation and translation (expression) of
CC an engineered KAS protein having altered substrate specificity with
CC respect to the native KAS protein. The present sequence represents a PCR
CC site-directed mutagenesis primer for E. coli KAS II, which is used in an
CC example from the present invention.

XX Sequence 32 BP; 5 A; 14 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 12; Length 32;

Best Local Similarity 76.2%; Pred. No. 1e+04; Mismatches 5; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCGAGTACTGGC 21
||||| ||| ||| ||| ||| ||| |||

Db 6 AACGCCCGCGGAGTACTGGC 26

RESULT 21
ADI80471/c
ID ADI80471 standard; DNA; 32 BP.
XX
AC ADI80471;
XX
DT 22-APR-2004 (first entry)
XX
DE E. coli KAS II PCR site-directed mutagenesis I197A sense primer.
XX
KW beta-ketoacyl-ACP synthase; KAS; enzyme; acyl-ACP substrate;
KW altered substrate specificity; PCR; site-directed mutagenesis; primer;
KW ss.
XX
OS Escherichia coli.
OS Synthetic.
XX
PN WO2004007744-A2.
XX
PD 22-JAN-2004.
XX
PF 31-JUL-2000; 2000WO-US022359.
XX
PR 31-JUL-2000; 2000WO-US022359.
XX
PA (CALJ) CALGENE LLC.
XX
PI Kaytayoon D, Val D;
XX
DR WPI; 2004-122971/12.
XX
PT Obtaining engineered approximately-beta-ketoacyl-ACP synthase (KAS), useful
PT for preparing constructs to direct expression in a host cell comprising
PT modifying a gene sequence encoding a first KAS protein to produce a
PT modified KAS gene sequence.
XX
PS Example 2; SEQ ID NO 15; 40pp; English.

CC The present invention describes a method for obtaining an engineered beta
CC -ketoacyl-ACP synthase (KAS) having an altered substrate specificity with
CC respect to the acyl-ACP substrates utilised by the KAS. Also described:
CC (1) an amino acid sequence encoding a KAS protein, where the sequence has
CC at least one substitution, insertion or deletion of at least one amino
CC acid residue selected from residue 105-120, 130-140, 190-205 and 340-400
CC and the protein has an altered substrate specificity; (2) a nucleic acid
CC construct comprising an operably linked components in the 5' to 3',
CC direction of transcription: (a) a transcriptional initiation region; and
CC (b) a polynucleotide sequence encoding a KAS having an altered substrate
CC specificity; and (3) a method for altering the fatty acid composition of
CC a host cell. The method is useful for obtaining an engineered KAS having
CC an altered substrate specificity with respect to the acyl-ACP substrates
CC utilised by the KAS. The engineered nucleic acid sequences are useful in
CC the preparation of constructs to direct expression in a host cell. It can
CC also be used in the preparation of plant expression constructs to alter
CC the fatty acid composition of a plant cell. The DNA constructs can be
CC used for transcription or translation and translation (expression) of
CC an engineered KAS protein having altered substrate specificity with
CC respect to the native KAS protein. The present sequence represents a PCR
CC site-directed mutagenesis primer for E. coli KAS II, which is used in an
CC example from the present invention.

XX Sequence 32 BP; 6 A; 7 C; 14 G; 5 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 12; Length 32;

Best Local Similarity 76.2%; Pred. No. 1e+04; Mismatches 5; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCGAGTACTGGC 21
||||| ||| ||| ||| ||| ||| |||
Db 27 AACGCCCGCGGAGTACTGGC 7

RESULT 22
AAH62283/c
ID AAH62283 standard; DNA; 21 BP.

XX AC AAH62283;
XX
XX 09-SEP-2004 (revised)
DT 12-SEP-2001 (first entry)
XX
XX NR1P1 polymorphism containing DNA fragment #184.
DE
XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW heart disease; paternity testing; forensic science; ds.
KW
XX Homo sapiens.
OS
OS Unidentified.
XX
XX Key Location/Qualifiers
FH variation 11
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200138576-A2.
XX
XX 31-MAY-2001.
PD
XX 17-NOV-2000; 2000WO-US031639.
PF
XX 24-NOV-1999; 99US-0167334P.
PR
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA
XX Cargill M, Ireland JS, Lander ES;
PI
XX WPI; 2001-367705/38.
DR
XX
XX New nucleic acid segments of the human genome, particularly from genes
PT including polymorphic sites, for phenotype correlation, forensics,
PT paternity testing, medicine and genetic analysis.
XX
XX Claim 1; Page 44; 80pp; English.
XX
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC contain single nucleotide polymorphisms (SNPs). A method is included in
CC the invention for analysing a nucleic acid sample, which consists of
CC determining the base occupying any one of the polymorphic sites given in
CC the SNP containing sequences. The nucleotide sequences can be used in the
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC a pharmaceutical. SNP containing oligonucleotides are useful in
CC applications such as phenotype correlation, forensics, paternity testing,
CC medicine and genetic analysis
CC
XX Revised record issued on 09-SEP-2004 : Correction to Feature Table Key

XX SQ Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGG 19
|||||
Db 21 GCATGCCAGATCCCTG 6

RESULT 23
ABS57999
ID ABS57999 standard; DNA; 23 BP.

XX ABS57999;
AC
XX 06-FEB-2003 (first entry)
DT
XX PCR primer, D2, used to amplify hSEZ-6 cDNA.
DE
XX Human; PCR; primer; ss; epilepsy; hSEZ-6; seizure-related gene;
KW epilepsy.
KW
XX Homo sapiens.
OS
XX CN1343774-A.
FN
XX 10-APR-2002.
PD
XX 28-MAY-2001; 2001CN-00112999.
PF
XX 28-MAY-2001; 2001CN-00112999.
PR
XX (UYFU-) UNIV FUDAN.
PA
XX Yu L, Jiang J;
PI
XX WPI; 2002-548896/59.
DR
XX Coding sequence of epilepsy associated protein, polypeptide coded by it,
PT and its preparing process and application.
PT
XX Example 1; Page 6 (disclosure); 19pp; Chinese.
PS
XX The invention discloses an human epilepsy associated protein hSEZ-6
CC (also referred to as a seizure-related gene) and the polynucleotide
CC encoding it. Also disclosed is a process for preparing hSEZ-6 by
CC recombinant techniques. The protein may be useful in the treatment of
CC disorders (e.g. epilepsy) related to the protein. The sequence presented
CC is the PCR primer, D2, which was used to amplify human SEZ-6 cDNA
XX
XX Sequence 23 BP; 4 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 6; Length 23;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGG 20
|||||
Db 1 CATGCCAAATTCCTGG 16

RESULT 24
AAD14408
ID AAD14408 standard; DNA; 24 BP.
XX
XX AAD14408;
AC
XX
XX 01-NOV-2001 (first entry)
DT
XX Human basic fibroblast growth factor (bFGF)-sense RT-PCR primer.
DE
XX Human; vascular endothelial cell growth factor; VEGF; hypotensive;
KW vasodilation; angiogenesis; vasoconstriction; pulmonary hypertension;
KW ischaemic wound; ischaemic cardiac condition; vasotropic; vulnery;
KW basic fibroblast growth factor; bFGF; relaxin; neovascularisation;
KW endothelin type B receptor; angiotensin-II; endothelin; wound healing;
KW angiogenic cytokine; cerebroprotective; enderfiltration; gene therapy;
KW stroke; Glomerular filtration rate; reverse transcription; RT;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200158468-A1.
FN
XX 16-AUG-2001.
PD

```
XX 09-FEB-2001; 2001WO-US004370.
XX 09-FEB-2000; 2000US-0181408P.
XX 28-APR-2000; 2000US-0200284P.
XX 20-OCT-2000; 2000US-0242216P.
XX (CONN-) CONNETICS CORP.
XX (UYPI-) UNIV PITTSBURGH.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Conrad KP, Lewis M, Unemori EN, Huang X, Tozzi CA;
XX WPI; 2001-514619/56.
XX Treating pulmonary or renal hypertension and an ischemic condition,
XX increasing vasodilation and renal function, promoting wound healing and
XX increasing production of angiogenic cytokine, comprises administering
XX relaxin.
XX Example 3; Page 32; 73pp; English.
XX The invention relates to methods of treating diseases related to
XX vasodilation by administering pharmacologically active relaxin. Relaxin
XX functions to increase both vasodilation and angiogenesis in males as well
XX as females and is therefore useful in treating a wide variety of diseases
XX relating to vasoconstriction. The method is used for treating renal or
XX pulmonary hypertension, treating ischaemic conditions such as ischaemic
XX wound, stroke or ischaemic cardiac conditional, for increasing production
XX of an angiogenic cytokine such as basic fibroblast growth factor (bFGF)
XX or a vascular endothelial growth factor, increasing vasodilation,
XX increasing renal function by increasing nitric oxide production in an
XX promoting wound healing, increasing nitric oxide production in an
XX endothelial cell of a blood vessel endothelium and for increasing
XX endothelin type B receptor activation in an endothelial cell in a blood
XX vessel endothelium. Relaxin is useful for treating diseases related to
XX vasoconstriction such as angiotensin-II-mediated vasoconstriction,
XX endothelin-mediated vasoconstriction and for increasing angiogenesis and
XX to promote neovascularisation in both males and females. It also promotes
XX renal vasodilation and hyperfiltration. The gene encoding relaxin is used
XX in gene therapy. The present sequence is a sense RT (reverse
XX transcription)-PCR primer used to amplify human bFGF
XX Sequence 24 BP; 9 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 5; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 ATGCCAGATTACTGGC 21
Db 9 ATGGAAGATTACTGGC 24
RESULT 25
ABQ05495/c
ID ABQ05495 standard; DNA; 24 BP.
XX AC ABQ05495;
XX 11-JUN-2002 (first entry)
XX OLigonucleotide adapter/capture probe 5486.
XX OLigonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX 28-FEB-2002.
XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX given capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CGCATGCCAGATTACT 18
Db 20 CGCATGCCAGATTCT 5
RESULT 26
ABQ11823/c
ID ABQ11823 standard; DNA; 24 BP.
XX AC ABQ11823;
XX 11-JUN-2002 (first entry)
XX OLigonucleotide adapter/capture probe 11814.
XX OLigonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX 28-FEB-2002.
XX 27-AUG-2001; 2001WO-US026519.
XX 25-AUG-2000; 2000US-0227948P.
XX 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
XX Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.
XX Claim 1; Page 235; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX given capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CGCATGCCAGATTACT 18
Db 20 CGCATGCCAGATTCT 5
RESULT 26
ABQ11823/c
ID ABQ11823 standard; DNA; 24 BP.
XX AC ABQ11823;
XX 11-JUN-2002 (first entry)
XX OLigonucleotide adapter/capture probe 11814.
XX OLigonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX 28-FEB-2002.
XX 27-AUG-2001; 2001WO-US026519.
XX 25-AUG-2000; 2000US-0227948P.
XX 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
XX Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.
XX Claim 1; Page 235; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
```

CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTCT 18
|||||
Db 20 CGCATGCCAAATTCCT 5

RESULT 27
ABQ00780/c
ID ABQ00780 standard; DNA; 24 BP.
XX
AC ABQ00780;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 771.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 62; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTCT 18
|||||
Db 20 CGCATGCCAAATTCCT 5

RESULT 29
ABQ11857
ID ABQ11857 standard; DNA; 24 BP.
XX
AC ABQ11857;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11848.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX

DB 20 CGCATGCCAAATTCCT 5

RESULT 28
ABQ05536
ID ABQ05536 standard; DNA; 24 BP.
XX
AC ABQ05536;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 5527.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 157; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 11 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTCT 18
|||||
Db 5 CGCATGCCAAATTCCT 20

RESULT 29
ABQ11857
ID ABQ11857 standard; DNA; 24 BP.
XX
AC ABQ11857;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11848.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX

CC comprises detecting the presence of the modified target nucleic acid
 XX Sequence 25 BP; 5 A; 3 C; 11 G; 6 T; 0 U; 0 Other;
 SQ

Query Match 61.0%; Score 12.8; DB 6; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1.2e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACT 18
 |||||
 Db 21 CGCATGCCAAATTCCT 6

RESULT 32
 ABQ13393
 ID ABQ13393 standard; DNA; 25 BP.

XX AC ABQ13393;

XX 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 13384.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US026519.

XX 25-AUG-2000; 2000US-0227948P.

XX 29-AUG-2000; 2000US-0228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.

XX Claim 1; Page 254; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

XX Sequence 25 BP; 5 A; 11 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 6; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1.2e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACT 18
 |||||
 Db 6 CGCATGCCAAATTCCT 21

RESULT 33
 AAQ46940/c
 ID AAQ46940 standard; DNA; 28 BP.

XX

AC AAQ46940;

XX 07-FEB-1994 (first entry)

XX Human bFGF primer 4.

XX Human fibronectin; FN; fibroblast cell growth factor; FGF; amplify;
 fusion; cell adhesion; cell growth; anti-aging; cosmetics; primer;
 wound healing; surgery; polymerase chain reaction; PCR; ss.

XX OS Synthetic.

XX PN JP05178897-A.

XX 20-JUL-1993.

XX 05-MAR-1992; 92JP-00083220.

XX 14-OCT-1991; 91JP-00291959.

XX (TAKI) TAKARA SHUZO CO LTD.

XX WPI; 1993-261656/33.

XX Synthetic functional polypeptide to promote wound healing, etc. - contg.
 cell adhesion polypeptide from fibronectin and fibroblast growth factor polypeptide, opt. linked by spacer.

XX Example 1; Page 11; 13pp; Japanese.

XX The sequences given in AAQ46937-42 are primers which were used in the amplification of the DNA encoding the human fibronectin (FN) and fibroblast cell growth factor (FGF) fragments which were used in the production of the fusion polypeptides of the invention. These polypeptides were able to stimulate cell adhesion and cell growth, and may be used for anti-aging cosmetics and in wound healing after surgery

XX Sequence 28 BP; 9 A; 8 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 28;
 Best Local Similarity 87.5%; Pred. No. 1.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGGC 21
 |||||

Db 27 ATGGAAGATTACTGGC 12

RESULT 34
 AAT59860
 ID AAT59860 standard; DNA; 28 BP.

XX AAT59860;

XX 09-DEC-1997 (first entry)

XX Sense primer #1 for phosphate translocator protein fragment.

XX Phosphate translocator protein; inner envelope membrane; plastid; pea;
 chloroplast; photosynthate; chimeric gene; promoter; transporter protein;
 permeability barrier; plant; translocator protein; membrane permeability;
 metabolism; starch production; plant growth; primer; PCR; amplify;
 polymerase chain reaction; ss.

XX OS Synthetic.

XX PN WO9708329-A1.

XX 06-MAR-1997.

XX 28-AUG-1996; 96WO-GB002129.

XX

```

PR 30-AUG-1995; 95GB-00017674.
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE.
XX Gray JC, Knight JS;
XX WPI; 1997-179286/16.
XX Chimeric polypeptide targetting the plastid inner envelope membrane -
XX used for affecting plastid metabolism, partic. increasing starch prodn.
XX Example 1; Page 19; 61pp; English.
XX AAT59858-T59866 represent amplification primers for a fragment of the pea
XX phosphate translocator protein (see AAT59857). The peptide encoded by the
XX amplified sequence is capable of directing a protein to the inner
XX envelope membrane. The phosphate translocator protein is the most
XX abundant chloroplast inner membrane protein. It catalyses the export of
XX photosynthate across the inner envelope membrane. These primers are used
XX in the construction of the chimeric gene of the invention. The chimeric
XX gene comprises a gene promoter, a sequence encoding a polypeptide that
XX targets the plastid inner envelope membrane (PIEM) of a plant (or its
XX variant, derivative or homologue), a coding sequence and a terminator.
XX The PIEM is the main permeability barrier of the plastids. Targetting
XX transporter or translocator proteins to the envelope may be carried out
XX to change the permeability of the membrane. The chimeric genes are used
XX to target a protein or polypeptide, for a particular plant
XX characteristic, to the PIEM and can be applied to a wide range of mono-
XX or di-cotyledonous plants. Especially, they are used to alter the
XX metabolism of plants. A particular application is increasing starch
XX production but also contemplated are production of plastics and other
XX polymers, control of plant growth etc
XX Sequence 28 BP; 4 A; 9 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 28;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTAC 17
DB 3 GCGCATGCCAGATTCC 18

RESULT 35
AAH48106
ID AAH48106 standard; DNA; 33 BP.
XX
XX AAH48106;
XX
XX 19-SEP-2001 (first entry)
XX
XX Ribulose biphosphate carboxylase 13 PCR primer #2.
XX
XX Ribulose biphosphate carboxylase 13; cytosstatic; coagulant; anti-HIV;
XX immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
XX haemopathy; HIV infection; immunological disease; inflammation;
XX PCR primer; ss.
XX
XX Unidentified.
XX
XX WO200148008-A1.
XX
XX 05-JUL-2001.
XX
XX 25-DEC-2000; 2000WO-CN000713.
XX
XX 27-DEC-1999; 99CN-00125375.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-418241/44.
XX
XX Ribulose biphosphate carboxylase 13 for diagnosing and treating
XX malignant tumor, hemopathy, human immunodeficiency virus, immunological
XX diseases and inflammation.
XX
XX Example 7; Page 20; 37pp; Chinese.
XX
XX The present invention relates to ribulose biphosphate carboxylase 13 and
XX its coding sequence (see AAH48104 and AAG64235). The ribulose
XX biphosphate carboxylase and its coding sequence are useful in the
XX diagnosis and treatment of malignant tumour, haemopathy, human
XX immunodeficiency virus (HIV) infection, immunological diseases and
XX various inflammations. The present sequence is a probe, which was used in
XX an example from the present invention
XX Sequence 41 BP; 11 A; 9 C; 9 G; 12 T; 0 U; 0 Other;

DR WPI; 2001-418241/44.
XX Ribulose biphosphate carboxylase 13 for diagnosing and treating
XX malignant tumor, hemopathy, human immunodeficiency virus, immunological
XX diseases and inflammation.
XX
XX Example 3; Page 17; 37pp; Chinese.
XX
XX The present invention relates to ribulose biphosphate carboxylase 13 and
XX its coding sequence (see AAH48104 and AAG64235). The ribulose
XX biphosphate carboxylase and its coding sequence are useful in the
XX diagnosis and treatment of malignant tumour, haemopathy, human
XX immunodeficiency virus (HIV) infection, immunological diseases and
XX various inflammations. The present sequence is a PCR primer, which was
XX used in an example from the present invention
XX Sequence 33 BP; 8 A; 7 C; 10 G; 8 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 4; Length 33;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTCG 20
DB 18 CATGCCAGAGGACTCG 33

RESULT 36
AAH48109
ID AAH48109 standard; DNA; 41 BP.
XX
XX AAH48109;
XX
XX 19-SEP-2001 (first entry)
XX
XX Ribulose biphosphate carboxylase 13 probe #1.
XX
XX Ribulose biphosphate carboxylase 13; cytosstatic; coagulant; anti-HIV;
XX immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
XX haemopathy; HIV infection; immunological disease; inflammation; probe;
XX ss.
XX
XX Unidentified.
XX
XX WO200148008-A1.
XX
XX 05-JUL-2001.
XX
XX 25-DEC-2000; 2000WO-CN000713.
XX
XX 27-DEC-1999; 99CN-00125375.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-418241/44.
XX
XX Ribulose biphosphate carboxylase 13 for diagnosing and treating
XX malignant tumor, hemopathy, human immunodeficiency virus, immunological
XX diseases and inflammation.
XX
XX Example 7; Page 20; 37pp; Chinese.
XX
XX The present invention relates to ribulose biphosphate carboxylase 13 and
XX its coding sequence (see AAH48104 and AAG64235). The ribulose
XX biphosphate carboxylase and its coding sequence are useful in the
XX diagnosis and treatment of malignant tumour, haemopathy, human
XX immunodeficiency virus (HIV) infection, immunological diseases and
XX various inflammations. The present sequence is a probe, which was used in
XX an example from the present invention
XX Sequence 41 BP; 11 A; 9 C; 9 G; 12 T; 0 U; 0 Other;

```

Query Match 61.0%; Score 12.8; DB 4; Length 41;
 Best Local Similarity 87.5%; Pred. No. 1.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGG 20
 |||||
 Db 8 CATGCCAGAGACTGG 23

RESULT 37
 AAT05760
 ID AAT05760 standard; DNA; 49 BP.
 XX
 AC AAT05760;
 XX
 DT 10-JUN-1996 (first entry)
 XX
 DE Thermophilic strand displacement amplification template oligo primer.
 XX
 KW Primer; template oligonucleotide; recognition; cleavage; site;
 KW restriction endonuclease; strand displacement assay; thermostable;
 KW strand displacement amplification reaction; diagnosis; HincII;
 KW genetic diseases; gene isolation; forensic medicine; ss.
 XX
 OS Synthetic.
 XX
 PN AU9514776-A.
 XX
 PD 26-OCT-1995.
 XX
 PF 13-MAR-1995; 95AU-00014776.
 XX
 PR 18-APR-1994; 94US-00229279.
 XX
 PA (BECT) BECTON DICKINSON CO.
 XX
 PI Fraiser MS, Spargo CA, Walker GT, Van Cleve M, Wright DU;
 XX
 DR WPI; 1995-383306/50.
 XX
 XX Amplifying target nucleic acid by strand displacement amplification -
 using thermophilic DNA polymerase and thermophilic restriction
 endonuclease.
 XX
 PS Example 5; Page 35; 47pp; English.
 XX
 CC The primer AAT05760 was used to prime the template oligonucleotide
 CC AAT05761, which contains a recognition/cleavage site for the restriction
 CC endonuclease HincII. The template was used in an thermophilic strand
 CC displacement amplification, to compare conventional and the claimed
 CC thermophilic strand displacement amplification reaction of the invention,
 CC which is useful in the diagnosis of genetic diseases, isolation of genes
 CC and forensic medicine
 XX
 SQ Sequence 49 BP; 12 A; 8 C; 16 G; 13 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 49;
 Best Local Similarity 87.5%; Pred. No. 1.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGG 20
 |||||
 Db 22 CATGCCCGGTACTGG 37

RESULT 38
 AAF82407
 ID AAF82407 standard; DNA; 19 BP.
 XX
 AC AAF82407;
 XX
 DT 26-JUN-2001 (first entry)

XX Mealworm encapsulation protein DNA primer #12.
 DE Mealworm; encapsulation; immunostimulant; primer; ss.
 XX
 KW Tenebrio molitor.
 OS
 XX JP2001037488-A.
 FN
 XX 13-FEB-2001.
 PD
 XX 29-NOV-1999; 99JP-00338594.
 PF
 XX 07-JUL-1999; 99KR-00027933.
 PR
 PR 26-JUL-1999; 99KR-00031172.
 XX
 PA (SAMY-) SAMYANG GENEX CORP.
 XX
 XX WPI; 2001-285602/30.
 DR
 XX Novel protein involved in encapsulation, used as an immunological
 PT activity enhancer.
 PT
 XX Example 4; Page 6; 23pp; Japanese.
 PS
 XX The present primer is provided in a specification relating a mealworm
 CC protein that participates in encapsulation, which is a cellular defensive
 CC reaction. The invention provides an encapsulation polypeptide comprising
 CC residues 1-754 or 18-754 of a 754 amino acid sequence, or 1-579 or 16-579
 CC of a 579 amino acid sequence, both fully defined in the specification, or
 CC a mutant having a replacement, deletion or insertion of an amino acid in
 CC at least one residue of the sequence. The protein can be used as an
 CC immunological activity enhancer
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 4; Length 19;
 Best Local Similarity 78.9%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCCCATGCCAGATTACTG 19
 |||||
 Db 1 AGCTCCAGCCAGATTCTCTG 19

RESULT 39
 AAX94343/C
 ID AAX94343 standard; DNA; 20 BP.
 XX
 AC AAX94343;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 XX neutralising epitope; PCR primer; ss.
 OS
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB001890.
 XX
 PR 21-NOV-1997; 97FR-00014673.
 PR 04-NOV-1998; 98US-0107078P.
 XX
 PA (GEST) GENSET.
 XX

PI Griffais R;
 XX WPI; 1999-357842/30.
 XX Genome sequence of Chlamydia pneumoniae.
 XX Page 1662; Disclosure; 1912pp; English.
 PS AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 2; Length 20;
 Best Local Similarity 78.9%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AGCGCATGCCAGATTACTG 19
 DB 20 AACGCTGCCAATTACAG 2
 RESULT 40
 AAZ21594
 ID AAZ21594 standard; DNA; 21 BP.
 XX
 AC AAZ21594;
 XX
 DT 02-DEC-1999 (first entry)
 XX
 DE PCR primer INSPR for amplifying HIV integrase cDNA.
 XX
 KW PCR primer; HIV; integrase; IN; inhibitor; DNA insertion; treatment;
 KW viral replication; reverse transcriptase; protease inhibitor;
 KW combination therapy; resistant strain; ss.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus.
 XX
 PN WO9948371-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 26-MAR-1999; 99WO-US006700.
 XX
 PR 27-MAR-1998; 98US-0079764P.
 PR 17-JUL-1998; 98US-0093208P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 XX Robinson WE, King PJ, Reinecke MG;
 FI WPI; 1999-571930/48.
 XX
 DR bis-(3,4-Dihydroxycinnamoyl)tartaric acid analogues for treatment of HIV
 XX infections.
 PT Disclosure; Page 35; 68pp; English.
 PS
 CC PCR primers AAZ21589-Z21594 are used to amplify the HIV integrase cDNA.
 CC This primer corresponds to nucleotides 4016-4036 of the integrase
 CC sequence. The HIV integrase (IN) cDNA was used in the generation of an L-
 CC chioric acid resistant strain of HIV. The invention relates to new
 CC compounds that are IN inhibitors. The inhibitors are novel compounds that

CC potentially and selectively inhibit HIV integrase. The inhibitors are
 CC structural analogues of bis-(3,4-Dihydroxycinnamoyl) tartaric acid.
 CC Integrase has the minimal activities needed for integration. In vitro the
 CC enzyme processes the HIV DNA for insertion in to the host cell's nucleus.
 CC IN also cleaves double stranded DNA and facilitates the insertion of the
 CC HIV DNA in to the cleavage site. IN also covalently links the HIV DNA to
 CC the cleaved ends of the host DNA. The new compounds block the actions of
 CC IN, and therefore block viral replication. The compounds are synergistic
 CC with reverse transcriptase and protease inhibitors, acting at a different
 CC part of the HIV replication cycle. The new inhibitors are used,
 CC preferably in combination therapy with reverse transcriptase inhibitors
 CC and protease inhibitors in the treatment of HIV
 XX
 SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 2; Length 21;
 Best Local Similarity 78.9%; Pred. No. 1.6e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AGCGCATGCCAGATTACTG 19
 DB 3 AGGGAATGCCAAATTCCTG 21
 Search completed: November 23, 2004, 17:27:12
 Job time : 145.708 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 24.3034 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0
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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
C 1	13.2	62.9	40	6	5521093-6	Patent No. 5521093
C 2	13	61.9	18	2	US-09-205-144-29	Sequence 29, Appl
C 3	13	61.9	32	4	US-09-591-279A-15	Sequence 15, Appl
C 4	13	61.9	32	4	US-09-591-279A-16	Sequence 16, Appl
C 5	12.8	61.0	24	4	US-09-780-752-20	Sequence 20, Appl
C 6	12.8	61.0	28	1	US-07-959-369-19	Sequence 19, Appl
C 7	12.8	61.0	28	3	US-09-029-341-5	Sequence 5, Appl
C 8	12.8	61.0	49	1	US-08-223-279-17	Sequence 17, Appl
C 9	12.8	61.0	49	1	US-08-701-269-17	Sequence 17, Appl
C 10	12.6	60.0	20	4	US-09-198-452A-3669	Sequence 3669, Ap
C 11	12.6	60.0	36	4	US-09-371-772B-12766	Sequence 7, Appl
C 12	12.4	59.0	21	3	US-09-179-231D-7	Sequence 7, Appl
C 13	12.4	59.0	42	3	US-08-721-979A-71	Sequence 71, Appl
C 14	12.4	59.0	42	3	US-08-721-979A-72	Sequence 72, Appl
C 15	12.4	59.0	42	3	US-08-836-501-71	Sequence 71, Appl
C 16	12.4	59.0	42	3	US-08-836-501-72	Sequence 72, Appl
C 17	12.4	59.0	42	4	US-09-654-289-71	Sequence 71, Appl
C 18	12.4	59.0	42	4	US-09-654-289-72	Sequence 72, Appl
C 19	12.4	59.0	42	4	US-09-582-876-71	Sequence 71, Appl
C 20	12.4	59.0	42	4	US-09-582-876-72	Sequence 72, Appl
C 21	12.4	59.0	42	4	US-09-626-830-71	Sequence 71, Appl
C 22	12.4	59.0	42	4	US-09-626-830-72	Sequence 72, Appl
C 23	12.4	59.0	42	4	US-10-091-257-71	Sequence 71, Appl
C 24	12.4	59.0	42	4	US-10-091-257-72	Sequence 72, Appl
C 25	12.4	59.0	45	5	PCT-US93-09070-5	Sequence 5, Appl
C 26	12.2	58.1	19	1	US-08-328-710A-15	Sequence 15, Appl
C 27	12.2	58.1	19	3	US-08-968-046-15	Sequence 15, Appl

30	1	US-07-915-922-9	Sequence 9, Appl
44	4	US-09-464-122A-13	Sequence 13, Appl
47	4	US-09-641-638-1195	Sequence 1195, Ap
47	4	US-10-170-097-1195	Sequence 1195, Ap
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33	3	US-08-776-511-6	Sequence 6, Appl
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36	1	US-08-045-806-21	Sequence 21, Appl
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36	4	US-09-479-005A-593	Sequence 593, App
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36	4	US-09-479-005A-1002	Sequence 1002, Ap
37	2	US-08-857-946-41	Sequence 41, Appl
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46	4	US-09-679-426-611	Sequence 611, App
46	4	US-09-679-426-615	Sequence 615, App
47	4	US-09-641-638-962	Sequence 962, App
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21	4	US-09-657-472-1808	Sequence 1808, Ap
21	4	US-09-657-472-2364	Sequence 2364, Ap
23	2	US-09-029-341-7	Sequence 7, Appl
28	2	US-08-305-764C-51	Sequence 51, Appl
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33	3	US-08-430-944D-52	Sequence 52, Appl
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33	3	US-08-431-184-52	Sequence 52, Appl
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34	2	US-08-505-448A-9	Sequence 9, Appl
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40	4	US-09-402-923A-185	Sequence 185, App
45	1	US-08-661-507-2	Sequence 2, Appl
45	2	US-08-840-236-14	Sequence 14, Appl
46	2	US-08-505-448A-14	Sequence 14, Appl
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50	3	US-09-012-097A-50	Sequence 50, Appl
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50	4	US-09-781-804-49	Sequence 49, Appl
50	4	US-09-060-299-383	Sequence 383, App
19	4	US-09-402-923A-383	Sequence 383, App
19	4	US-09-696-791-271	Sequence 271, App
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23	3	US-09-175-828-48	Sequence 48, Appl
23	3	US-09-129-075-5	Sequence 5, Appl
26	3	US-07-850-770-23	Sequence 23, Appl
26	4	US-09-544-123-5	Sequence 5, Appl
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30	1	US-08-313-168-4	Sequence 4, Appl

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c 102	11.2	53.3	34	4	US-09-086-118-19	Sequence 19, Appl	175	10.8	51.4	25	2	US-08-738-922-3	Sequence 3, Appl
103	11.2	53.3	34	4	US-09-769-864-49	Sequence 49, Appl	176	10.8	51.4	25	3	US-09-474-922A-7	Sequence 7, Appl
104	11.2	53.3	36	4	US-09-371-772B-12844	Sequence 12844, A	177	10.8	51.4	26	1	US-08-148-310-4	Sequence 4, Appl
105	11.2	53.3	36	4	US-09-479-005A-674	Sequence 674, App	178	10.8	51.4	26	3	US-08-448-937A-4	Sequence 4, Appl
106	11.2	53.3	37	4	US-09-479-005A-1102	Sequence 1102, Ap	c 179	10.8	51.4	26	3	US-09-245-041-74	Sequence 74, Appl
107	11.2	53.3	41	4	US-09-479-123-15	Sequence 15, Appl	c 180	10.8	51.4	26	4	US-09-358-055B-75	Sequence 75, Appl
108	11.2	53.3	41	4	US-09-484-997-15	Sequence 15, Appl	c 181	10.8	51.4	26	4	US-09-893-238-74	Sequence 74, Appl
109	11.2	53.3	41	4	US-09-481-355-15	Sequence 15, Appl	c 182	10.8	51.4	28	3	US-09-446-504-90	Sequence 90, Appl
110	11.2	53.3	41	4	US-09-481-282-15	Sequence 15, Appl	c 183	10.8	51.4	28	3	US-09-712-266-90	Sequence 90, Appl
111	11.2	53.3	41	4	US-09-455-659A-15	Sequence 15, Appl	c 184	10.8	51.4	28	4	US-09-786-684-9	Sequence 9, Appl
112	11.2	53.3	41	4	US-09-484-996-15	Sequence 15, Appl	c 185	10.8	51.4	28	4	US-09-786-684-9	Sequence 9, Appl
113	11.2	53.3	41	4	US-09-479-123-15	Sequence 15, Appl	186	10.8	51.4	32	3	US-08-991-743C-129	Sequence 129, App
114	11.2	53.3	41	4	US-09-484-317A-15	Sequence 15, Appl	187	10.8	51.4	32	4	US-09-851-486-129	Sequence 129, App
115	11.2	53.3	41	4	US-08-435-350-52	Sequence 52, Appl	188	10.8	51.4	33	3	US-08-437-569-16	Sequence 16, Appl
116	11.2	52.4	14	1	US-09-474-432B-419	Sequence 419, App	189	10.8	51.4	33	3	US-08-169-715-37	Sequence 37, Appl
117	11.2	52.4	17	4	US-09-474-432B-420	Sequence 420, App	190	10.8	51.4	35	1	US-08-479-852-38	Sequence 38, Appl
118	11.2	52.4	17	4	US-09-476-387-419	Sequence 419, App	191	10.8	51.4	35	1	US-08-479-852-38	Sequence 38, Appl
119	11.2	52.4	17	4	US-09-476-387-419	Sequence 419, App	192	10.8	51.4	35	2	US-08-462-646-38	Sequence 38, Appl
120	11.2	52.4	18	4	US-10-066-130-14	Sequence 14, Appl	193	10.8	51.4	35	2	US-08-462-646-38	Sequence 38, Appl
121	11.2	52.4	20	3	US-09-488-744A-70	Sequence 70, Appl	194	10.8	51.4	35	3	US-09-013-406-118	Sequence 118, App
122	11.2	52.4	22	4	US-08-469-260A-114	Sequence 114, App	195	10.8	51.4	35	3	US-09-013-406-118	Sequence 118, App
123	11.2	52.4	22	4	US-08-469-260A-114	Sequence 114, App	196	10.8	51.4	35	4	US-09-766-095-38	Sequence 38, Appl
124	11.2	52.4	22	4	US-08-467-344A-114	Sequence 114, App	197	10.8	51.4	35	4	US-09-766-095-38	Sequence 38, Appl
125	11.2	52.4	22	4	US-08-424-550B-114	Sequence 114, App	198	10.8	51.4	36	4	US-09-479-005A-778	Sequence 778, App
126	11.2	52.4	23	4	US-09-181-585-6	Sequence 6, Appl	199	10.8	51.4	37	4	US-09-196-270-21	Sequence 21, Appl
127	11.2	52.4	24	3	US-09-139-617-16	Sequence 16, Appl	c 200	10.8	51.4	37	4	US-09-823-823-62	Sequence 62, Appl
128	11.2	52.4	24	4	US-09-561-741A-16	Sequence 16, Appl	201	10.8	51.4	39	2	US-08-467-963C-37	Sequence 37, Appl
129	11.2	52.4	24	4	US-09-558-795-16	Sequence 16, Appl	202	10.8	51.4	39	2	US-08-838-189D-37	Sequence 37, Appl
130	11.2	52.4	25	4	US-09-402-631A-48	Sequence 48, Appl	203	10.8	51.4	39	3	US-08-852-344D-37	Sequence 37, Appl
c 131	11.2	52.4	27	1	US-07-796-106-10	Sequence 10, Appl	204	10.8	51.4	39	3	US-08-344-639E-37	Sequence 37, Appl
132	11.2	52.4	27	3	US-08-584-040-430	Sequence 430, App	205	10.8	51.4	40	3	US-08-975-703-22	Sequence 22, Appl
133	11.2	52.4	28	4	US-09-067-453-3	Sequence 3, Appl	206	10.8	51.4	40	3	US-09-515-884-22	Sequence 22, Appl
134	11.2	52.4	28	4	US-09-067-453-4	Sequence 4, Appl	c 207	10.8	51.4	41	3	US-09-109-063-7	Sequence 7, Appl
c 135	11.2	52.4	29	2	US-08-794-795-3	Sequence 3, Appl	c 208	10.8	51.4	41	4	US-09-448-310-7	Sequence 7, Appl
c 136	11.2	52.4	29	3	US-09-249-200-3	Sequence 3, Appl	c 209	10.8	51.4	42	2	US-08-418-848A-61	Sequence 61, Appl
c 137	11.2	52.4	29	3	US-09-304-232-784	Sequence 784, Appl	c 210	10.8	51.4	43	4	US-09-553-867A-39	Sequence 39, Appl
c 138	11.2	52.4	30	1	US-08-104-072B-20	Sequence 20, Appl	211	10.8	51.4	45	1	US-08-661-507-1	Sequence 1, Appl
c 139	11.2	52.4	35	3	US-08-959-212-11	Sequence 11, Appl	212	10.8	51.4	45	2	US-08-855-085-2	Sequence 2, Appl
c 140	11.2	52.4	36	4	US-09-371-772B-12728	Sequence 12728, A	213	10.8	51.4	45	2	US-09-186-030-2	Sequence 2, Appl
c 141	11.2	52.4	36	4	US-09-371-772B-12746	Sequence 12746, A	214	10.8	51.4	45	2	US-08-865-675-2	Sequence 2, Appl
c 142	11.2	52.4	36	4	US-09-371-772B-12813	Sequence 12813, A	215	10.8	51.4	45	2	US-08-933-749-3	Sequence 3, Appl
c 143	11.2	52.4	36	4	US-09-371-772B-13005	Sequence 13005, A	216	10.8	51.4	45	2	US-09-237-510-2	Sequence 2, Appl
c 144	11.2	52.4	36	4	US-09-371-772B-13027	Sequence 13027, A	217	10.8	51.4	45	3	US-09-120-916-2	Sequence 2, Appl
c 145	11.2	52.4	36	4	US-09-371-772B-13150	Sequence 13150, A	218	10.8	51.4	45	3	US-08-964-020-6	Sequence 6, Appl
c 146	11.2	52.4	36	4	US-09-371-772B-14097	Sequence 14097, A	219	10.8	51.4	45	3	US-09-235-583-3	Sequence 3, Appl
c 147	11.2	52.4	36	4	US-09-479-005A-683	Sequence 683, App	220	10.8	51.4	45	3	US-09-599-164-3	Sequence 3, Appl
c 148	11.2	52.4	36	4	US-09-479-005A-920	Sequence 920, App	c 221	10.8	51.4	47	4	US-09-422-978-323	Sequence 323, App
c 149	11.2	52.4	36	4	US-09-479-005A-993	Sequence 993, App	c 222	10.8	51.4	47	4	US-09-422-978-323	Sequence 323, App
c 150	11.2	52.4	36	4	US-09-479-005A-1001	Sequence 1001, Ap	223	10.8	51.4	47	4	US-09-270-767-25514	Sequence 25514, A
c 151	11.2	52.4	36	4	US-09-479-005A-1003	Sequence 1003, Ap	224	10.8	51.4	50	4	US-08-292-620A-1811	Sequence 1811, Ap
c 152	11.2	52.4	36	4	US-09-479-005A-1012	Sequence 1012, Ap	c 225	10.6	50.5	17	3	US-09-071-845-1811	Sequence 1811, Ap
c 153	11.2	52.4	37	4	US-09-552-322-20	Sequence 20, Appl	c 226	10.6	50.5	17	3	US-08-633-575B-3	Sequence 3, Appl
c 154	11.2	52.4	37	4	US-09-479-005A-1104	Sequence 1104, Ap	c 227	10.6	50.5	20	2	US-08-433-819-11	Sequence 11, Appl
c 155	11.2	52.4	38	2	US-09-479-005A-1166	Sequence 1166, Ap	228	10.6	50.5	20	3	US-09-488-744A-59	Sequence 59, Appl
c 156	11.2	52.4	38	2	US-09-097-759-5	Sequence 5, Appl	229	10.6	50.5	20	3	US-09-199-542B-3	Sequence 3, Appl
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c 158	11.2	52.4	38	4	US-09-371-772B-7548	Sequence 7548, Ap	c 231	10.6	50.5	21	2	US-09-574-779B-154	Sequence 154, App
c 159	11.2	52.4	38	4	US-09-371-772B-11378	Sequence 11378, A	c 232	10.6	50.5	21	2	US-08-357-642A-11	Sequence 11, Appl
c 160	11.2	52.4	40	4	US-09-849-069-44	Sequence 44, Appl	233	10.6	50.5	21	2	US-08-460-626-11	Sequence 11, Appl
c 161	11.2	52.4	40	4	US-10-001-052-36	Sequence 36, Appl	234	10.6	50.5	21	2	US-08-460-626-23	Sequence 23, Appl
c 162	11.2	52.4	42	3	US-08-952-973-19	Sequence 19, Appl	235	10.6	50.5	24	1	US-08-467-284-12	Sequence 12, Appl
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c 165	11.2	52.4	47	4	US-09-422-978-1654	Sequence 1654, Ap	c 238	10.6	50.5	25	3	US-09-245-041-26	Sequence 26, Appl
c 166	11.2	52.4	48	4	US-08-439-813-7	Sequence 7, Appl	c 239	10.6	50.5	25	3	US-09-358-055B-27	Sequence 27, Appl
c 167	11.2	52.4	48	4	US-10-001-052-123	Sequence 123, App	c 240	10.6	50.5	25	4	US-09-893-238-25	Sequence 25, Appl
c 168	10.8	51.4	19	4	US-09-475-947A-46	Sequence 46, Appl	c 241	10.6	50.5	25	4	US-08-411-795B-57	Sequence 57, Appl
c 169	10.8	51.4	20	4	US-09-529-239D-65	Sequence 65, Appl	c 242	10.6	50.5	26	1	US-08-469-319A-57	Sequence 57, Appl
c 170	10.8	51.4	21	4	US-09-657-472-1455	Sequence 1455, Ap	c 243	10.6	50.5	26	1	US-08-469-319A-57	Sequence 57, Appl
c 171	10.8	51.4	21	4	US-09-657-472-2292	Sequence 2292, Ap	c 244	10.6	50.5	26	4	US-08-764-114-57	Sequence 57, Appl
c 172	10.8	51.4	22	1	US-08-464-523B-21	Sequence 21, Appl	c 245	10.6	50.5	26	4	US-08-469-419-57	Sequence 57, Appl
c 173	10.8	51.4	24	2	US-08-448-267A-7	Sequence 7, Appl	c 246	10.6	50.5	26	4	US-09-199-542B-82	Sequence 82, Appl

C 247	10.6	50.5	27	1	US-08-242-402-3	Sequence 3, Appli	C 320	10.6	50.5	47	4	US-09-422-978-3505	Sequence 3505, Ap
C 248	10.6	50.5	27	1	US-08-270-180-4	Sequence 4, Appli	C 321	10.6	50.5	48	1	US-08-137-117D-81	Sequence 81, Appl
C 249	10.6	50.5	27	1	US-08-682-423-4	Sequence 4, Appli	C 322	10.6	50.5	48	1	US-08-436-717-81	Sequence 81, Appl
C 250	10.6	50.5	27	3	US-09-246-277A-8	Sequence 8, Appli	C 323	10.4	49.5	17	3	US-08-584-040-5368	Sequence 5368, Ap
C 251	10.6	50.5	27	5	PCT-US95-05141-4	Sequence 4, Appli	C 324	10.4	49.5	17	3	US-08-584-040-5369	Sequence 5369, Ap
C 252	10.6	50.5	28	1	US-08-455-633A-24	Sequence 24, Appl	C 325	10.4	49.5	17	4	US-09-371-772B-2270	Sequence 2270, Ap
C 253	10.6	50.5	28	2	US-08-456-460C-24	Sequence 24, Appl	C 326	10.4	49.5	17	4	US-09-371-772B-2271	Sequence 2271, Ap
C 254	10.6	50.5	28	3	US-08-812-121-6	Sequence 6, Appli	C 327	10.4	49.5	18	3	US-08-584-040-6215	Sequence 6215, Ap
C 255	10.6	50.5	28	3	US-08-928-805-3	Sequence 3, Appli	C 328	10.4	49.5	18	4	US-09-157-864-14	Sequence 14, Appl
C 256	10.6	50.5	28	3	US-09-403-672-6	Sequence 6, Appli	C 329	10.4	49.5	18	4	US-09-371-772B-2977	Sequence 2977, Ap
C 257	10.6	50.5	28	5	PCT-US94-05354-24	Sequence 24, Appl	C 330	10.4	49.5	19	1	US-08-221-579A-47	Sequence 47, Appl
C 258	10.6	50.5	29	1	US-08-032-846-25	Sequence 25, Appl	C 331	10.4	49.5	19	1	US-08-753-147-6	Sequence 6, Appli
C 259	10.6	50.5	29	2	US-08-993-228-29	Sequence 29, Appl	C 332	10.4	49.5	19	1	US-08-512-681-11	Sequence 11, Appl
C 260	10.6	50.5	29	3	US-09-029-341-11	Sequence 11, Appl	C 333	10.4	49.5	19	2	US-08-704-701-47	Sequence 47, Appl
C 261	10.6	50.5	29	3	US-08-474-636-25	Sequence 25, Appl	C 334	10.4	49.5	19	2	US-08-979-385B-51	Sequence 51, Appl
C 262	10.6	50.5	30	4	US-09-522-955A-17	Sequence 17, Appl	C 335	10.4	49.5	19	3	US-09-321-461-47	Sequence 47, Appl
C 263	10.6	50.5	32	3	US-09-252-292-10	Sequence 10, Appl	C 336	10.4	49.5	19	3	US-08-357-398A-39	Sequence 39, Appl
C 264	10.6	50.5	33	4	US-09-531-056A-11	Sequence 11, Appl	C 337	10.4	49.5	19	4	US-09-422-978-9097	Sequence 9097, Ap
C 265	10.6	50.5	35	4	US-09-823-823-38	Sequence 38, Appl	C 338	10.4	49.5	19	5	PCT-US95-16206A-39	Sequence 39, Appl
C 266	10.6	50.5	35	4	US-09-736-116-65	Sequence 65, Appl	C 339	10.4	49.5	20	3	US-08-928-881-4	Sequence 4, Appli
C 267	10.6	50.5	35	4	US-09-736-116-94	Sequence 94, Appl	C 340	10.4	49.5	20	3	US-09-167-375-15	Sequence 15, Appl
C 268	10.6	50.5	36	4	US-09-371-772B-12943	Sequence 12743, A	C 341	10.4	49.5	20	3	US-09-467-642-46	Sequence 46, Appl
C 269	10.6	50.5	36	4	US-09-371-772B-12940	Sequence 12940, A	C 342	10.4	49.5	20	3	US-09-543-921-4	Sequence 4, Appli
C 270	10.6	50.5	36	4	US-09-371-772B-13109	Sequence 13109, A	C 343	10.4	49.5	20	4	US-09-517-467B-223	Sequence 223, App
C 271	10.6	50.5	36	4	US-09-479-005A-571	Sequence 571, App	C 344	10.4	49.5	20	4	US-09-266-014-9	Sequence 9, Appli
C 272	10.6	50.5	36	4	US-09-479-005A-595	Sequence 595, App	C 345	10.4	49.5	20	4	US-09-659-845A-171	Sequence 171, App
C 273	10.6	50.5	36	4	US-09-479-005A-688	Sequence 688, App	C 346	10.4	49.5	20	4	US-09-422-978-11045	Sequence 11045, A
C 274	10.6	50.5	36	4	US-09-479-005A-838	Sequence 838, App	C 347	10.4	49.5	20	4	US-09-491-759-4	Sequence 4, Appli
C 275	10.6	50.5	36	4	US-09-479-005A-903	Sequence 903, App	C 348	10.4	49.5	20	4	US-09-526-193A-147	Sequence 147, App
C 276	10.6	50.5	36	4	US-09-479-005A-975	Sequence 975, App	C 349	10.4	49.5	21	3	US-09-336-447A-66	Sequence 66, Appl
C 277	10.6	50.5	36	4	US-09-004-068-7	Sequence 7, Appli	C 350	10.4	49.5	21	3	US-09-710-200-3	Sequence 3, Appli
C 278	10.6	50.5	37	1	US-08-477-877B-27	Sequence 27, Appl	C 351	10.4	49.5	21	4	US-09-975-408-3	Sequence 3, Appli
C 279	10.6	50.5	37	2	US-08-472-281A-27	Sequence 27, Appl	C 352	10.4	49.5	21	4	US-09-422-978-11666	Sequence 11666, A
C 280	10.6	50.5	37	2	US-08-477-989B-27	Sequence 27, Appl	C 353	10.4	49.5	21	4	US-09-657-472-1826	Sequence 1826, Ap
C 281	10.6	50.5	37	4	US-09-662-386-17	Sequence 17, Appl	C 354	10.4	49.5	21	4	US-09-522-267B-66	Sequence 66, Appl
C 282	10.6	50.5	37	4	US-09-479-005A-1078	Sequence 1078, Ap	C 355	10.4	49.5	23	1	US-08-242-035A-9	Sequence 9, Appl
C 283	10.6	50.5	38	4	US-10-112-802-68	Sequence 68, Appl	C 356	10.4	49.5	23	3	US-09-018-584A-47	Sequence 47, Appl
C 284	10.6	50.5	38	4	US-10-112-802-69	Sequence 69, Appl	C 357	10.4	49.5	23	4	US-09-784-423-47	Sequence 47, Appl
C 285	10.6	50.5	39	2	US-08-714-070A-21	Sequence 21, Appl	C 358	10.4	49.5	24	1	US-08-508-778A-13	Sequence 13, Appl
C 286	10.6	50.5	40	4	US-09-496-346-10	Sequence 10, Appl	C 359	10.4	49.5	24	2	US-08-202-044-14	Sequence 14, Appl
C 287	10.6	50.5	41	2	US-08-985-337A-4	Sequence 4, Appli	C 360	10.4	49.5	24	3	US-08-751-344B-14	Sequence 14, Appl
C 288	10.6	50.5	41	2	US-08-985-144A-4	Sequence 4, Appli	C 361	10.4	49.5	24	3	US-08-818-082-6	Sequence 6, Appli
C 289	10.6	50.5	41	3	US-08-985-320A-4	Sequence 4, Appli	C 362	10.4	49.5	24	4	US-09-815-585-21	Sequence 21, Appl
C 290	10.6	50.5	41	3	US-08-984-732A-4	Sequence 4, Appli	C 363	10.4	49.5	24	4	US-09-692-056-6	Sequence 6, Appli
C 291	10.6	50.5	41	3	US-09-195-578-16	Sequence 16, Appl	C 364	10.4	49.5	25	1	US-07-989-160-10	Sequence 10, Appl
C 292	10.6	50.5	41	3	US-09-170-951-16	Sequence 16, Appl	C 365	10.4	49.5	25	3	US-08-891-789B-18	Sequence 18, Appl
C 293	10.6	50.5	41	3	US-09-164-482-16	Sequence 16, Appl	C 366	10.4	49.5	25	3	US-08-849-602C-6	Sequence 6, Appli
C 294	10.6	50.5	41	3	US-09-332-769-11	Sequence 11, Appl	C 367	10.4	49.5	25	3	US-09-149-322-41	Sequence 41, Appl
C 295	10.6	50.5	41	3	US-09-456-153-11	Sequence 11, Appl	C 368	10.4	49.5	25	5	PCT-US92-08090-10	Sequence 10, Appl
C 296	10.6	50.5	41	3	US-09-167-180-16	Sequence 16, Appl	C 369	10.4	49.5	26	1	US-08-044-621D-15	Sequence 15, Appl
C 297	10.6	50.5	41	3	US-09-455-627-11	Sequence 11, Appl	C 370	10.4	49.5	26	3	US-09-534-407-28	Sequence 28, Appl
C 298	10.6	50.5	41	3	US-09-426-533-11	Sequence 11, Appl	C 371	10.4	49.5	26	4	US-09-007-288E-2	Sequence 2, Appli
C 299	10.6	50.5	41	3	US-09-609-205-12	Sequence 12, Appl	C 372	10.4	49.5	26	4	US-09-007-288E-137	Sequence 137, App
C 300	10.6	50.5	41	3	US-09-516-945-11	Sequence 11, Appl	C 373	10.4	49.5	26	4	US-09-999-201B-28	Sequence 28, Appl
C 301	10.6	50.5	41	3	US-09-757-218-12	Sequence 12, Appl	C 374	10.4	49.5	26	4	US-10-281-673A-28	Sequence 28, Appl
C 302	10.6	50.5	41	3	US-09-516-757-11	Sequence 11, Appl	C 375	10.4	49.5	27	4	US-09-630-250B-2	Sequence 2, Appli
C 303	10.6	50.5	41	3	US-09-516-750-11	Sequence 11, Appl	C 376	10.4	49.5	28	1	US-08-446-729-11	Sequence 11, Appl
C 304	10.6	50.5	41	3	US-09-342-577-12	Sequence 12, Appl	C 377	10.4	49.5	28	4	US-09-157-864-12	Sequence 12, Appl
C 305	10.6	50.5	41	3	US-09-516-756-11	Sequence 11, Appl	C 378	10.4	49.5	29	1	US-08-306-871-23	Sequence 23, Appl
C 306	10.6	50.5	41	3	US-09-828-061A-12	Sequence 12, Appl	C 379	10.4	49.5	29	2	US-08-569-959-23	Sequence 23, Appl
C 307	10.6	50.5	41	3	US-09-463-917-11	Sequence 11, Appl	C 380	10.4	49.5	29	2	US-08-930-605-5	Sequence 5, Appli
C 308	10.6	50.5	41	4	US-09-347-673-12	Sequence 12, Appl	C 381	10.4	49.5	30	1	US-08-373-124A-25	Sequence 25, Appl
C 309	10.6	50.5	41	4	US-09-757-213-12	Sequence 12, Appl	C 382	10.4	49.5	30	1	US-08-667-079B-8	Sequence 8, Appli
C 310	10.6	50.5	41	4	US-09-656-653-11	Sequence 11, Appl	C 383	10.4	49.5	30	1	US-08-435-628-25	Sequence 25, Appl
C 311	10.6	50.5	41	4	US-09-757-231-12	Sequence 12, Appl	C 384	10.4	49.5	30	2	US-08-678-039A-20	Sequence 20, Appl
C 312	10.6	50.5	41	4	US-09-828-259A-12	Sequence 12, Appl	C 385	10.4	49.5	30	3	US-08-643-704A-27	Sequence 27, Appl
C 313	10.6	50.5	41	4	US-09-719-878-12	Sequence 12, Appl	C 386	10.4	49.5	30	4	US-09-052-919-30	Sequence 30, Appl
C 314	10.6	50.5	41	4	US-09-757-217A-12	Sequence 12, Appl	C 387	10.4	49.5	30	4	US-09-953-052-30	Sequence 30, Appl
C 315	10.6	50.5	41	4	US-09-828-325A-12	Sequence 12, Appl	C 388	10.4	49.5	31	2	US-08-859-998-463	Sequence 463, App
C 316	10.6	50.5	41	4	US-09-756-248-11	Sequence 11, Appl	C 389	10.4	49.5	31	3	US-08-836-329-14	Sequence 14, Appl
C 317	10.6	50.5	44	1	US-08-340-011-20	Sequence 20, Appl	C 390	10.4	49.5	31	3	US-03-225-928-463	Sequence 463, App
C 318	10.6	50.5	44	3	US-08-901-710-20	Sequence 20, Appl	C 391	10.4	49.5	32	1	US-09-225-201B-463	Sequence 463, App
C 319	10.6	50.5	46	3	US-09-065-104-14	Sequence 14, Appl	C 392	10.4	49.5	32	1	US-08-765-081-8	Sequence 8, Appli

C 539	10.2	48.6	32	3	US-09-234-393-2	Sequence 2, Appli	c 612	10.2	48.6	48	3	US-08-986-659B-13	Sequence 13, Appl
C 540	10.2	48.6	32	3	US-09-865-171-2	Sequence 2, Appli	613	10.2	48.6	49	3	US-09-235-451-13	Sequence 13, Appl
C 541	10.2	48.6	33	4	US-09-043-239-15	Sequence 15, Appl	614	10.2	48.6	49	4	US-09-978-303-13	Sequence 13, Appl
C 542	10.2	48.6	33	4	US-09-080-983-22	Sequence 22, Appl	615	10.2	48.6	50	3	US-09-043-239-7	Sequence 7, Appli
C 543	10.2	48.6	33	4	US-09-495-901-15	Sequence 15, Appl	616	10.2	48.6	50	4	US-09-495-901-7	Sequence 7, Appli
C 544	10.2	48.6	34	2	US-08-381-691-9	Sequence 9, Appli	617	10.2	48.6	50	4	US-08-956-171E-2231	Sequence 2231, Ap
C 545	10.2	48.6	34	4	US-08-463-260A-128	Sequence 128, App	618	10.2	48.6	50	4	US-08-781-986A-2231	Sequence 2231, Ap
C 546	10.2	48.6	34	4	US-08-468-446-128	Sequence 128, App	c 619	10	47.6	14	4	US-07-209-504-1	Sequence 1, Appli
C 547	10.2	48.6	34	4	US-08-467-344A-128	Sequence 128, App	620	10	47.6	17	3	US-09-446-504-28	Sequence 28, Appl
C 548	10.2	48.6	34	4	US-08-424-550B-128	Sequence 128, App	621	10	47.6	17	3	US-09-712-266-38	Sequence 28, Appl
C 549	10.2	48.6	34	4	US-09-971-611-10	Sequence 11, Appl	622	10	47.6	18	1	US-07-702-163B-2	Sequence 2, Appli
C 550	10.2	48.6	34	4	US-09-971-611-11	Sequence 11, Appl	623	10	47.6	18	1	US-08-060-984-2	Sequence 2, Appli
C 551	10.2	48.6	36	4	US-09-371-772B-12820	Sequence 12820, A	624	10	47.6	18	1	US-08-143-219-10	Sequence 10, Appl
C 552	10.2	48.6	37	1	US-08-290-592E-15	Sequence 15, Appl	625	10	47.6	18	1	US-08-383-742-2	Sequence 2, Appli
C 553	10.2	48.6	37	5	PCT-US95-10053-12	Sequence 12, Appl	626	10	47.6	18	2	US-08-532-979-1	Sequence 1, Appli
C 554	10.2	48.6	37	5	PCT-US96-09448-15	Sequence 15, Appl	627	10	47.6	18	2	US-08-532-979-4	Sequence 4, Appli
C 555	10.2	48.6	38	2	US-08-857-946-127	Sequence 127, App	628	10	47.6	18	2	US-08-532-979-6	Sequence 6, Appli
C 556	10.2	48.6	38	3	US-08-970-740-127	Sequence 127, App	629	10	47.6	18	3	US-08-540-699-1	Sequence 1, Appli
C 557	10.2	48.6	38	4	US-09-371-772B-8119	Sequence 8119, Ap	c 630	10	47.6	18	4	US-09-250-609-56	Sequence 56, Appl
C 558	10.2	48.6	39	3	US-09-198-723A-28	Sequence 28, Appl	c 631	10	47.6	18	4	US-09-250-611-56	Sequence 56, Appl
C 559	10.2	48.6	39	3	US-09-198-723A-29	Sequence 29, Appl	632	10	47.6	18	4	US-09-587-934B-20	Sequence 20, Appl
C 560	10.2	48.6	39	3	US-09-198-723A-36	Sequence 36, Appl	633	10	47.6	18	4	US-09-321-249-20	Sequence 20, Appl
C 561	10.2	48.6	39	3	US-09-198-723A-37	Sequence 37, Appl	634	10	47.6	18	4	US-09-375-248-10	Sequence 10, Appl
C 562	10.2	48.6	39	3	US-09-198-723A-44	Sequence 44, Appl	635	10	47.6	18	4	US-08-835-370-39	Sequence 39, Appl
C 563	10.2	48.6	39	3	US-09-198-723A-45	Sequence 45, Appl	636	10	47.6	19	1	US-08-221-579A-48	Sequence 48, Appl
C 564	10.2	48.6	39	3	US-09-198-723A-51	Sequence 51, Appl	637	10	47.6	19	2	US-08-704-701-48	Sequence 48, Appl
C 565	10.2	48.6	39	3	US-09-198-723A-52	Sequence 52, Appl	638	10	47.6	19	2	US-08-979-385B-52	Sequence 52, Appl
C 566	10.2	48.6	39	3	US-09-198-723A-58	Sequence 58, Appl	639	10	47.6	19	3	US-09-321-461-48	Sequence 48, Appl
C 567	10.2	48.6	39	3	US-09-198-723A-59	Sequence 59, Appl	640	10	47.6	19	3	US-08-357-398A-40	Sequence 40, Appl
C 568	10.2	48.6	39	3	US-09-198-723A-61	Sequence 61, Appl	641	10	47.6	19	5	PCT-US95-16206A-40	Sequence 40, Appl
C 569	10.2	48.6	39	3	US-09-198-723A-62	Sequence 62, Appl	642	10	47.6	20	2	US-08-418-848A-43	Sequence 43, Appl
C 570	10.2	48.6	39	3	US-09-198-723A-75	Sequence 75, Appl	c 643	10	47.6	20	2	US-08-418-848A-46	Sequence 46, Appl
C 571	10.2	48.6	39	3	US-09-198-723A-76	Sequence 76, Appl	644	10	47.6	20	3	US-09-167-375-18	Sequence 18, Appl
C 572	10.2	48.6	39	3	US-09-198-723A-81	Sequence 81, Appl	c 645	10	47.6	20	3	US-09-489-765A-27	Sequence 27, Appl
C 573	10.2	48.6	39	3	US-09-198-723A-82	Sequence 82, Appl	c 646	10	47.6	20	3	US-03-561-437-53	Sequence 53, Appl
C 574	10.2	48.6	39	4	US-09-477-135A-163	Sequence 163, App	647	10	47.6	20	4	US-08-211-823C-13	Sequence 13, Appl
C 575	10.2	48.6	39	4	US-09-684-881-28	Sequence 28, Appl	c 648	10	47.6	21	1	US-08-728-259A-20	Sequence 20, Appl
C 576	10.2	48.6	39	4	US-09-684-881-29	Sequence 29, Appl	c 649	10	47.6	21	2	US-08-473-486-20	Sequence 20, Appl
C 577	10.2	48.6	39	4	US-09-684-881-36	Sequence 36, Appl	c 650	10	47.6	21	4	US-09-360-545-35	Sequence 35, Appl
C 578	10.2	48.6	39	4	US-09-684-881-37	Sequence 37, Appl	c 651	10	47.6	21	4	US-09-657-472-307	Sequence 307, App
C 579	10.2	48.6	39	4	US-09-684-881-44	Sequence 44, Appl	c 652	10	47.6	22	3	US-09-099-749-3	Sequence 3, Appli
C 580	10.2	48.6	39	4	US-09-684-881-45	Sequence 45, Appl	653	10	47.6	22	3	US-09-341-587-11	Sequence 11, Appl
C 581	10.2	48.6	39	4	US-09-684-881-51	Sequence 51, Appl	c 654	10	47.6	23	3	US-08-964-877-14	Sequence 14, Appl
C 582	10.2	48.6	39	4	US-09-684-881-52	Sequence 52, Appl	655	10	47.6	23	3	US-09-540-699-6	Sequence 6, Appli
C 583	10.2	48.6	39	4	US-09-684-881-58	Sequence 58, Appl	656	10	47.6	23	3	US-09-540-699-10	Sequence 10, Appl
C 584	10.2	48.6	39	4	US-09-684-881-59	Sequence 59, Appl	c 657	10	47.6	24	1	US-08-117-329-2	Sequence 2, Appli
C 585	10.2	48.6	39	4	US-09-684-881-61	Sequence 61, Appl	c 658	10	47.6	24	2	US-08-859-398-776	Sequence 776, App
C 586	10.2	48.6	39	4	US-09-684-881-62	Sequence 62, Appl	659	10	47.6	24	3	US-09-225-928-776	Sequence 776, App
C 587	10.2	48.6	39	4	US-09-684-881-75	Sequence 75, Appl	660	10	47.6	24	3	US-09-540-699-4	Sequence 4, Appli
C 588	10.2	48.6	39	4	US-09-684-881-76	Sequence 76, Appl	661	10	47.6	24	3	US-09-540-699-7	Sequence 7, Appli
C 589	10.2	48.6	39	4	US-09-684-881-81	Sequence 81, Appl	c 662	10	47.6	24	4	US-09-806-354-19	Sequence 19, Appl
C 590	10.2	48.6	39	4	US-09-684-881-82	Sequence 82, Appl	663	10	47.6	24	4	US-09-225-201B-776	Sequence 776, App
C 591	10.2	48.6	40	1	US-07-972-387-57	Sequence 57, Appl	c 664	10	47.6	25	1	US-08-368-281-9	Sequence 9, Appli
C 592	10.2	48.6	40	1	US-08-431-412-57	Sequence 57, Appl	665	10	47.6	25	2	US-08-666-392A-8	Sequence 8, Appli
C 593	10.2	48.6	40	1	US-08-057-971-57	Sequence 57, Appl	c 666	10	47.6	25	3	US-08-737-607-10	Sequence 10, Appl
C 594	10.2	48.6	40	2	US-08-235-515A-53	Sequence 53, Appl	c 667	10	47.6	25	3	US-08-513-974B-213	Sequence 213, App
C 595	10.2	48.6	40	2	US-08-455-968E-45	Sequence 45, Appl	668	10	47.6	25	3	US-09-199-926-8	Sequence 8, Appli
C 596	10.2	48.6	40	3	US-08-929-329-19	Sequence 19, Appl	c 669	10	47.6	25	3	US-09-203-231B-86	Sequence 86, Appl
C 597	10.2	48.6	44	1	US-08-168-917-10	Sequence 10, Appl	670	10	47.6	25	3	US-09-150-766-4	Sequence 4, Appli
C 598	10.2	48.6	44	2	US-08-460-510-10	Sequence 10, Appl	671	10	47.6	25	3	US-09-540-699-8	Sequence 8, Appli
C 599	10.2	48.6	44	2	US-08-460-490-10	Sequence 10, Appl	672	10	47.6	25	3	US-09-540-699-11	Sequence 11, Appl
C 600	10.2	48.6	44	4	US-09-281-851-3	Sequence 3, Appli	673	10	47.6	25	4	US-09-422-936-9	Sequence 9, Appli
C 601	10.2	48.6	44	5	PCT-US92-00730-10	Sequence 5, Appli	674	10	47.6	25	4	US-09-422-936-64	Sequence 64, Appl
C 602	10.2	48.6	45	2	US-08-687-355A-13	Sequence 13, Appl	675	10	47.6	25	4	US-09-866-108A-12068	Sequence 12068, A
C 603	10.2	48.6	45	3	US-08-986-659B-12	Sequence 12, Appl	676	10	47.6	25	4	US-09-866-108A-12069	Sequence 12069, A
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ALIGNMENTS

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; APPLICANT: LEMOINE, YVES; NGUYEN, MARTINE; ACHSTETTER, TILMAN
; TITLE OF INVENTION: YEAST VECTOR CODING FOR HETEROLOGOUS
; GENE FUSIONS LINKED VIA KEX2 CLEAVAGE SITE AND CODING FOR
; TRUNCATED KEX2 GENES
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,025
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 191,354
; FILING DATE: 07-FEB-1994
; APPLICATION NUMBER: 26,121
; FILING DATE: 04-MAR-1993
; APPLICATION NUMBER: 500,885
; FILING DATE: 29-MAR-1990
; SEQ ID NO: 6
; LENGTH: 40
5521093-6

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; Patent No. 5958771
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESS
; FILE REFERENCE: RTS-0021
; CURRENT APPLICATION NUMBER: US/09/205,144
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 47

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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-144-29

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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for No. 6770465el Substrate
; FILE REFERENCE: 16516.117
; CURRENT APPLICATION NUMBER: US/09/591,279A
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/138,308
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
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; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for No. 6770465el Substrate
; FILE REFERENCE: 16516.117
; CURRENT APPLICATION NUMBER: US/09/591,279A
; CURRENT FILING DATE: 2000-06-09
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; PRIOR FILING DATE: 1999-06-09
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US-09-591-279A-16


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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
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; LENGTH: 28 bases
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; MOLECULE TYPE: other nucleic acid
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; ANTI-SENSE: Yes
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; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
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; CELL LINE:
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; IMMEDIATE SOURCE:
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; AUTHORS:
; TITLE:
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; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-959-369-19
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; Db 27 ATCGAGATTACTGGC 12
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; US-09-029-341-5
; Sequence 5, Application US/09029341
; Patent No. 6197588
; GENERAL INFORMATION:
; APPLICANT: Gray, John C.
; APPLICANT: Knight, Jacqueline S.
; TITLE OF INVENTION: PLASTID INNER ENVELOPE MEMBRANE

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;/ TITLE OF INVENTION: TARGETING POLYPEPTIDES, MANUFACTURE AND
;/ TITLE OF INVENTION: USE THEREOF
;/ NUMBER OF SEQUENCES: 12
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: PENNIE & EDMONDS LLP
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: NY
;/ COUNTRY: USA
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
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;/ SOFTWARE: FastSeq Version 2.0
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;/ APPLICATION NUMBER: US/09/029,341
;/ FILING DATE: 27-FEB-1998
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: GB 9517674.9
;/ FILING DATE: 30-AUG-1995
;/ APPLICATION NUMBER: PCT/GB96/02129
;/ FILING DATE: 28-AUG-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Coruzzi, Laura A
;/ REGISTRATION NUMBER: 30,742
;/ REFERENCE/DOCKET NUMBER: 9341-012-999
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212)7909090
;/ TELEFAX: (212)8699741
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 5:
;/ SEQUENCE CHARACTERISTICS:
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Query Match 61.0%; Score 12.8; DB 3; Length 28;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTAC 17
Db 3 GCGCATGCCGATTC 18

RESULT 8
US-08-229-279-17
; Sequence 17, Application US/08229279
; Patent No. 5648211
; GENERAL INFORMATION:
; APPLICANT: Fraiser, Melinda S.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Walker, George T.
; APPLICANT: Van Cleve, Mark
; APPLICANT: Wright, David J.
; TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM: Floppy disk

;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/229,279
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Fugit, Donna R.
;/ REGISTRATION NUMBER: 32,135
;/ REFERENCE/DOCKET NUMBER: P-2961
;/ INFORMATION FOR SEQ ID NO: 17:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 49 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
;/ US-08-229-279-17
;/ Query Match 61.0%; Score 12.8; DB 1; Length 49;
;/ Best Local Similarity 87.5%; Pred. No. 1.6e+03;
;/ Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;/ Qy 5 CATGCCAGATTACTGG 20
;/ Db 22 CATGCCCGTTACTGG 37
;/ RESULT 9
;/ US-08-701-269-17
;/ Sequence 17, Application US/08701269
;/ Patent No. 5744311
;/ GENERAL INFORMATION:
;/ APPLICANT: Fraiser, Melinda S.
;/ APPLICANT: Spargo, Catherine A.
;/ APPLICANT: Walker, George T.
;/ APPLICANT: Van Cleve, Mark
;/ APPLICANT: Wright, David J.
;/ TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
;/ NUMBER OF SEQUENCES: 19
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
;/ ADDRESSEE: Company
;/ STREET: 1 Becton Drive
;/ CITY: Franklin Lakes
;/ STATE: NJ
;/ COUNTRY: US
;/ ZIP: 07417
;/ COMPUTER READABLE FORM: Floppy disk
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/701,269
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/229,279
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Fugit, Donna R.
;/ REGISTRATION NUMBER: 32,135
;/ REFERENCE/DOCKET NUMBER: P-2961
;/ INFORMATION FOR SEQ ID NO: 17:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 49 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)

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US-08-701-269-17
Query Match      61.0%; Score 12.8; DB 1; Length 49;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGG 20
Db 22 CATGCCGGTTACTGG 37

RESULT 10
US-09-198-452A-3669/c
; Sequence 3669, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3669
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3669

Query Match      60.0%; Score 12.6; DB 4; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTG 19
Db 20 AACGCGTCCCAATTACAG 2

RESULT 11
US-09-371-772B-12766/c
; Sequence 12766, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12766
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12766

Query Match      60.0%; Score 12.6; DB 4; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTG 19

US-08-701-269-17
Db 19 AGTGCATGCCATCATCTG 1

RESULT 12
US-09-179-221D-7
; Sequence 7, Application US/09179221D
; Patent No. 6291168
; GENERAL INFORMATION:
; APPLICANT: Musso, Richard
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES DIAGNOSTIC FOR PATHOGENIC E.
; TITLE OF INVENTION: COLI 0157, METHODS OF IDENTIFICATION AND KIT THEREFOR
; FILE REFERENCE: 922.6496P
; CURRENT APPLICATION NUMBER: US/09/179,221D
; CURRENT FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: No. 6291168epad
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-179-221D-7

Query Match      59.0%; Score 12.4; DB 3; Length 21;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTAC 17
Db 8 GCATGCCGGATTAC 21

RESULT 13
US-08-721-979A-71/c
; Sequence 71, Application US/08721979A
; Patent No. 6113911
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Baussant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; TITLE OF INVENTION: SYNCTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; STREET: Avenue
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/721,979A
; FILING DATE: October 4, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 04009
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
; TELECOMMUNICATION INFORMATION:
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;
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..42
; OTHER INFORMATION: /product= "GIV"
; OTHER INFORMATION: /note= "sequence 174-187"
US-08-721-979A-71

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
DB 27 GCATGCAAGATTAC 14

RESULT 14
US-08-721-979A-72/c
; Sequence 72, Application US/08721979A
; Patent No. 6113911
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Baussant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; TITLE OF INVENTION: SYNCTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/721,979A
; FILING DATE: October 4, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: FR 94 04009
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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;
; NAME/KEY: CDS
; LOCATION: 1..42
; OTHER INFORMATION: /product= "GIVdeltaC"
; OTHER INFORMATION: /note= "sequence 174-187"
US-08-721-979A-72

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
DB 27 GCATGCAAGATTAC 14

RESULT 15
US-08-836-501-71/c
; Sequence 71, Application US/08836501
; Patent No. 6149911
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR IMPROVING THE IMMUNOGENICITY
; TITLE OF INVENTION: OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE
; TITLE OF INVENTION: PREPARATION OF VACCINES
; NUMBER OF SEQUENCES: 78
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,501
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: FR 9413310
; FILING DATE: 07-NOV-1994
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..42
US-08-836-501-71

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
DB 27 GCATGCAAGATTAC 14

RESULT 16
US-08-836-501-72/c
; Sequence 72, Application US/08836501
; Patent No. 6149911
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR IMPROVING THE IMMUNOGENICITY
; TITLE OF INVENTION: OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE
; TITLE OF INVENTION: PREPARATION OF VACCINES
; NUMBER OF SEQUENCES: 78
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,501
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9413310
FILING DATE: 07-NOV-1994
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
US-08-836-501-72

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
|||||
Db 27 GCATGCCAGATTAC 14

RESULT 17

US-09-654-289-71/c
Sequence 71, Application US/09654289
Patent No. 6410030
GENERAL INFORMATION:

APPLICANT: Binz, Hans
APPLICANT: N'Guyen, Ngoc Thien
APPLICANT: Baussant, Thierry
APPLICANT: Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/654,289
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,979
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
OTHER INFORMATION: /product= "GlV"
OTHER INFORMATION: /note= "sequence 174-187"
US-09-654-289-71

Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
|||||
Db 27 GCATGCCAGATTAC 14

RESULT 18

US-09-654-289-72/c
Sequence 72, Application US/09654289
Patent No. 6410030
GENERAL INFORMATION:

APPLICANT: Binz, Hans
APPLICANT: N'Guyen, Ngoc Thien
APPLICANT: Baussant, Thierry
APPLICANT: Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/654,289
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,979
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
OTHER INFORMATION: /product= "GlVdeltaC"
OTHER INFORMATION: /note= "sequence 174-187"

US-09-654-289-72

Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
DB 27 GCATGCAAGATTAC 14

RESULT 19

US-09-582-876-71/c

; Sequence 71, Application US/09582876

; Patent No. 6537556

; GENERAL INFORMATION:

; APPLICANT: Binz, Hans

; N'Guyen, Ngoc Thien

; Baussant, Thierry

; Trudel, Michel

; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY

; SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL

; COMPOSITION CONTAINING IT AND PREPARATION PROCESS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gordon W. Hueschen

; STREET: 715 The "H" Bldg., 310 East Michigan

; Avenue

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/582,876

; FILING DATE: 30-Jun-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/721,979

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Hueschen, Gordon W.

; REGISTRATION NUMBER: 16,157

; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 616-382-0030

; TELEFAX: 616-382-2030

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..42

; OTHER INFORMATION: /product= "G1V"

; /note= "sequence 174-187"

; SEQUENCE DESCRIPTION: SEQ ID NO: 71:

US-09-582-876-71

Query Match 59.0%; Score 12.4; DB 4; Length 42;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17

DB 27 GCATGCAAGATTAC 14

Db 27 GCATGCAAGATTAC 14

RESULT 20

US-09-582-876-72/c

; Sequence 72, Application US/09582876

; Patent No. 6537556

; GENERAL INFORMATION:

; APPLICANT: Binz, Hans

; N'Guyen, Ngoc Thien

; Baussant, Thierry

; Trudel, Michel

; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY

; SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL

; COMPOSITION CONTAINING IT AND PREPARATION PROCESS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gordon W. Hueschen

; STREET: 715 The "H" Bldg., 310 East Michigan

; Avenue

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/582,876

; FILING DATE: 30-Jun-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/721,979

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Hueschen, Gordon W.

; REGISTRATION NUMBER: 16,157

; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 616-382-0030

; TELEFAX: 616-382-2030

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..42

; OTHER INFORMATION: /product= "GIVdeltaC"

; /note= "sequence 174-187"

; SEQUENCE DESCRIPTION: SEQ ID NO: 72:

US-09-582-876-72

Query Match 59.0%; Score 12.4; DB 4; Length 42;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17

DB 27 GCATGCAAGATTAC 14

RESULT 21

US-09-626-830-71/c

; Sequence 71, Application US/09626830

; Patent No. 6558673

; GENERAL INFORMATION:

APPLICANT: PROCESS FOR IMPROVING THE IMMUNOGENICITY
TITLE OF INVENTION: OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE
TITLE OF INVENTION: PREPARATION OF VACCINES
NUMBER OF SEQUENCES: 78
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/626,830
FILING DATE: 27-JULY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,501
FILING DATE: 07-NOV-1994
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
US-09-626-830-71

Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
|||||
Db 27 GCATGCCAGATTAC 14

RESULT 22
US-09-626-830-72/c
Sequence 72, Application US/09626830
Patent No. 6558673
GENERAL INFORMATION:
APPLICANT: PROCESS FOR IMPROVING THE IMMUNOGENICITY
TITLE OF INVENTION: OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE
TITLE OF INVENTION: PREPARATION OF VACCINES
NUMBER OF SEQUENCES: 78
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/626,830
FILING DATE: 27-JULY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,501
FILING DATE: 07-NOV-1994
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
US-09-626-830-72

Query Match 59.0%; Score 12.4; DB 4; Length 42;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 GCATGCCAGATTAC 17
|||||
Db 27 GCATGCCAGATTAC 14

RESULT 23
US-10-091-257-71/c
Sequence 71, Application US/10091257
Patent No. 6616930
GENERAL INFORMATION:
APPLICANT: Binz, Hans
N'Guyen, Ngoc Thien
Bausant, Thierry
Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
(EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/091,257
FILING DATE: 05-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/721,979A
FILING DATE: October 4, 1996
APPLICATION NUMBER: FR 94 04009
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
OTHER INFORMATION: /product= "G1V"
/note= "sequence 174-187"
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-091-257-71

Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 GCATGCCAGATTAC 17
|||||
Db 27 GCATGCCAGATTAC 14

RESULT 24
US-10-091-257-72/c
; Sequence 72, Application US/10091257
; Patent No. 6616930
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; N'Guyen, Ngoc Thien
; Baussant, Thierry
; Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; SYNCTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; Avenue
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/091,257
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/721,979A
; FILING DATE: October 4, 1996
; APPLICATION NUMBER: FR 94 04009
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..42
; OTHER INFORMATION: /product= "G1VdeltaC"
; /note= "sequence 174-187"
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-091-257-72
Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GCATGCCAGATTAC 17
Db 27 GCATGCCAGATTAC 14
RESULT 25
PCT-US93-09070-5
; Sequence 5, Application PC/TUS9309070
; GENERAL INFORMATION:
; APPLICANT: Lee, William T.L.
; APPLICANT: Serbin, John J.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Barber, Jack R.
; APPLICANT: Chang, Stephen M.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TREATING
; TITLE OF INVENTION: FELINE LEUKEMIA VIRUS AND FELINE
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09070
; FILING DATE: N/A
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.415PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
PCT-US93-09070-5
Query Match 59.0%; Score 12.4; DB 5; Length 45;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGCATGCCAGATT 15
Db 7 GGCATGCCAGATT 20
RESULT 26
US-08-328-710A-15/c
; Sequence 15, Application US/08328710A
; Patent No. 5795717
; GENERAL INFORMATION:
; APPLICANT: Nakayama, Tomoko
; APPLICANT: Tada, Jun
; APPLICANT: Fukushima, Shigeru
; APPLICANT: Ohashi, Tetsuo
; TITLE OF INVENTION: Oligonucleotides for detecting bacteria and detection
; TITLE OF INVENTION: process
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: PO Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,710A
FILING DATE: 25-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
US-08-328-710A-15

Query Match 58.1%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGG 20
| ||| ||||| |||||
Db 17 GAATGTCAGATACTGG 1

RESULT 27
US-08-968-046-15/c
Sequence 15, Application US/08968046
Patent No. 6218110
GENERAL INFORMATION:
APPLICANT: Nakayama, Tomoko
APPLICANT: Tada, Jun
APPLICANT: Fukushima, Shigeru
APPLICANT: Ohashi, Tetsuo
TITLE OF INVENTION: Oligonucleotides for detecting bacteria
TITLE OF INVENTION: and detection process
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,046
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,710
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S
REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
US-08-968-046-15

Query Match 58.1%; Score 12.2; DB 3; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGG 20
| ||| ||||| |||||
Db 17 GAATGTCAGATACTGG 1

RESULT 28
US-07-915-922-9
Sequence 9, Application US/07915922
Patent No. 5422342
GENERAL INFORMATION:
APPLICANT: Young, Karen K.Y.
TITLE OF INVENTION: Mycobacterium Primers and Probes
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,922
FILING DATE: 19920717
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8616
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 522-1285
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-915-922-9

Query Match 58.1%; Score 12.2; DB 1; Length 30;
Best Local Similarity 82.4%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTAC 17
| ||| ||||| |||||

Wed Nov 24 08:46:01 2004

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Db      7 AGTGCAGGCCAGATTGC 23

RESULT 29
US-09-464-122A-13/c
; Sequence 13, Application US/09464122A
; Patent No. 6489103
; GENERAL INFORMATION:
; APPLICANT: MEDICAL RESEARCH COUNCIL
; TITLE OF INVENTION: IN VITRO SORTING METHOD
; FILE REFERENCE: 18396/1080
; CURRENT APPLICATION NUMBER: US/09/464,122A
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/GB98/01889
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: GB 97/14300.2
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: GB 98/06393.6
; PRIOR FILING DATE: 1998-03-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-464-122A-13

Query Match      58.1%; Score 12.2; DB 4; Length 44;
Best Local Similarity 82.4%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GCGCATGCCAGATTACT 18
Db      43 GTGCATGCGCTGATACT 27

RESULT 30
US-09-641-638-1195.
; Sequence 1195, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1195
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-8-39 : polymorphic base A or C
US-09-641-638-1195

Query Match      58.1%; Score 12.2; DB 4; Length 47;
Best Local Similarity 82.4%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db      7 AGTGCAGGCCAGATTGC 23

RESULT 31
US-10-170-097-1195
; Sequence 1195, Application US/10170097
; Patent No. 6794143
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1195
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-8-39 : polymorphic base A or C
US-10-170-097-1195

Query Match      58.1%; Score 12.2; DB 4; Length 47;
Best Local Similarity 73.7%; Pred. No. 3.2e+03;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      3 CGCATGCCAGATTACTGGC 21
Db      11 CCCAGGCCAGTTMCCGGC 29

RESULT 32
US-09-488-744A-71
; Sequence 71, Application US/09488744A
; Patent No. 6287860
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Donna T. Ward
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK2 EXPRESSION
; FILE REFERENCE: RTS-0108
; CURRENT APPLICATION NUMBER: US/09/488,744A
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,511
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jervis, Herbert H.
; REGISTRATION NUMBER: 31,171
; REFERENCE/DOCKET NUMBER: SBC P50349-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; US-08-776-511-6

Query Match          57.1%; Score 12; DB 3; Length 38;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 9 AGAGCAAGCCACATAGCTGG 28

RESULT 37
US-09-485-737B-29/c
; Sequence 29, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: GENOMIC
; US-09-485-737B-29

Query Match          57.1%; Score 12; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 9 AGAGCAAGCCACATAGCTGG 28

RESULT 38
US-09-485-737B-30
; Sequence 30, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 30
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: GENOMIC
; US-09-485-737B-30

Query Match          57.1%; Score 12; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 21 ACCGCTCGCCAGGTGTCTGG 40

RESULT 39
US-09-527-154-13/c
; Sequence 13, Application US/09527154
; Patent No. 6228648
; GENERAL INFORMATION:
; APPLICANT: Thomas P. Condon
; APPLICANT: Shin Cheng Fluoroy
; TITLE OF INVENTION: ANTISENSE MODULATION OF ADAM10 EXPRESSION
; FILE REFERENCE: ISPH-0446
; CURRENT APPLICATION NUMBER: US/09/527,154
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-527-154-13

Query Match          56.2%; Score 11.8; DB 3; Length 20;
Best Local Similarity 86.7%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACTGG 20
Db 20 ATACCAGATGACTGG 6

RESULT 40
US-08-553-501A-38/c
; Sequence 38, Application US/08553501A
; Patent No. 5856135
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; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553.501A
; FILING DATE: 20-FEB-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-553-501A-38

```

```

Query Match          56.2%; Score 11.8; DB 2; Length 39;
Best Local Similarity 86.7%; Pred. No. Se+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      24 CATGCTAAATTACTG 10

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Search completed: November 23, 2004, 22:25:58
Job time : 36.3034 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 98.4719 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21

Sequence: 1 agcgtgcccagattactggc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	15	US-10-419-022-1
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4	13.2	62.9	22	18	US-10-813-805-42
5	13.2	62.9	32	17	US-10-250-997-24
6	13.2	62.9	32	17	US-10-250-997-25
7	13.2	62.9	32	17	US-10-250-997-39
8	13.2	62.9	35	17	US-10-641-455A-117
9	13	61.9	18	14	US-10-197-290-29
10	13	61.9	18	15	US-10-388-263-182
11	13	61.9	20	17	US-10-317-278-17
12	13	61.9	20	17	US-10-317-278-51
13	13	61.9	20	17	US-10-317-278-51

32	18	61.9	13	13	US-10-851-894-15	Sequence 15, Appl
32	18	61.9	13	13	US-10-851-894-16	Sequence 16, Appl
37	10	61.9	13	13	US-09-930-423-2899	Sequence 2899, Ap
37	10	61.9	13	13	US-09-745-237A-2899	Sequence 2899, Ap
24	9	61.0	17	12.8	US-09-780-752-20	Sequence 20, Appl
24	10	61.0	18	12.8	US-09-940-185-787	Sequence 787, App
24	15	61.0	19	12.8	US-10-320-231A-8	Sequence 8, Appl
25	10	61.0	20	12.8	US-09-940-185-4752	Sequence 4752, Ap
20	16	60.0	21	12.6	US-10-289-762-3669	Sequence 3669, Ap
25	10	60.0	22	12.6	US-09-754-853A-418	Sequence 418, App
36	16	60.0	23	12.6	US-10-138-674-15043	Sequence 15043, A
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42	14	59.0	30	12.4	US-10-091-257-72	Sequence 72, Appl
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26	15	58.1	40	12.2	US-10-072-622-26	Sequence 26, Appl
27	15	58.1	41	12.2	US-10-072-622-25	Sequence 25, Appl
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32	17	58.1	43	12.2	US-10-250-997-45	Sequence 45, Appl
41	16	58.1	44	12.2	US-10-035-833A-1679	Sequence 1679, Ap
41	16	58.1	45	12.2	US-10-035-833A-7227	Sequence 7227, Ap
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25	14	57.1	55	12	US-10-060-756A-3209	Sequence 3209, Ap
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37	10	57.1	62	12	US-09-877-478-4135	Sequence 4135, Ap
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25	15	56.2	74	11.8	US-10-098-263B-103084	Sequence 103084,
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25	14	55.2	80	11.6	US-10-060-756A-3211	Sequence 3211, Ap
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31	15	55.2	83	11.6	US-10-401-343-32	Sequence 32, Appl
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C 89	11.6	55.2	37	16	US-09-877-478-4087	Sequence 4087, A	C 162	11.4	54.3	50	15	US-10-341-967-68	Sequence 68, Appl
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C 91	11.6	55.2	37	17	US-10-665-841-8978	Sequence 8978, A	C 164	11.2	53.3	18	9	US-09-969-373-3139	Sequence 3139, A
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C 94	11.6	55.2	46	9	US-09-759-143-611	Sequence 611, App	C 167	11.2	53.3	19	15	US-10-005-956-80	Sequence 80, Appl
C 95	11.6	55.2	46	9	US-09-759-143-615	Sequence 615, App	C 168	11.2	53.3	19	15	US-10-331-907-383	Sequence 383, App
C 96	11.6	55.2	46	9	US-09-780-669-611	Sequence 611, App	C 169	11.2	53.3	20	17	US-10-303-165-20	Sequence 20, Appl
C 97	11.6	55.2	46	9	US-09-780-669-611	Sequence 611, App	C 170	11.2	53.3	20	17	US-10-303-165-20	Sequence 20, Appl
C 98	11.6	55.2	46	9	US-09-822-827-611	Sequence 611, App	C 171	11.2	53.3	20	17	US-10-619-739-45	Sequence 45, Appl
C 99	11.6	55.2	46	9	US-09-822-827-615	Sequence 615, App	C 172	11.2	53.3	21	17	US-10-257-344A-8	Sequence 8, Appl
C 100	11.6	55.2	46	9	US-09-895-793-611	Sequence 611, App	C 173	11.2	53.3	23	9	US-09-753-143-48	Sequence 48, Appl
C 101	11.6	55.2	46	9	US-09-895-793-615	Sequence 615, App	C 174	11.2	53.3	23	15	US-10-401-194-72	Sequence 72, Appl
C 102	11.6	55.2	46	9	US-09-895-814-611	Sequence 611, App	C 175	11.2	53.3	24	10	US-09-940-185-349	Sequence 349, App
C 103	11.6	55.2	46	9	US-09-895-814-615	Sequence 615, App	C 176	11.2	53.3	24	10	US-09-940-185-349	Sequence 349, App
C 104	11.6	55.2	46	13	US-10-012-896-611	Sequence 611, App	C 177	11.2	53.3	25	10	US-09-940-185-349	Sequence 349, App
C 105	11.6	55.2	46	13	US-10-012-896-615	Sequence 615, App	C 178	11.2	53.3	25	14	US-10-215-112-4318	Sequence 4318, App
C 106	11.6	55.2	46	15	US-10-144-678A-611	Sequence 611, App	C 179	11.2	53.3	25	15	US-10-098-263B-5933	Sequence 5933, App
C 107	11.6	55.2	46	15	US-10-144-678A-615	Sequence 615, App	C 180	11.2	53.3	25	15	US-10-098-263B-5933	Sequence 5933, App
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C 115	11.4	54.3	17	15	US-10-339-884-11	Sequence 884, App	C 188	11.2	53.3	31	9	US-09-801-274-1627	Sequence 1627, App
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C 118	11.4	54.3	20	17	US-10-317-278-68	Sequence 68, Appl	C 191	11.2	53.3	34	9	US-09-086-118-19	Sequence 19, Appl
C 119	11.4	54.3	22	10	US-09-974-591-25	Sequence 25, Appl	C 192	11.2	53.3	34	9	US-09-769-864-49	Sequence 49, Appl
C 120	11.4	54.3	22	10	US-09-777-789-88	Sequence 88, Appl	C 193	11.2	53.3	34	16	US-10-387-806-19	Sequence 19, Appl
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C 129	11.4	54.3	33	10	US-09-996-954B-7	Sequence 7, Appl	C 202	11.2	53.3	41	15	US-10-005-956-269	Sequence 269, App
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c 437	11	52.4	50	10	US-09-978-585A-344	Sequence 344, Appl	510	11	52.4	50	15	US-10-013-923A-344	Sequence 344, App
c 438	11	52.4	50	10	US-09-978-191A-344	Sequence 344, Appl	511	11	52.4	50	15	US-10-013-925A-344	Sequence 344, App
c 439	11	52.4	50	10	US-09-978-403A-344	Sequence 344, Appl	512	11	52.4	50	15	US-10-013-927A-344	Sequence 344, App
c 440	11	52.4	50	10	US-09-978-564A-344	Sequence 344, Appl	513	11	52.4	50	16	US-10-145-093A-344	Sequence 344, App
c 441	11	52.4	50	10	US-09-999-833A-344	Sequence 344, Appl	514	11	52.4	50	16	US-10-013-919A-344	Sequence 344, App
c 442	11	52.4	50	10	US-09-981-915A-344	Sequence 344, Appl	515	11	52.4	50	16	US-10-013-920A-344	Sequence 344, App
c 443	11	52.4	50	10	US-09-978-824-344	Sequence 344, Appl	516	11	52.4	50	16	US-10-131-827-1648	Sequence 344, App
c 444	11	52.4	50	10	US-09-918-585A-344	Sequence 344, Appl	517	11	52.4	50	16	US-10-131-827-2778	Sequence 344, App
c 445	11	52.4	50	10	US-09-999-834A-344	Sequence 344, Appl	518	11	52.4	50	16	US-10-131-827-4215	Sequence 344, App
c 446	11	52.4	50	10	US-09-978-423A-344	Sequence 344, Appl	519	11	52.4	50	16	US-10-131-827-4390	Sequence 344, App
c 447	11	52.4	50	10	US-09-978-193A-344	Sequence 344, Appl	520	11	52.4	50	16	US-10-164-749A-344	Sequence 344, App
c 448	11	52.4	50	10	US-09-999-830A-344	Sequence 344, Appl	521	11	52.4	50	16	US-10-013-917A-344	Sequence 344, App
c 449	11	52.4	50	10	US-09-978-757A-344	Sequence 344, Appl	522	11	52.4	50	18	US-10-152-388B-344	Sequence 344, App
c 450	11	52.4	50	10	US-09-978-187B-344	Sequence 344, Appl	523	11	52.4	17	15	US-10-340-192-82	Sequence 82, Appl

c 524	10.8	51.4	20	14	US-10-005-338B-136	Sequence 136, App	597	10.6	50.5	17	17	US-10-287-949B-7740	Sequence 7740, App
c 525	10.8	51.4	20	14	US-10-005-338B-138	Sequence 138, App	598	10.6	50.5	17	18	US-10-712-633-823	Sequence 823, App
c 526	10.8	51.4	20	14	US-10-032-585-4860	Sequence 4860, App	599	10.6	50.5	17	18	US-10-712-633-8238	Sequence 8238, App
c 527	10.8	51.4	20	15	US-10-159-266-74	Sequence 147, Appl	600	10.6	50.5	18	9	US-09-969-373-2799	Sequence 2799, App
c 528	10.8	51.4	20	15	US-10-159-266-147	Sequence 147, App	601	10.6	50.5	18	17	US-10-182-952A-9	Sequence 9, Appli
c 529	10.8	51.4	20	16	US-10-139-674-41	Sequence 41, Appl	c 602	10.6	50.5	19	16	US-10-280-183A-414	Sequence 414, App
c 530	10.8	51.4	20	16	US-10-199-674-100	Sequence 100, App	603	10.6	50.5	19	17	US-10-665-951-2244	Sequence 2244, App
c 531	10.8	51.4	20	16	US-10-292-337-14	Sequence 14, Appl	604	10.6	50.5	19	17	US-10-665-951-2264	Sequence 2264, App
c 532	10.8	51.4	20	16	US-10-292-337-85	Sequence 85, Appl	605	10.6	50.5	19	17	US-10-665-951-2265	Sequence 2265, App
c 533	10.8	51.4	20	17	US-10-317-500-98	Sequence 98, Appl	c 606	10.6	50.5	20	9	US-09-454-394-70	Sequence 70, Appl
c 534	10.8	51.4	20	17	US-10-619-739-2008	Sequence 2008, App	607	10.6	50.5	20	9	US-09-454-394-71	Sequence 71, Appl
c 535	10.8	51.4	20	18	US-10-741-789A-65	Sequence 65, Appl	608	10.6	50.5	20	9	US-09-969-373-3127	Sequence 3127, App
c 536	10.8	51.4	21	15	US-10-002-623-518	Sequence 518, App	c 609	10.6	50.5	20	9	US-09-969-373-3128	Sequence 3128, App
c 537	10.8	51.4	21	15	US-10-184-085A-43	Sequence 43, Appl	610	10.6	50.5	20	10	US-09-770-107-20	Sequence 20, Appl
c 538	10.8	51.4	21	15	US-10-184-085A-635	Sequence 635, App	611	10.6	50.5	20	10	US-09-846-863-70	Sequence 70, Appl
c 539	10.8	51.4	23	10	US-09-945-943-1	Sequence 1, Appli	612	10.6	50.5	20	15	US-09-846-863-71	Sequence 71, Appl
c 540	10.8	51.4	24	13	US-10-027-632-52767	Sequence 52767, A	613	10.6	50.5	20	15	US-10-181-856-69	Sequence 69, Appl
c 541	10.8	51.4	24	15	US-10-027-632-52767	Sequence 52767, A	c 614	10.6	50.5	20	15	US-10-370-143-18	Sequence 18, Appl
c 542	10.8	51.4	25	10	US-09-754-853A-748	Sequence 748, App	c 615	10.6	50.5	20	16	US-10-452-510-116	Sequence 116, App
c 543	10.8	51.4	25	14	US-10-215-112-2106	Sequence 2106, App	c 616	10.6	50.5	20	16	US-10-617-334-116	Sequence 116, App
c 544	10.8	51.4	25	15	US-10-098-263B-47551	Sequence 47551, A	617	10.6	50.5	20	16	US-10-298-953-25	Sequence 25, Appl
c 545	10.8	51.4	25	15	US-10-098-263B-65678	Sequence 65678, A	618	10.6	50.5	20	16	US-10-298-953-59	Sequence 59, Appl
c 546	10.8	51.4	25	15	US-10-098-263B-81467	Sequence 81467, A	c 619	10.6	50.5	20	17	US-10-360-854-7	Sequence 7, Appli
c 547	10.8	51.4	25	15	US-10-098-263B-85311	Sequence 85311, A	c 620	10.6	50.5	20	17	US-10-744-465-116	Sequence 116, App
c 548	10.8	51.4	25	15	US-10-098-263B-85312	Sequence 85312, A	c 621	10.6	50.5	20	17	US-10-833-679-116	Sequence 116, App
c 549	10.8	51.4	25	15	US-10-098-263B-96895	Sequence 96895, A	c 622	10.6	50.5	20	18	US-10-659-473-72	Sequence 72, Appl
c 550	10.8	51.4	25	15	US-10-098-263B-105618	Sequence 105618, A	623	10.6	50.5	21	8	US-08-987-689A-11	Sequence 11, Appl
c 551	10.8	51.4	25	15	US-10-098-263B-112284	Sequence 112284, A	624	10.6	50.5	21	8	US-08-987-689A-23	Sequence 23, Appl
c 552	10.8	51.4	25	15	US-10-168-771-7	Sequence 7, Appli	625	10.6	50.5	21	15	US-10-292-524-11	Sequence 11, Appl
c 553	10.8	51.4	25	16	US-10-188-186-290	Sequence 290, App	626	10.6	50.5	21	15	US-10-292-524-23	Sequence 23, Appl
c 554	10.8	51.4	25	17	US-10-775-169-827	Sequence 827, App	c 627	10.6	50.5	21	15	US-10-072-622-23	Sequence 23, Appl
c 555	10.8	51.4	26	9	US-09-893-238-74	Sequence 74, Appl	628	10.6	50.5	21	15	US-10-072-622-24	Sequence 24, Appl
c 556	10.8	51.4	26	9	US-09-893-238-74	Sequence 74, Appl	629	10.6	50.5	21	15	US-10-214-670-27	Sequence 27, Appl
c 557	10.8	51.4	27	16	US-10-161-493-271	Sequence 271, App	630	10.6	50.5	21	16	US-10-464-805-11	Sequence 11, Appl
c 558	10.8	51.4	28	9	US-09-971-309-90	Sequence 90, Appl	631	10.6	50.5	21	16	US-10-464-805-23	Sequence 23, Appl
c 559	10.8	51.4	28	15	US-10-435-633-9	Sequence 9, Appli	632	10.6	50.5	21	16	US-10-420-194-427	Sequence 427, App
c 560	10.8	51.4	28	15	US-10-434-837-8	Sequence 8, Appli	633	10.6	50.5	21	16	US-10-420-194-430	Sequence 430, App
c 561	10.8	51.4	28	16	US-10-188-186-308	Sequence 308, App	c 634	10.6	50.5	21	16	US-10-420-194-937	Sequence 937, App
c 562	10.8	51.4	29	10	US-09-374-046A-228	Sequence 228, App	c 635	10.6	50.5	21	16	US-10-420-194-940	Sequence 940, App
c 563	10.8	51.4	29	16	US-10-616-263-228	Sequence 228, App	c 636	10.6	50.5	21	17	US-10-665-951-2275	Sequence 2275, App
c 564	10.8	51.4	30	17	US-10-644-355A-102	Sequence 102, App	c 637	10.6	50.5	21	17	US-10-665-951-2278	Sequence 2278, App
c 565	10.8	51.4	31	9	US-09-746-284-51	Sequence 51, Appl	c 638	10.6	50.5	21	17	US-10-665-951-2373	Sequence 2373, App
c 566	10.8	51.4	32	10	US-09-851-486-129	Sequence 129, App	639	10.6	50.5	21	17	US-10-665-951-2374	Sequence 2374, App
c 567	10.8	51.4	32	15	US-10-339-674-1210	Sequence 1210, App	c 640	10.6	50.5	21	17	US-10-665-951-2385	Sequence 2385, App
c 568	10.8	51.4	33	10	US-09-826-509-112	Sequence 112, App	c 641	10.6	50.5	21	17	US-10-665-951-2386	Sequence 2386, App
c 569	10.8	51.4	35	9	US-09-766-095-38	Sequence 38, Appl	642	10.6	50.5	21	17	US-10-728-491-17	Sequence 17, Appl
c 570	10.8	51.4	35	9	US-09-766-095-118	Sequence 118, App	c 643	10.6	50.5	21	18	US-10-786-720-1231	Sequence 1231, App
c 571	10.8	51.4	36	14	US-09-897-778-444	Sequence 444, App	c 644	10.6	50.5	21	18	US-10-786-720-1232	Sequence 1232, App
c 572	10.8	51.4	36	14	US-10-007-700-444	Sequence 444, App	645	10.6	50.5	21	18	US-10-786-720-1233	Sequence 1233, App
c 573	10.8	51.4	36	15	US-10-117-982-444	Sequence 444, App	646	10.6	50.5	21	18	US-10-786-720-13186	Sequence 13186, A
c 574	10.8	51.4	36	15	US-10-313-986-444	Sequence 444, App	c 647	10.6	50.5	21	18	US-10-786-720-13188	Sequence 13188, A
c 575	10.8	51.4	38	9	US-09-823-829-62	Sequence 62, Appl	648	10.6	50.5	21	18	US-10-786-720-13300	Sequence 13300, A
c 576	10.8	51.4	38	9	US-09-823-829-62	Sequence 62, Appl	c 649	10.6	50.5	21	18	US-10-786-720-13302	Sequence 13302, A
c 577	10.8	51.4	38	10	US-09-839-575-42	Sequence 42, Appl	c 650	10.6	50.5	22	16	US-10-114-270-369	Sequence 369, App
c 578	10.8	51.4	38	11	US-10-164-433-8	Sequence 8, Appli	c 651	10.6	50.5	22	16	US-10-262-511-420	Sequence 420, App
c 579	10.8	51.4	39	11	US-09-923-917-6	Sequence 6, Appli	c 652	10.6	50.5	22	16	US-10-287-226-459	Sequence 459, App
c 580	10.8	51.4	41	9	US-09-892-864A-6	Sequence 6, Appli	653	10.6	50.5	23	16	US-10-420-194-1046	Sequence 1046, App
c 581	10.8	51.4	41	9	US-09-896-561-7	Sequence 7, Appli	654	10.6	50.5	23	16	US-10-420-194-1155	Sequence 1155, App
c 582	10.8	51.4	41	9	US-09-884-948-7	Sequence 7, Appli	c 655	10.6	50.5	23	16	US-10-420-194-1158	Sequence 1158, App
c 583	10.8	51.4	41	14	US-10-092-750-149	Sequence 149, App	c 656	10.6	50.5	23	16	US-09-940-185-375	Sequence 375, App
c 584	10.8	51.4	41	16	US-10-035-833A-1534	Sequence 1534, App	c 657	10.6	50.5	24	10	US-09-940-185-375	Sequence 375, App
c 585	10.8	51.4	41	16	US-10-035-833A-4031	Sequence 4031, App	c 658	10.6	50.5	24	16	US-10-401-077-3	Sequence 3, Appli
c 586	10.8	51.4	42	11	US-09-923-917-7	Sequence 7, Appli	c 659	10.6	50.5	25	9	US-09-893-238-36	Sequence 26, Appli
c 587	10.8	51.4	42	15	US-10-040-206A-4	Sequence 4, Appli	660	10.6	50.5	25	10	US-09-754-853A-410	Sequence 410, App
c 588	10.8	51.4	42	15	US-10-243-509-4	Sequence 4, Appli	c 661	10.6	50.5	25	10	US-09-940-185-4350	Sequence 4350, App
c 589	10.8	51.4	47	16	US-10-349-143-323	Sequence 323, App	c 662	10.6	50.5	25	14	US-10-060-756A-3212	Sequence 3212, App
c 590	10.8	51.4	47	16	US-10-349-143-2538	Sequence 2538, App	c 663	10.6	50.5	25	15	US-10-098-263B-34248	Sequence 34248, A
c 591	10.8	51.4	47	16	US-10-349-143-3718	Sequence 3718, App	664	10.6	50.5	25	15	US-10-098-263B-51667	Sequence 51667, A
c 592	10.8	51.4	50	16	US-10-131-827-1182	Sequence 1182, App	665	10.6	50.5	25	15	US-10-098-263B-77507	Sequence 77507, A
c 593	10.8	51.4	50	16	US-10-131-827-3481	Sequence 3481, App	c 666	10.6	50.5	25	15	US-10-098-263B-115942	Sequence 115942, A
c 594	10.6	50.5	17	14	US-10-060-756A-1206	Sequence 1206, App	c 667	10.6	50.5	25	15	US-10-098-263B-119515	Sequence 119515, A
c 595	10.6	50.5	17	14	US-10-060-756A-1207	Sequence 1207, App	c 668	10.6	50.5	25	15	US-10-098-263B-130624	Sequence 130624, A
c 596	10.6	50.5	17	16	US-10-138-674A-7740	Sequence 7740, App	c 669	10.6	50.5	25	17	US-10-717-597-762	Sequence 762, App

670	10.6	50.5	26	10	US-09-981-151A-118	Sequence 118, App	743	10.6	50.5	41	9	US-09-828-359A-12	Sequence 12, Appl
671	10.6	50.5	26	10	US-09-981-151A-130	Sequence 130, App	744	10.6	50.5	41	9	US-09-784-818-11	Sequence 11, Appl
c 672	10.6	50.5	26	15	US-10-090-182A-57	Sequence 57, Appl	745	10.6	50.5	41	10	US-09-756-248-11	Sequence 11, Appl
c 673	10.6	50.5	26	15	US-10-078-113-57	Sequence 57, Appl	746	10.6	50.5	41	11	US-09-828-317A-12	Sequence 12, Appl
c 674	10.6	50.5	27	15	US-10-084-839-2961	Sequence 2961, App	747	10.6	50.5	41	15	US-10-244-215-77	Sequence 77, Appl
c 675	10.6	50.5	28	10	US-09-905-253A-20	Sequence 20, Appl	748	10.6	50.5	41	16	US-10-035-833A-1817	Sequence 1817, App
c 676	10.6	50.5	28	10	US-09-905-253A-28	Sequence 28, Appl	c 749	10.6	50.5	41	16	US-10-035-833A-1915	Sequence 1915, App
c 677	10.6	50.5	28	10	US-09-817-748-6	Sequence 6, Appl	c 750	10.6	50.5	41	16	US-10-035-833A-4510	Sequence 4510, App
c 678	10.6	50.5	28	15	US-10-201-187-20	Sequence 20, Appl	751	10.6	50.5	41	16	US-10-035-833A-5919	Sequence 5919, App
c 679	10.6	50.5	28	15	US-10-201-187-28	Sequence 28, Appl	752	10.6	50.5	44	11	US-09-765-534B-20	Sequence 20, Appl
c 680	10.6	50.5	28	16	US-10-603-566-23	Sequence 23, Appl	753	10.6	50.5	44	18	US-10-774-802-20	Sequence 20, Appl
c 681	10.6	50.5	28	16	US-10-603-566-31	Sequence 31, Appl	c 754	10.6	50.5	44	18	US-10-349-143-3505	Sequence 3505, App
c 682	10.6	50.5	29	15	US-10-284-084-51	Sequence 51, Appl	c 755	10.6	50.5	48	10	US-09-860-840-5	Sequence 5, Appl
c 683	10.6	50.5	29	17	US-10-469-125-38	Sequence 38, Appl	756	10.6	50.5	48	16	US-10-371-771-30	Sequence 30, Appl
c 684	10.6	50.5	30	17	US-10-469-125-37	Sequence 37, Appl	c 757	10.6	50.5	48	16	US-10-444-683-5	Sequence 5, Appl
c 685	10.6	50.5	30	18	US-10-419-020-165	Sequence 165, App	c 758	10.6	50.5	48	16	US-10-332-340-12	Sequence 12, Appl
c 686	10.6	50.5	30	18	US-10-419-020-166	Sequence 166, App	c 759	10.6	50.5	50	9	US-09-179-536B-302	Sequence 302, Appl
c 687	10.6	50.5	31	9	US-09-801-274-1453	Sequence 1453, App	c 760	10.6	50.5	50	10	US-09-897-623-21	Sequence 21, Appl
c 688	10.6	50.5	31	9	US-09-974-300-4394	Sequence 4394, App	761	10.6	50.5	50	10	US-09-897-623-22	Sequence 22, Appl
c 689	10.6	50.5	31	16	US-10-193-377-8	Sequence 8, Appl	c 762	10.6	50.5	50	10	US-09-978-917A-21	Sequence 21, Appl
c 690	10.6	50.5	32	9	US-09-943-388-30	Sequence 30, Appl	763	10.6	50.5	50	10	US-09-978-917A-22	Sequence 22, Appl
c 691	10.6	50.5	32	9	US-09-943-388-44	Sequence 44, Appl	c 764	10.6	50.5	50	10	US-09-297-576A-302	Sequence 302, App
c 692	10.6	50.5	32	16	US-10-433-836-7	Sequence 7, Appl	c 765	10.6	50.5	50	16	US-10-131-827-1715	Sequence 1715, App
c 693	10.6	50.5	32	17	US-10-772-656-62	Sequence 62, Appl	c 766	10.6	50.5	50	16	US-10-131-827-1987	Sequence 1987, App
c 694	10.6	50.5	35	9	US-09-823-829-38	Sequence 38, Appl	c 767	10.6	50.5	50	16	US-10-131-827-2069	Sequence 2069, App
c 695	10.6	50.5	35	9	US-09-976-414-5	Sequence 5, Appl	c 768	10.6	50.5	50	16	US-10-131-827-2333	Sequence 2333, App
c 696	10.6	50.5	35	9	US-09-823-823-38	Sequence 38, Appl	c 769	10.6	50.5	50	16	US-10-131-827-2408	Sequence 2408, App
c 697	10.6	50.5	35	10	US-09-736-116-65	Sequence 65, Appl	770	10.6	50.5	50	16	US-10-131-827-2987	Sequence 2987, App
c 698	10.6	50.5	35	10	US-09-736-116-94	Sequence 94, Appl	771	10.6	50.5	50	16	US-10-131-827-4546	Sequence 4546, App
c 699	10.6	50.5	36	9	US-09-004-068-7	Sequence 7, Appl	772	10.6	50.5	50	16	US-10-131-827-4547	Sequence 4547, App
c 700	10.6	50.5	36	16	US-10-138-674-15020	Sequence 15020, A	773	10.6	50.5	50	16	US-10-131-827-5318	Sequence 5318, App
c 701	10.6	50.5	36	16	US-10-138-674-15217	Sequence 15217, A	c 774	10.6	50.5	50	16	US-10-131-827-1569	Sequence 1569, App
c 702	10.6	50.5	36	16	US-10-138-674-15386	Sequence 15386, A	c 775	10.4	49.5	16	17	US-10-712-672-1570	Sequence 1570, App
c 703	10.6	50.5	36	17	US-10-287-949A-15020	Sequence 15020, A	c 776	10.4	49.5	17	10	US-09-740-332-1889	Sequence 1889, App
c 704	10.6	50.5	36	17	US-10-287-949A-15217	Sequence 15217, A	777	10.4	49.5	17	10	US-09-740-332-1890	Sequence 1890, App
c 705	10.6	50.5	36	17	US-10-287-949A-15386	Sequence 15386, A	c 778	10.4	49.5	17	10	US-09-740-332-2665	Sequence 2665, App
c 706	10.6	50.5	36	17	US-10-712-672-4317	Sequence 4317, App	c 779	10.4	49.5	17	10	US-09-740-332-2666	Sequence 2666, App
c 707	10.6	50.5	36	17	US-10-712-672-4355	Sequence 4355, App	780	10.4	49.5	17	10	US-09-817-879-1889	Sequence 1889, App
c 708	10.6	50.5	36	17	US-10-712-672-4419	Sequence 4419, App	c 781	10.4	49.5	17	10	US-09-817-879-1890	Sequence 1890, App
c 709	10.6	50.5	36	17	US-10-712-672-4602	Sequence 4602, App	c 782	10.4	49.5	17	10	US-09-817-879-2665	Sequence 2665, App
c 710	10.6	50.5	36	18	US-10-728-766-7	Sequence 7, Appl	c 783	10.4	49.5	17	10	US-09-817-879-2666	Sequence 2666, App
c 711	10.6	50.5	37	10	US-09-927-046-3589	Sequence 3589, App	784	10.4	49.5	17	15	US-10-338-777-286	Sequence 286, App
c 712	10.6	50.5	37	10	US-09-927-046-3600	Sequence 3600, App	785	10.4	49.5	17	15	US-10-338-777-286	Sequence 286, App
c 713	10.6	50.5	37	10	US-09-877-478-4104	Sequence 4104, App	786	10.4	49.5	17	16	US-10-138-674-2271	Sequence 2271, App
c 714	10.6	50.5	37	10	US-09-877-478-4109	Sequence 4109, App	787	10.4	49.5	17	16	US-10-287-949A-2270	Sequence 2270, App
c 715	10.6	50.5	37	10	US-09-877-478-4113	Sequence 4113, App	788	10.4	49.5	17	17	US-10-287-949A-2271	Sequence 2271, App
c 716	10.6	50.5	37	10	US-09-930-423-2895	Sequence 2895, App	c 789	10.4	49.5	17	17	US-10-712-672-620	Sequence 620, App
c 717	10.6	50.5	37	10	US-09-930-423-2913	Sequence 2913, App	c 790	10.4	49.5	17	17	US-10-669-841-4482	Sequence 4482, App
c 718	10.6	50.5	37	10	US-09-745-237A-2895	Sequence 2895, App	791	10.4	49.5	17	17	US-10-669-841-4483	Sequence 4483, App
c 719	10.6	50.5	37	10	US-09-745-237A-2913	Sequence 2913, App	c 792	10.4	49.5	17	17	US-10-669-841-5258	Sequence 5258, App
c 720	10.6	50.5	37	15	US-10-408-878-17	Sequence 17, Appl	c 793	10.4	49.5	17	17	US-10-669-841-5259	Sequence 5259, App
c 721	10.6	50.5	37	16	US-10-342-902-4104	Sequence 4104, App	794	10.4	49.5	18	14	US-10-174-654-14	Sequence 14, Appl
c 722	10.6	50.5	37	16	US-10-342-902-4109	Sequence 4109, App	795	10.4	49.5	18	16	US-10-138-674-2977	Sequence 2977, App
c 723	10.6	50.5	37	16	US-10-342-902-4113	Sequence 4113, App	796	10.4	49.5	18	17	US-10-138-674-2977	Sequence 2977, App
c 724	10.6	50.5	37	17	US-10-669-841-8995	Sequence 8995, App	c 797	10.4	49.5	19	10	US-09-880-313A-253	Sequence 253, App
c 725	10.6	50.5	37	17	US-10-669-841-9000	Sequence 9000, App	c 798	10.4	49.5	19	13	US-10-076-900-39	Sequence 39, Appl
c 726	10.6	50.5	37	17	US-10-669-841-9004	Sequence 9004, App	799	10.4	49.5	19	16	US-10-349-143-9097	Sequence 9097, App
c 727	10.6	50.5	37	18	US-10-685-838-5	Sequence 5, Appl	800	10.4	49.5	20	9	US-09-805-293-4	Sequence 4, Appl
c 728	10.6	50.5	38	14	US-10-112-802-68	Sequence 68, Appl	801	10.4	49.5	20	9	US-09-795-668-89	Sequence 89, Appl
c 729	10.6	50.5	38	14	US-10-112-802-69	Sequence 69, Appl	802	10.4	49.5	20	9	US-09-795-668-89	Sequence 89, Appl
c 730	10.6	50.5	40	15	US-10-131-841-174	Sequence 174, App	803	10.4	49.5	20	9	US-09-946-807-89	Sequence 89, Appl
c 731	10.6	50.5	40	15	US-10-131-841-187	Sequence 187, App	804	10.4	49.5	20	10	US-09-040-736-46	Sequence 46, Appl
c 732	10.6	50.5	40	18	US-10-469-851-174	Sequence 174, App	805	10.4	49.5	20	14	US-10-165-060-9	Sequence 9, Appl
c 733	10.6	50.5	40	18	US-10-469-851-177	Sequence 177, App	806	10.4	49.5	20	14	US-10-271-887-171	Sequence 171, App
c 734	10.6	50.5	41	9	US-09-770-967-11	Sequence 11, Appl	c 807	10.4	49.5	20	15	US-10-165-968-9	Sequence 9, Appl
c 735	10.6	50.5	41	9	US-09-858-369-11	Sequence 11, Appl	808	10.4	49.5	20	15	US-10-003-354-21	Sequence 21, Appl
c 736	10.6	50.5	41	9	US-09-819-522-11	Sequence 11, Appl	809	10.4	49.5	20	15	US-10-318-905-4	Sequence 4, Appl
c 737	10.6	50.5	41	9	US-09-828-061A-12	Sequence 12, Appl	810	10.4	49.5	20	15	US-10-240-689-25	Sequence 25, Appl
c 738	10.6	50.5	41	9	US-09-757-251-12	Sequence 12, Appl	c 811	10.4	49.5	20	15	US-10-148-355A-46	Sequence 46, Appl
c 739	10.6	50.5	41	9	US-09-784-897A-11	Sequence 11, Appl	812	10.4	49.5	20	15	US-10-167-034-66	Sequence 66, Appl
c 740	10.6	50.5	41	9	US-09-770-983-11	Sequence 11, Appl	c 813	10.4	49.5	20	15	US-10-167-034-130	Sequence 130, App
c 741	10.6	50.5	41	9	US-09-828-325A-12	Sequence 12, Appl	814	10.4	49.5	20	16	US-10-349-143-11045	Sequence 11045, A
c 742	10.6	50.5	41	9	US-09-757-217A-12	Sequence 12, Appl	c 815	10.4	49.5	20	16	US-10-452-510-147	Sequence 147, App

C 816	10.4	49.5	20	16	US-10-617-334-147	Sequence 147, App	C 889	10.4	49.5	30	10	US-09-854-867-595	Sequence 595, App
C 817	10.4	49.5	20	16	US-10-371-701-46	Sequence 46, Appl	C 890	10.4	49.5	30	15	US-10-215-062-20	Sequence 20, Appl
C 818	10.4	49.5	20	17	US-10-317-280-75	Sequence 75, Appl	C 891	10.4	49.5	30	15	US-10-310-734-58	Sequence 58, Appl
C 819	10.4	49.5	20	17	US-10-317-280-147	Sequence 147, App	C 892	10.4	49.5	30	16	US-10-471-171-1	Sequence 1, Appl
C 820	10.4	49.5	20	17	US-10-317-278-35	Sequence 35, Appl	C 893	10.4	49.5	30	17	US-10-416-621-49	Sequence 49, Appl
C 821	10.4	49.5	20	17	US-10-317-278-65	Sequence 65, Appl	C 894	10.4	49.5	31	9	US-09-801-274-373	Sequence 373, App
C 822	10.4	49.5	20	17	US-10-728-491-4	Sequence 4, Appl	C 895	10.4	49.5	31	9	US-09-801-274-1125	Sequence 1125, App
C 823	10.4	49.5	20	17	US-10-744-465-147	Sequence 147, App	C 896	10.4	49.5	31	9	US-09-801-274-1299	Sequence 1299, App
C 824	10.4	49.5	20	17	US-10-833-679-147	Sequence 147, App	C 897	10.4	49.5	31	10	US-09-912-263-297	Sequence 297, App
C 825	10.4	49.5	21	9	US-09-975-408-3	Sequence 3, Appl	C 898	10.4	49.5	31	15	US-10-163-552-1466	Sequence 1466, App
C 826	10.4	49.5	21	10	US-09-952-267-66	Sequence 66, Appl	C 899	10.4	49.5	31	16	US-10-395-741B-67	Sequence 67, Appl
C 827	10.4	49.5	21	10	US-09-996-008B-18	Sequence 18, Appl	C 900	10.4	49.5	31	18	US-10-807-837-24	Sequence 24, Appl
C 828	10.4	49.5	21	13	US-10-075-579-3	Sequence 3, Appl	C 901	10.4	49.5	32	14	US-10-221-841-3	Sequence 3, Appl
C 829	10.4	49.5	21	16	US-10-349-143-11666	Sequence 11666, A	C 902	10.4	49.5	32	17	US-10-220-481-175	Sequence 175, App
C 830	10.4	49.5	21	16	US-10-287-971-291	Sequence 291, App	C 903	10.4	49.5	32	17	US-10-220-481-404	Sequence 404, App
C 831	10.4	49.5	22	9	US-09-798-584-11	Sequence 11, Appl	C 904	10.4	49.5	33	17	US-10-467-479-5	Sequence 5, Appl
C 832	10.4	49.5	22	15	US-10-209-372-21	Sequence 21, Appl	C 905	10.4	49.5	33	14	US-10-121-857-75	Sequence 75, Appl
C 833	10.4	49.5	22	15	US-10-005-041A-172	Sequence 172, App	C 906	10.4	49.5	33	15	US-10-208-018-75	Sequence 75, Appl
C 834	10.4	49.5	22	15	US-10-024-212-233	Sequence 233, App	C 907	10.4	49.5	33	15	US-10-336-566-76	Sequence 76, Appl
C 835	10.4	49.5	22	17	US-10-333-068-142	Sequence 142, App	C 908	10.4	49.5	33	15	US-10-336-566-77	Sequence 77, Appl
C 836	10.4	49.5	23	9	US-09-784-423-47	Sequence 47, Appl	C 909	10.4	49.5	33	15	US-10-363-427-25	Sequence 25, Appl
C 837	10.4	49.5	23	17	US-10-465-498-124	Sequence 124, App	C 910	10.4	49.5	33	17	US-10-338-552-14	Sequence 14, Appl
C 838	10.4	49.5	24	9	US-09-815-585-21	Sequence 21, Appl	C 911	10.4	49.5	33	17	US-10-338-627-14	Sequence 14, Appl
C 839	10.4	49.5	24	10	US-09-940-185-221	Sequence 221, App	C 912	10.4	49.5	33	17	US-10-772-227-81	Sequence 81, Appl
C 840	10.4	49.5	24	10	US-09-940-185-507	Sequence 507, App	C 913	10.4	49.5	34	9	US-09-978-758-14	Sequence 14, Appl
C 841	10.4	49.5	24	10	US-09-940-185-2507	Sequence 2507, App	C 914	10.4	49.5	34	16	US-10-001-052-50	Sequence 50, Appl
C 842	10.4	49.5	24	10	US-09-841-994-39	Sequence 39, Appl	C 915	10.4	49.5	34	17	US-10-766-421-14	Sequence 14, Appl
C 843	10.4	49.5	24	15	US-10-322-138-68	Sequence 68, Appl	C 916	10.4	49.5	35	16	US-10-420-194-648	Sequence 648, App
C 844	10.4	49.5	24	15	US-10-317-832-154	Sequence 154, App	C 917	10.4	49.5	35	17	US-10-751-928-12	Sequence 12, Appl
C 845	10.4	49.5	24	16	US-10-336-603A-117	Sequence 117, App	C 918	10.4	49.5	36	9	US-09-010-733-23	Sequence 23, Appl
C 846	10.4	49.5	24	18	US-08-469-172-10	Sequence 10, Appl	C 919	10.4	49.5	36	9	US-09-996-634-164	Sequence 164, App
C 847	10.4	49.5	25	10	US-09-940-185-4202	Sequence 4202, App	C 920	10.4	49.5	36	10	US-09-997-182-164	Sequence 164, App
C 848	10.4	49.5	25	10	US-09-940-185-4477	Sequence 4477, App	C 921	10.4	49.5	36	10	US-09-997-181-164	Sequence 164, App
C 849	10.4	49.5	25	14	US-10-060-756A-2785	Sequence 2785, App	C 922	10.4	49.5	36	15	US-10-045-674-617	Sequence 617, App
C 850	10.4	49.5	25	14	US-10-060-756A-2786	Sequence 2786, App	C 923	10.4	49.5	37	10	US-09-730-289B-2772	Sequence 2772, App
C 851	10.4	49.5	25	14	US-10-060-756A-2787	Sequence 2787, App	C 924	10.4	49.5	37	10	US-09-780-533A-4319	Sequence 4319, App
C 852	10.4	49.5	25	14	US-10-060-756A-2788	Sequence 2788, App	C 925	10.4	49.5	37	10	US-09-927-046-3466	Sequence 3466, App
C 853	10.4	49.5	25	14	US-10-060-756A-2789	Sequence 2789, App	C 926	10.4	49.5	37	10	US-09-927-046-3614	Sequence 3614, App
C 854	10.4	49.5	25	14	US-10-060-756A-2790	Sequence 2790, App	C 927	10.4	49.5	37	10	US-09-927-046-3617	Sequence 3617, App
C 855	10.4	49.5	25	15	US-10-060-756A-2791	Sequence 2791, App	C 928	10.4	49.5	37	10	US-09-877-478-4112	Sequence 4112, App
C 856	10.4	49.5	25	15	US-10-098-263B-2476	Sequence 2476, App	C 929	10.4	49.5	37	10	US-09-877-478-4144	Sequence 4144, App
C 857	10.4	49.5	25	15	US-10-098-263B-10614	Sequence 10614, A	C 930	10.4	49.5	37	10	US-09-877-478-4146	Sequence 4146, App
C 858	10.4	49.5	25	15	US-10-098-263B-26683	Sequence 26683, A	C 931	10.4	49.5	37	10	US-09-877-478-4151	Sequence 4151, App
C 859	10.4	49.5	25	15	US-10-098-263B-35494	Sequence 35494, A	C 932	10.4	49.5	37	10	US-09-776-474-1952	Sequence 1952, App
C 860	10.4	49.5	25	15	US-10-098-263B-56690	Sequence 56690, A	C 933	10.4	49.5	37	10	US-09-930-423-2740	Sequence 2740, App
C 861	10.4	49.5	25	15	US-10-098-263B-87196	Sequence 87196, A	C 934	10.4	49.5	37	10	US-09-930-423-2796	Sequence 2796, App
C 862	10.4	49.5	25	15	US-10-098-263B-114687	Sequence 114687, A	C 935	10.4	49.5	37	10	US-09-930-423-2802	Sequence 2802, App
C 863	10.4	49.5	25	15	US-10-098-263B-114688	Sequence 114688, A	C 936	10.4	49.5	37	10	US-09-930-423-2885	Sequence 2885, App
C 864	10.4	49.5	25	15	US-10-098-263B-126636	Sequence 126636, A	C 937	10.4	49.5	37	10	US-09-930-423-2896	Sequence 2896, App
C 865	10.4	49.5	25	15	US-10-098-263B-129144	Sequence 129144, A	C 938	10.4	49.5	37	10	US-09-930-423-2902	Sequence 2902, App
C 866	10.4	49.5	25	15	US-10-231-115-18	Sequence 18, Appl	C 939	10.4	49.5	37	10	US-09-780-164-1790	Sequence 1790, App
C 867	10.4	49.5	25	15	US-10-331-285-21	Sequence 21, Appl	C 940	10.4	49.5	37	10	US-09-792-818-1423	Sequence 1423, App
C 868	10.4	49.5	25	17	US-10-717-597-2160	Sequence 10, Appl	C 941	10.4	49.5	37	10	US-09-792-818-1447	Sequence 1447, App
C 869	10.4	49.5	25	17	US-10-788-779-10	Sequence 10, Appl	C 942	10.4	49.5	37	10	US-09-745-237A-2740	Sequence 2740, App
C 870	10.4	49.5	25	17	US-10-716-029-80	Sequence 80, Appl	C 943	10.4	49.5	37	10	US-09-745-237A-2796	Sequence 2796, App
C 871	10.4	49.5	25	17	US-10-716-029-95	Sequence 95, Appl	C 944	10.4	49.5	37	10	US-09-745-237A-2802	Sequence 2802, App
C 872	10.4	49.5	25	17	US-10-775-169-3937	Sequence 3937, App	C 945	10.4	49.5	37	10	US-09-745-237A-2885	Sequence 2885, App
C 873	10.4	49.5	26	9	US-09-985-694A-3	Sequence 3, Appl	C 946	10.4	49.5	37	10	US-09-745-237A-2896	Sequence 2896, App
C 874	10.4	49.5	26	13	US-10-176-079-3	Sequence 3, Appl	C 947	10.4	49.5	37	10	US-09-745-237A-2902	Sequence 2902, App
C 875	10.4	49.5	26	13	US-10-281-673-28	Sequence 28, Appl	C 948	10.4	49.5	37	16	US-10-342-902-4112	Sequence 4112, App
C 876	10.4	49.5	26	15	US-10-232-544-2	Sequence 2, Appl	C 949	10.4	49.5	37	16	US-10-342-902-4144	Sequence 4144, App
C 877	10.4	49.5	26	15	US-10-232-544-137	Sequence 137, App	C 950	10.4	49.5	37	16	US-10-342-902-4146	Sequence 4146, App
C 878	10.4	49.5	26	16	US-10-600-389-18	Sequence 18, Appl	C 951	10.4	49.5	37	16	US-10-342-902-4151	Sequence 4151, App
C 879	10.4	49.5	27	15	US-10-076-047A-73	Sequence 73, Appl	C 952	10.4	49.5	37	17	US-10-669-841-9003	Sequence 9003, App
C 880	10.4	49.5	27	15	US-10-182-033-7	Sequence 7, Appl	C 953	10.4	49.5	37	17	US-10-669-841-9035	Sequence 9035, App
C 881	10.4	49.5	28	9	US-09-764-619-6	Sequence 6, Appl	C 954	10.4	49.5	37	17	US-10-669-841-9037	Sequence 9037, App
C 882	10.4	49.5	28	13	US-10-038-001-9	Sequence 9, Appl	C 955	10.4	49.5	37	17	US-10-669-841-9042	Sequence 9042, App
C 883	10.4	49.5	28	14	US-10-174-654-12	Sequence 12, Appl	C 956	10.4	49.5	38	15	US-10-408-878-13	Sequence 13, Appl
C 884	10.4	49.5	28	17	US-10-220-481-245	Sequence 245, App	C 957	10.4	49.5	38	15	US-10-149-736-49	Sequence 49, Appl
C 885	10.4	49.5	28	17	US-10-220-481-270	Sequence 270, App	C 958	10.4	49.5	38	15	US-10-149-736-50	Sequence 50, Appl
C 886	10.4	49.5	29	10	US-09-746-783-199	Sequence 199, App	C 959	10.4	49.5	39	13	US-10-027-075-16	Sequence 16, Appl
C 887	10.4	49.5	29	15	US-10-258-073-15	Sequence 15, Appl	C 960	10.4	49.5	39	13	US-10-027-075-17	Sequence 17, Appl
C 888	10.4	49.5	30	9	US-09-953-052-30	Sequence 30, Appl	C 961	10.4	49.5	39	15	US-10-134-645-6	Sequence 6, Appl

; Publication No. US20040191902A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER INC.
; APPLICANT: Hambor, John E.
; APPLICANT: Roach, Marsha L.
; TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF STEM CELLS
; FILE REFERENCE: PC25028A
; CURRENT APPLICATION NUMBER: US/10/813,805
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US 60/459,449
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-813-805-42

Query Match 62.9%; Score 13.2; DB 18; Length 22;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGATGCCAGATTACTG 19
| ||||| |||||
Db 21 GAGCATGCCAAATTAGTG 4

RESULT 5
US-10-250-997-24/c
; Sequence 24, Application US/10250997
; Publication No. US20040110251A1
; GENERAL INFORMATION:
; APPLICANT: Grabowski et al.
; TITLE OF INVENTION: DETECTION OF PATHOGENIC BACTERIA
; FILE REFERENCE: 223374
; CURRENT APPLICATION NUMBER: US/10/250,997
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/11901
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: DE 10100493.1
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 24
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-250-997-24

Query Match 62.9%; Score 13.2; DB 17; Length 32;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21
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Db 26 GAATGTCAGATAACTGGC 9

RESULT 6
US-10-250-997-25/c
; Sequence 25, Application US/10250997
; Publication No. US20040110251A1
; GENERAL INFORMATION:
; APPLICANT: Grabowski et al.
; TITLE OF INVENTION: DETECTION OF PATHOGENIC BACTERIA
; FILE REFERENCE: 223374
; CURRENT APPLICATION NUMBER: US/10/250,997
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/11901
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: DE 10100493.1
; PRIOR FILING DATE: 2001-01-08

; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 25
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-250-997-25

Query Match 62.9%; Score 13.2; DB 17; Length 32;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21
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RESULT 7
US-10-250-997-39
; Sequence 39, Application US/10250997
; Publication No. US20040110251A1
; GENERAL INFORMATION:
; APPLICANT: Grabowski et al.
; TITLE OF INVENTION: DETECTION OF PATHOGENIC BACTERIA
; FILE REFERENCE: 223374
; CURRENT APPLICATION NUMBER: US/10/250,997
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/11901
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; PRIOR APPLICATION NUMBER: DE 10100493.1
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 39
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-250-997-39

Query Match 62.9%; Score 13.2; DB 17; Length 32;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21
| ||||| |||||
Db 7 GAATGTCAGATAACTGGC 24

RESULT 8
US-10-641-455A-117/c
; Sequence 117, Application US/10641455A
; Publication No. US20040171566A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; APPLICANT: McKay, Robert
; APPLICANT: Popoff, Ian
; APPLICANT: Wong, Wai Shiu Fred
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of p38 Mitogen
; TITLE OF INVENTION: Activated Protein Kinase Expression
; FILE REFERENCE: ISPH-0762
; CURRENT APPLICATION NUMBER: US/10/641,455A
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/238,442
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/640,101
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 09/286,904
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117

```
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-641-455A-117

Query Match          62.9%; Score 13.2; DB 17; Length 35;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGGC 21
Db 34 GCATACCAGATTACAGCC 17

RESULT 9
US-10-197-290-29/c
; Sequence 29, Application US/10197290
; Publication No. US20030083300A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2
; FILE REFERENCE: RTSP-0421
; CURRENT APPLICATION NUMBER: US/10/197,290
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 09/857,299
; PRIOR FILING DATE: 2001-20-04
; PRIOR APPLICATION NUMBER: PCT/US99/22083
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-197-290-29

Query Match          61.9%; Score 13; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACT 18
Db 16 ATGCCAGATTACT 4

RESULT 10
US-10-388-263-182/c
; Sequence 182, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; MODULATION BY OLIGONUCLEOTIDES AND
; GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-182

Query Match          61.9%; Score 13; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACT 18
Db 16 ATGCCAGATTACT 4

RESULT 11
US-10-317-278-17
; Sequence 17, Application US/10317278
; Publication No. US20040110702A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MAGE-D1 EXPRESSION
; FILE REFERENCE: HTS-0041
; CURRENT APPLICATION NUMBER: US/10/317,278
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-278-17

Query Match          61.9%; Score 13; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGCCAGATTACTG 19
Db 8 TGCCAGATTACTG 20

RESULT 12
US-10-317-278-51/c
; Sequence 51, Application US/10317278
; Publication No. US20040110702A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MAGE-D1 EXPRESSION
; FILE REFERENCE: HTS-0041
; CURRENT APPLICATION NUMBER: US/10/317,278
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-317-278-51

Query Match          61.9%; Score 13; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGCCAGATTACTG 19
```



```
Db      13 TGCCGAGTACTG 1
|||||
RESULT 13
US-10-851-894-15/c
; Sequence 15, Application US/10851894
; Publication No. US20040216185A1
; GENERAL INFORMATION:
; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for Novel Substrate Specific
; FILE REFERENCE: 16518.137
; CURRENT APPLICATION NUMBER: US/10/851,894
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 09/591,279
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/138,308
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (..)
; OTHER INFORMATION: Oligonucleotide Primer L197A Sense
US-10-851-894-15
Query Match      61.9%; Score 13; DB 18; Length 32;
Best Local Similarity 76.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      27 AACGCCCGCGAGTACTGGC 7
|||||

RESULT 14
US-10-851-894-16
; Sequence 16, Application US/10851894
; Publication No. US20040216185A1
; GENERAL INFORMATION:
; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for Novel Substrate Specific
; FILE REFERENCE: 16518.137
; CURRENT APPLICATION NUMBER: US/10/851,894
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 09/591,279
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/138,308
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (..)
; OTHER INFORMATION: Oligonucleotide Primer L197A Antisense
US-10-851-894-16
Query Match      61.9%; Score 13; DB 18; Length 32;
Best Local Similarity 76.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      6 AACGCCCGCGAGTACTGGC 26
|||||
```

```
RESULT 15
US-09-930-423-2899/c
; Sequence 2899, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2899
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2899
Query Match      61.9%; Score 13; DB 10; Length 37;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      22 AGTGCATGCCATCATGCTGGC 2
|||||

RESULT 16
US-09-745-237A-2899/c
; Sequence 2899, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2899
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2899
Query Match      61.9%; Score 13; DB 10; Length 37;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      22 AGTGCATGCCATCATGCTGGC 2
|||||

RESULT 17
US-09-780-752-20
; Sequence 20, Application US/09780752
; Patent No. US20020019349A1
; GENERAL INFORMATION:
; APPLICANT: Conrad, Kirk P.
; APPLICANT: Martyn Lewis
; APPLICANT: Elaine N. Unemori
; APPLICANT: Xinfan Huang
; APPLICANT: Carol A. Tozzi
```

```
; TITLE OF INVENTION: Use of Relaxin to Treat Diseases Related
; TITLE OF INVENTION: to Vasoconstriction
; FILE REFERENCE: CONN-001
; CURRENT APPLICATION NUMBER: US/09/780,752
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,408
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/200,284
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/242,216
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-752-20

Query Match          61.0%; Score 12.8; DB 9; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 ATGCCAGATTACTGGC 21
Db      9 ATGGAAGATTACTGGC 24
      ||| . ||||| |||||
RESULT 18
US-09-940-185-787/c
; Sequence 787, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 787
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-787

Query Match          61.0%; Score 12.8; DB 10; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CGCATGCCAGATTACT 18
Db      20 CGCATGCCAAATTCCT 5
      ||| ||||| ||||| |||
RESULT 19
US-10-320-231A-8/c
; Sequence 8, Application US/10320231A
; Publication No. US20030194403A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
```

```
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-8

Query Match          61.0%; Score 12.8; DB 15; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTG 19
Db      19 GCATACCAGAACTACTG 4
      ||| ||||| |||||
RESULT 20
US-09-940-185-4752/c
; Sequence 4752, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4752
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4752

Query Match          61.0%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CGCATGCCAGATTACT 18
Db      21 CGCATGCCAAATTCCT 6
      ||| ||||| ||||| |||
RESULT 21
US-10-289-762-3669/c
; Sequence 3669, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffaiss, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3669
; LENGTH: 20
; TYPE: DNA
```

; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3669

Query Match 60.0%; Score 12.6; DB 16; Length 20;
Best Local Similarity 78.9%; Pred. No. 9.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTG 19
||| ||||| |||||
Db 20 AACGCTGCCAAATTACAG 2

RESULT 22

US-09-754-853A-418
; Sequence 418, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Soybean Cyst Nematode Resistance
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 418
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 240017_region_G3_50537_17_Reverse_Primer
US-09-754-853A-418

Query Match 60.0%; Score 12.6; DB 10; Length 25;
Best Local Similarity 78.9%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTG 19
||| ||||| |||||
Db 4 AGAGCATCCCAATTAAATG 22

RESULT 23

US-10-138-674-15043/c
; Sequence 15043, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15043
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-15043

Query Match 60.0%; Score 12.6; DB 16; Length 36;
Best Local Similarity 78.9%; Pred. No. 1e+04;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTG 19
||| ||||| |||||
Db 19 AGTGCATGCCCATACTG 1

RESULT 24

US-10-287-949A-15043/c
; Sequence 15043, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15043
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-15043

Query Match 60.0%; Score 12.6; DB 17; Length 36;
Best Local Similarity 78.9%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTG 19
||| ||||| |||||
Db 19 AGTGCATGCCCATACTG 1

RESULT 25

US-10-318-970-29/c
; Sequence 29, Application US/10318970
; Publication No. US2004002080A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, Nancy D.
; TITLE OF INVENTION: PRIMERS FOR USE IN DETECTING BETA LACTAMASES
; FILE REFERENCE: 180.0009 0101
; CURRENT APPLICATION NUMBER: US/10/318,970
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/340,466
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Primer
US-10-318-970-29

Query Match 59.0%; Score 12.4; DB 16; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTAC 17
||| ||||| |||||
Db 15 GCGTGCCAGATTAC 2

RESULT 26

ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan

ZIP: 49007
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
(EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/091,257
FILING DATE: 05-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/721,979A
FILING DATE: October 4, 1996
APPLICATION NUMBER: FR 94 04009
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
OTHER INFORMATION: /product= "GivdeltaC"
/note= "sequence 174-187"
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-091-257-72

Query Match 59.0%; Score 12.4; DB 14; Length 42;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTAC 17
Db 27 GCATGCCAGATTAC 14

RESULT 30
US-10-035-833A-2502
; Sequence 2502, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2502
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: t is present or absent.
US-10-035-833A-2502

Query Match 59.0%; Score 12.4; DB 16; Length 49;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACT 18
Db 30 CTTGCCAGATTACT 43

RESULT 31
US-10-035-833A-4898
; Sequence 4898, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4898
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: t is present or absent.
US-10-035-833A-4898

Query Match 59.0%; Score 12.4; DB 16; Length 49;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACT 18
Db 30 CTTGCCAGATTACT 43

RESULT 32
US-10-138-381-15/c
; Sequence 15, Application US/10138381
; Publication No. US20030064388A1
; GENERAL INFORMATION:
; APPLICANT: NAKAYAMA, Tomoko
; APPLICANT: TADA, Jun
; APPLICANT: FUKUSHIMA, Shigeru
; APPLICANT: OHASHI, Tetsuo
; TITLE OF INVENTION: Oligonucleotides for Detecting Bacteria and
; TITLE OF INVENTION: Detection Process
; FILE REFERENCE: 1422-0430P
; CURRENT APPLICATION NUMBER: US/10/138,381
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/614,681
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 08/968,046
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 08/328,710
; PRIOR FILING DATE: 1994-10-25
; PRIOR APPLICATION NUMBER: 6-48174 JAPAN
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 6-30277 JAPAN
; PRIOR FILING DATE: 1994-02-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-138-381-15

Query Match 58.1%; Score 12.2; DB 14; Length 19;

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Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGG 20
DB 17 GAATGTCAGATAACTGG 1

RESULT 33
US-10-084-839-3754/c
; Sequence 3754, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Lymaicheva, Natalie B.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Testska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT FILING DATE: 2002-02-26
; CURRENT APPLICATION NUMBER: US/10/084,839
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3754
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3754

Query Match 58.1%; Score 12.2; DB 15; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACT 18
DB 19 GCGCAGCAGACAGATTCT 3

RESULT 34
US-10-085-239A-14/c
; Sequence 14, Application US/10085239A
; Publication No. US2003019715A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Ward, Simon
; APPLICANT: Bavik, Claes
; APPLICANT: Corfk, Michael
; APPLICANT: Tazi-aahini, Rachid
; TITLE OF INVENTION: Treatment of Hyperproliferative Diseases
; FILE REFERENCE: 674569-2001
; CURRENT APPLICATION NUMBER: US/10/085,239A

Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGG 20
DB 17 GAATGTCAGATAACTGG 1

RESULT 35
US-09-754-853A-786
; Sequence 786, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE OF INVENTION: Soybean Cyst Nematode Resistance
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 786
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 318013_region_A3_140551_15_Reverse_Primer_Seq
US-09-754-853A-786

Query Match 58.1%; Score 12.2; DB 10; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTAC 17
DB 3 AACGCATACCAGATGAC 19

RESULT 36
US-10-098-263B-115941/c
; Sequence 115941, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115941
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-115941
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Query Match      58.1%; Score 12.2; DB 15; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGCC 21
Db 23 CTTGACAGATTACTGCC 7

RESULT 37
US-10-098-263B-119516
; Sequence 119516, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 119516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-119516

Query Match      58.1%; Score 12.2; DB 15; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACT 18
Db 3 GAGAAATGTCAGATTACT 19

RESULT 38
US-10-084-839-3753
; Sequence 3753, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chenak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: JP, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Teetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004

Query Match      58.1%; Score 12.2; DB 15; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGCC 21
Db 23 CTTGACAGATTACTGCC 7

RESULT 39
US-10-072-622-26
; Sequence 26, Application US/10072622
; Publication No. US20030158102A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; APPLICANT: Bajorath, Jorgen
; TITLE OF INVENTION: ICOS Mutants
; FILE REFERENCE: 07039-331001
; CURRENT APPLICATION NUMBER: US/10/072,622
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-072-622-26

Query Match      58.1%; Score 12.2; DB 15; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGG 20
Db 9 GCATGCTAAATTTGCTGG 25

RESULT 40
US-10-072-622-25/c
; Sequence 25, Application US/10072622
; Publication No. US20030158102A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; APPLICANT: Bajorath, Jorgen
; TITLE OF INVENTION: ICOS Mutants
; FILE REFERENCE: 07039-331001
; CURRENT APPLICATION NUMBER: US/10/072,622
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-072-622-25

Query Match      58.1%; Score 12.2; DB 15; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Oy 4 GCATGCCAGATTACTGG 20
|||
Db 19 GCATGCTAAATTGCTGG 3
|||

Search completed: November 24, 2004, 03:41:54
Job time : 113.572 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1006.82 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21

Sequence: 1 agcgatgcccagattactggc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gssi:*

9: gb_gssi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13	61.9	34	9	BX547835 Arabidops
C 2	12.8	61.0	38	9	DR10119T
C 3	12.6	60.0	37	1	AL182864
C 4	12.6	60.0	46	1	AI284041 qt72d04.x
C 5	12.2	58.1	37	1	AI561150
C 6	12.2	58.1	48	9	AG203065
C 7	12	57.1	39	9	CG709763
C 8	12	57.1	43	1	AI182198
C 9	12	57.1	43	8	BH635056
C 10	12	57.1	45	2	BE907096
C 11	12	57.1	48	9	CL423735
C 12	12	57.1	50	1	AU102389
C 13	11.8	56.2	36	9	TA329D01Q
C 14	11.8	56.2	44	9	CR358600
C 15	11.8	56.2	50	9	CG711376
C 16	11.8	56.2	50	9	AG215560 Drosophil
C 17	11.6	55.2	28	1	AU255721
C 18	11.6	55.2	31	6	CD036166 mgmt009xB
C 19	11.6	55.2	32	8	AZ828889
C 20	11.6	55.2	41	8	AZ471345
C 21	11.6	55.2	42	9	TA92F10Q
C 22	11.6	55.2	49	8	AZ503905
C 23	11.6	55.2	50	9	AB082362 Drosophil
C 24	11.4	54.3	31	9	BX651219 Arabidops

C	25	11.4	54.3	34	1	AV857727
C	26	11.4	54.3	35	6	CD533621
C	27	11.4	54.3	41	8	AZ804337
C	28	11.4	54.3	47	8	AZ369672
C	29	11.4	54.3	48	9	CL302431
C	30	11.4	54.3	50	1	AU104945
C	31	11.2	53.3	34	1	AA641303
C	32	11.2	53.3	35	1	AU040922
C	33	11.2	53.3	35	1	AU040926
C	34	11.2	53.3	35	9	DR4J11T
C	35	11.2	53.3	37	8	AZ821751
C	36	11.2	53.3	40	9	AL760654
C	37	11.2	53.3	41	8	AZ471345
C	38	11	52.4	32	6	CA853264
C	39	11	52.4	41	1	AU746715
C	40	11	52.4	43	8	AZ447897
C	41	11	52.4	43	8	AZ872071
C	42	11	52.4	44	9	CNS07F95
C	43	11	52.4	50	1	AU106987
C	44	10.8	51.4	28	8	AZ502451
C	45	10.8	51.4	29	8	AZ948785
C	46	10.8	51.4	31	8	AZ596685
C	47	10.8	51.4	33	9	DR13K9T
C	48	10.8	51.4	34	9	DR43K2T
C	49	10.8	51.4	35	1	AJ655516
C	50	10.8	51.4	36	8	AZ353586
C	51	10.8	51.4	37	8	BH910433
C	52	10.8	51.4	38	8	AZ779310
C	53	10.8	51.4	38	9	TA170E05Q
C	54	10.8	51.4	43	7	D19557
C	55	10.8	51.4	43	8	BH850810
C	56	10.8	51.4	43	8	BH910174
C	57	10.8	51.4	45	9	CG719990
C	58	10.8	51.4	47	8	BH740833
C	59	10.8	51.4	50	1	AU103992
C	60	10.8	51.4	50	1	AU107439
C	61	10.6	50.5	25	1	AA880161
C	62	10.6	50.5	33	9	TA61D02P
C	63	10.6	50.5	34	1	AA630482
C	64	10.6	50.5	37	9	DR43D23T
C	65	10.6	50.5	39	2	BE732614
C	66	10.6	50.5	39	4	BJ524497
C	67	10.6	50.5	39	8	AZ372602
C	68	10.6	50.5	39	9	CG723167
C	69	10.6	50.5	40	8	BH852184
C	70	10.6	50.5	40	8	BZ764204
C	71	10.6	50.5	42	7	N74525
C	72	10.6	50.5	42	8	BH906566
C	73	10.6	50.5	43	1	AA780094
C	74	10.6	50.5	43	7	N71938
C	75	10.6	50.5	46	9	TA316D03P
C	76	10.6	50.5	47	1	AV842025
C	77	10.6	50.5	48	2	AW497611
C	78	10.6	50.5	48	9	CG721564
C	79	10.6	50.5	49	1	AA871018
C	80	10.6	50.5	50	1	AU102221
C	81	10.6	50.5	50	1	AU106993
C	82	10.4	49.5	23	6	CF317783
C	83	10.4	49.5	25	9	AJ587447
C	84	10.4	49.5	29	8	AZ310013
C	85	10.4	49.5	31	8	AZ849227
C	86	10.4	49.5	35	9	AG189387
C	87	10.4	49.5	37	8	AZ643581
C	88	10.4	49.5	39	4	BJ055437
C	89	10.4	49.5	40	1	AJ749535
C	90	10.4	49.5	40	8	AZ480737
C	91	10.4	49.5	41	4	BI596584
C	92	10.4	49.5	41	4	BI602229
C	93	10.4	49.5	42	8	CC025121
C	94	10.4	49.5	42	9	BX650299
C	95	10.4	49.5	43	9	BX287314
C	96	10.4	49.5	45	1	AA683880
C	97	10.4	49.5	47	8	CC020084

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AZ369672	1M0120821	AZ369672
CL302431	G058B11 G	CL302431
AU104945	AU104945	AU104945
AA641303	nr78d09.8	AA641303
AU040922	AU040922	AU040922
AU040926	AU040926	AU040926
AL736749	Danio rer	AL736749
AZ821751	2M0094H09	AZ821751
AL760654	Arabidops	AL760654
AZ471345	1M0285119	AZ471345
CA853264	B06C01.8e	CA853264
AJ746715	AJ746715	AJ746715
AZ447897	1M0245G17	AZ447897
AZ872071	2M0185B13	AZ872071
AL608171	Anopheles	AL608171
AU106987	AU106987	AU106987
AZ502451	1M0341D17	AZ502451
AZ948785	2M0211F21	AZ948785
AZ596685	1M0410A07	AZ596685
DR13K9T	Danio rer	DR13K9T
DR43K2T	Danio rer	DR43K2T
AJ655516	AJ655516	AJ655516
AZ353586	1M0092105	AZ353586
BH910433	SALK 0596	BH910433
AZ779310	2M0015M05	AZ779310
TA170E05Q	T. brucei	TA170E05Q
D19557	MUSGS00957	D19557
BH850810	SALK_0718	BH850810
BH910174	SALK_0581	BH910174
CG719990	1119060A1	CG719990
BH740833	KG04903-3	BH740833
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AU107439	AU107439	AU107439
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AL456624	T. brucei	AL456624
AA630482	ab98f09.8	AA630482
DR43D23T	Danio rer	DR43D23T
BE732614	601571185	BE732614
BJ524497	603051689	BJ524497
AZ372602	1M0124J02	AZ372602
CG723167	1119075A0	CG723167
BH852184	SALK_0742	BH852184
BZ764204	SALK_1241	BZ764204
N74525	za06c08.s1	N74525
BH906566	SALK_0339	BH906566
AA780094	af36509.s	AA780094
N71938	y295a03.s1	N71938
AL491175	T. brucei	AL491175
AV842025	AV842025	AV842025
AW497611	RARG5B34	AW497611
CG721564	1119067H1	CG721564
AA871018	vq23c04.r	AA871018
AU102221	AU102221	AU102221
AU106993	AU106993	AU106993
CF317783	HD--07-J1	CF317783
AJ587447	Arabidops	AJ587447
AZ310013	1M0018B12	AZ310013
AZ849227	2M0150N02	AZ849227
AG189387	Pan trogl	AG189387
AZ643581	1M0507B10	AZ643581
BJ055437	BJ055437	BJ055437
AJ749535	at30b05.x	AJ749535
AZ480737	1M0302A06	AZ480737
BI596584	603243143	BI596584
BI602229	603244161	BI602229
CC025121	3591.1.42	CC025121
BX650299	Arabidops	BX650299
BX287314	Arabidops	BX287314
AA683880	vr06c09.r	AA683880
CC020084	3591_1_18	CC020084

98	10.4	49.5	48	9	CL423502	CL423502 01S0557-0	c 171	10	47.6	49	1	AA122130	AA122130 zn82f09.r
99	10.4	49.5	49	8	AI671091	BH636470 1008011E0	c 172	10	47.6	49	8	AI966717	AI966717 SC56504.Y
100	10.4	49.5	49	8	BH636470	BH755942 SALK_0525	c 173	10	47.6	49	8	AZ784737	AZ784737 2M0027L14
101	10.4	49.5	49	8	BH755942	AU102514 AU102514	c 174	10	47.6	49	8	AZ817223	AZ817223 2M0086N19
102	10.4	49.5	50	1	AU102514	AU102516 AU102516	c 175	10	47.6	49	9	BX131309	BX131309 Danilo rer
103	10.4	49.5	50	1	AU102516	AU103904 AU103904	c 176	10	47.6	50	1	AU103679	AU103679 AU103679
104	10.4	49.5	50	1	AU103904	AU104912 AU104912	c 177	10	47.6	50	1	AU104966	AU104966 AU104966
105	10.4	49.5	50	1	AU104912	AU104927 AU104927	c 178	10	47.6	50	1	AU104967	AU104967 AU104967
106	10.4	49.5	50	1	AU104927	AU106996 AU106996	c 179	10	47.6	50	1	AU105067	AU105067 AU105067
107	10.4	49.5	50	1	AU106996	AU107003 AU107003	c 180	10	47.6	50	1	AU105707	AU105707 AU105707
108	10.4	49.5	50	1	AU107003	AG202039 Pan trogl	c 181	10	47.6	50	1	AU105973	AU105973 AU105973
109	10.2	48.6	22	9	AG202039	AZ827167 2M0103N22	c 182	10	47.6	50	1	AU106349	AU106349 AU106349
110	10.2	48.6	26	8	AZ827167	BH789439 AJ789439	c 183	10	47.6	50	1	AA406919	AA406919 MBFAFCZ6G1
111	10.2	48.6	27	1	AJ789439	AZ650214 1M0520G15	c 184	10	47.6	50	7	CO578886	CO578886 tai59f10.
112	10.2	48.6	29	8	AZ650214	AZ784520 2M0027H10	c 185	10	47.6	50	8	AZ510728	AZ510728 1M0355I10
113	10.2	48.6	29	8	AZ784520	CG723474 1119076E1	c 186	10	47.6	50	8	BH856729	BH856729 SALK_0792
114	10.2	48.6	31	9	CG723474	CA795338 Cac BL_23	c 187	9.8	46.7	19	8	AZ482658	AZ482658 1M0307L16
115	10.2	48.6	33	6	CA795338	BZ770289 SALK_1432	c 188	9.8	46.7	21	8	AZ313684	AZ313684 1M030D08
116	10.2	48.6	33	8	BZ770289	BZ770290 SALK_1432	c 189	9.8	46.7	24	9	TA386G12P	TA386G12P T. brucei
117	10.2	48.6	33	8	BZ770290	AL743042 Danilo rer	c 190	9.8	46.7	26	9	TA157A01Q	TA157A01Q T. brucei
118	10.2	48.6	33	9	DR7G2T	AL743042 Danilo rer	c 191	9.8	46.7	27	8	AZ404641	AZ404641 1M0173G08
119	10.2	48.6	33	9	TA131H12P	AL743042 Danilo rer	c 192	9.8	46.7	28	8	AZ404641	AZ404641 1M0173G08
120	10.2	48.6	34	4	BJ055330	BJ055330 BJ055330	c 193	9.8	46.7	29	9	TA174H12P	TA174H12P T. brucei
121	10.2	48.6	36	8	AZ867774	AZ788205 2M0035H09	c 194	9.8	46.7	29	9	TA300E08Q	TA300E08Q T. brucei
122	10.2	48.6	36	8	AZ867774	BZ380454 SALK_1151	c 195	9.8	46.7	30	4	BI763468	BI763468 603047483
123	10.2	48.6	37	8	BZ380454	CL524306 SA07D11 F	c 196	9.8	46.7	31	4	BG432088	BG432088 602496951
124	10.2	48.6	39	9	CL524306	CL218856 GG75G08.X	c 197	9.8	46.7	31	9	AL767632	AL767632 Arabidops
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126	10.2	48.6	40	1	AA137304	W88034 mf68d04.r1	c 199	9.8	46.7	32	9	DR43118T	DR43118T Danilo rer
127	10.2	48.6	40	7	W88034	AZ666338 1M0348G21	c 200	9.8	46.7	32	9	DR43118T	DR43118T Danilo rer
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129	10.2	48.6	43	1	AJ655037	CG720647 1119063C0	c 202	9.8	46.7	33	2	BE275474	BE275474 601121496
130	10.2	48.6	43	9	TA102809Q	AL460487 T. brucei	c 203	9.8	46.7	33	9	AG196275	AG196275 Pan trogl
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133	10.2	48.6	45	8	AZ666338	AZ788205 2M0035H09	c 206	9.8	46.7	34	9	DR3F10T	DR3F10T Danilo rer
134	10.2	48.6	45	9	CG720647	AJ655037 AJ655037	c 207	9.8	46.7	34	9	DR3F10T	DR3F10T Danilo rer
135	10.2	48.6	45	9	CG720647	AL460487 T. brucei	c 208	9.8	46.7	34	9	TA294F06P	TA294F06P T. brucei
136	10.2	48.6	45	8	CL001730	AL460487 T. brucei	c 209	9.8	46.7	36	8	AZ468285	AZ468285 1M0281O12
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139	10.2	48.6	49	9	DR1307T	AL737772 Danilo rer	c 212	9.8	46.7	36	9	AL952164	AL952164 Arabidops
140	10.2	48.6	50	1	AU102397	AU102397 AU102397	c 213	9.8	46.7	37	1	AI240580	AI240580 qh52e10.X
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145	10	47.6	23	8	AZ629873	AZ629873 1M0483E10	c 218	9.8	46.7	38	8	AZ768399	AZ768399 1M0568E19
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C 406	9.4	44.8	43	8	CC455427	CC455427	C 479	9.2	43.8	33	1	AU255073	AU255073
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C 409	9.4	44.8	44	9	AJ595690	ARabidops	C 482	9.2	43.8	33	9	BX894791	ARabidops
C 410	9.4	44.8	44	9	AG023552	Oryza.sst	C 483	9.2	43.8	33	1	AA390119	mr37C04.r
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C 412	9.4	44.8	45	7	CF660851	CCLM09A32	C 485	9.2	43.8	34	8	AZ829250	2M0106K17
C 413	9.4	44.8	45	8	AZ452557	1M0252C01	C 486	9.2	43.8	34	8	AQ254767	EP(X)1346
C 414	9.4	44.8	45	8	BZ596472	SALK_0926	C 487	9.2	43.8	34	8	BH406304	RPCI-23-3
C 415	9.4	44.8	45	9	BX651841	ARabidops	C 488	9.2	43.8	34	9	AJ597693	ARabidops
C 416	9.4	44.8	45	9	TA54E07Q	T. brucei	C 489	9.2	43.8	34	9	TA82C11P	T. brucei
C 417	9.4	44.8	46	1	AJ950926	AJ950926	C 490	9.2	43.8	35	6	CA913569	PCSC09477
C 418	9.4	44.8	46	1	AJ650474	AJ650474	C 491	9.2	43.8	35	7	N94609	ZB79D03.s1
C 419	9.4	44.8	46	1	AA622161	rq56f10.s	C 492	9.2	43.8	35	8	AZ823097	2M0096K19
C 420	9.4	44.8	46	2	BF682270	602117413	C 493	9.2	43.8	35	9	TA129B11P	T. brucei
C 421	9.4	44.8	46	8	AZ436091	1M0233C08	C 494	9.2	43.8	36	8	AZ658185	1M0534M18
C 422	9.4	44.8	46	8	AZ831992	2M0112L06	C 495	9.2	43.8	36	8	AZ817178	2M0086C21
C 423	9.4	44.8	46	9	TA300F12P	T. brucei	C 496	9.2	43.8	37	1	AI591377	ts10G07.x
C 424	9.4	44.8	46	9	CC884049	SALK_1028	C 497	9.2	43.8	37	1	AZ644324	1M0508A13
C 425	9.4	44.8	47	6	CF107684	Shultzomi	C 498	9.2	43.8	37	9	TA371B02Q	T. brucei
C 426	9.4	44.8	47	8	AZ663255	1M0542K15	C 499	9.2	43.8	38	1	AJ652946	AJ652946
C 427	9.4	44.8	47	8	AZ801261	2M0059H08	C 500	9.2	43.8	38	8	AZ339876	1M0071J03
C 428	9.4	44.8	47	9	AL760555	ARabidops	C 501	9.2	43.8	38	8	AZ662464	1M0541003
C 429	9.4	44.8	47	9	AB082006	Drosophila	C 502	9.2	43.8	38	8	BZ664429	BZ664429
C 430	9.4	44.8	48	8	AZ603425	1M0422P01	C 503	9.2	43.8	39	7	N75693	YN52A01.r1
C 431	9.4	44.8	48	8	AZ810742	2M0076C06	C 504	9.2	43.8	39	8	AZ360831	1M0104F14
C 432	9.4	44.8	48	8	BH910369	SALK_0591	C 505	9.2	43.8	39	8	AZ834606	2M0117G22
C 433	9.4	44.8	48	9	CL265882	03F3660-0	C 506	9.2	43.8	39	8	BH811161	SALK_0575
C 434	9.4	44.8	49	1	AI148915	QC59G08.x	C 507	9.2	43.8	39	9	BX654933	ARabidops
C 435	9.4	44.8	49	1	AZ232796	2r47a03.r	C 508	9.2	43.8	40	1	AA138030	mq02f11.r
C 436	9.4	44.8	49	1	AA400193	AA400193	C 509	9.2	43.8	40	1	AI499269	tc09C08.x
C 437	9.4	44.8	49	6	CA935081	CA935081	C 510	9.2	43.8	40	1	AI766423	wh49h03.x
C 438	9.4	44.8	49	7	CK583962	1ST-W15_5	C 511	9.2	43.8	40	1	AI959989	sc36B11.x
C 439	9.4	44.8	49	7	W30135	mc27E11.r1	C 512	9.2	43.8	40	6	CF299766	7LEAF--03
C 440	9.4	44.8	49	9	BX179896	Danio rer	C 513	9.2	43.8	40	7	D19133	MUGSG01349
C 441	9.4	44.8	49	9	CR402501	ARabidops	C 514	9.2	43.8	40	8	BH846353	SALK_0074
C 442	9.4	44.8	49	9	CT979707	SALK_1455	C 515	9.2	43.8	40	9	CG713594	1119032E0
C 443	9.4	44.8	49	9	CL300934	CL300934	C 516	9.2	43.8	40	9	CL653498	PR101118c
C 444	9.4	44.8	49	9	CL694976	PR10165C-	C 517	9.2	43.8	41	4	BG614845	602642382
C 445	9.4	44.8	50	1	AL932753	AL932753	C 518	9.2	43.8	41	9	AG189043	Pan trogl
C 446	9.4	44.8	50	1	AU102518	AU102518	C 519	9.2	43.8	42	6	CD743540	IRB14_B02
C 447	9.4	44.8	50	1	AU103816	AU103816	C 520	9.2	43.8	42	8	AZ606691	1M0428C15
C 448	9.4	44.8	50	1	AU104251	AU104251	C 521	9.2	43.8	42	6	CF281213	14ETL--08
C 449	9.4	44.8	50	1	AU105592	AU105592	C 522	9.2	43.8	43	8	AZ834960	2M0117L19
C 450	9.4	44.8	50	1	AU105973	AU105973	C 523	9.2	43.8	43	1	AV956799	AV956799
C 451	9.4	44.8	50	1	AU106018	AU106018	C 524	9.2	43.8	44	8	AZ341899	1M0074D10
C 452	9.4	44.8	50	1	AU106020	AU106020	C 525	9.2	43.8	44	8	AZ419512	1M0196W02
C 453	9.4	44.8	50	1	AU106985	AU106985	C 526	9.2	43.8	44	8	BH864323	SALK_0957
C 454	9.4	44.8	50	1	AU107581	AU107581	C 527	9.2	43.8	44	9	CG711064	1119020A0
C 455	9.4	44.8	50	4	BM319246	ki70c02.y	C 528	9.2	43.8	45	1	AA861335	ak15h10.s
C 456	9.4	44.8	50	5	BX628742	BX628742	C 529	9.2	43.8	45	8	AZ588295	1M0396G03
C 457	9.4	44.8	50	6	CB046639	NISC_gf05	C 530	9.2	43.8	45	9	AJ593903	ARabidops
C 458	9.4	44.8	50	8	AZ330881	1M056101	C 531	9.2	43.8	45	9	EX229715	Danio rer
C 459	9.4	44.8	50	8	AZ466564	1M0277B23	C 532	9.2	43.8	45	9	CL436746	PS13730-N
C 460	9.4	44.8	50	9	CG785978	98F0079-0	C 533	9.2	43.8	46	1	AA782439	ak154h08.s
C 461	9.4	44.8	50	9	CL265883	03F3660-0	C 534	9.2	43.8	46	1	AA834374	of67e02.s
C 462	9.2	43.8	19	8	AZ336303	1M0066G03	C 535	9.2	43.8	46	1	AA501996	nes3q01.s

C 536	9.2	43.8	46	4	B1646968	BI646968	603278737		609	9	42.9	33	8	AZ607132	AZ607132	1M0429J23
C 537	9.2	43.8	46	8	A2991900	AZ991900	2M0276P17		C 610	9	42.9	34	1	AA530516	AA530516	VJ39e05.r
C 538	9.2	43.8	46	8	BZ291224	BZ291224	SALK 1125		611	9	42.9	34	7	N57329	N57329	YH81G01.r1
C 539	9.2	43.8	46	8	BZ769984	BZ769984	SALK 1429		C 612	9	42.9	34	7	N77004	N77004	YV50F05.r1
C 540	9.2	43.8	46	9	BX290413	BX290413	Arabidops		C 613	9	42.9	34	8	AZ345514	AZ345514	1M0080J05
C 541	9.2	43.8	46	9	TA123H08P	TA123H08P			C 614	9	42.9	34	8	AZ462629	AZ462629	1M0269B10
C 542	9.2	43.8	46	9	CL436498	CL436498	FST3118-N		C 615	9	42.9	34	8	AZ648259	AZ648259	1M0517M11
C 543	9.2	43.8	47	1	AJ789432	AJ789432	AJ789432		C 616	9	42.9	34	8	AZ877651	AZ877651	BG00655-3
C 544	9.2	43.8	47	8	AQ097186	AQ097186	GSSTC0919		C 617	9	42.9	34	8	CC057359	CC057359	SALK 1408
C 545	9.2	43.8	47	8	AZ79546	AZ79546	2M0016C09		C 618	9	42.9	34	9	AL940060	AL940060	Arabidops
C 546	9.2	43.8	47	8	BZ288624	BZ288624	SALK 0220		C 619	9	42.9	35	7	CF861066	CF861066	PSZ0003iH
C 547	9.2	43.8	47	9	BX658228	BX658228	Arabidops		C 620	9	42.9	35	8	AZ371076	AZ371076	1M0122A01
C 548	9.2	43.8	47	9	CL256760	CL256760	XS0700 Sa		C 621	9	42.9	35	9	AL944678	AL944678	Arabidops
C 549	9.2	43.8	47	9	CU519316	CU519316	DAGIH09 F		C 622	9	42.9	36	4	BI246232	BI246232	602958773
C 550	9.2	43.8	48	8	AZ447190	AZ447190	1M0243N19		C 623	9	42.9	36	4	BI697010	BI697010	603348471
C 551	9.2	43.8	48	8	AZ830212	AZ830212	2M0109M16		C 624	9	42.9	36	6	CA797391	CA797391	Cac BL 44
C 552	9.2	43.8	48	8	BH851849	BH851849	SALK 0736		C 625	9	42.9	36	8	AZ423700	AZ423700	1M0202H22
C 553	9.2	43.8	48	8	BZ765762	BZ765762	SALK 1342		C 626	9	42.9	36	8	AZ479941	AZ479941	1M0301I04
C 554	9.2	43.8	48	8	CC456314	CC456314	SALK 0971		C 627	9	42.9	36	8	AZ794093	AZ794093	2M0047012
C 555	9.2	43.8	49	1	AA648244	AA648244	ns07h03.r		C 628	9	42.9	36	8	AZ796083	AZ796083	2M0051G03
C 556	9.2	43.8	49	1	AA798166	AA798166	vx67G05.r		C 629	9	42.9	36	8	BH852549	BH852549	SALK 0751
C 557	9.2	43.8	49	1	AA109169	AA109169	mp38f04.r		C 630	9	42.9	36	8	BH852550	BH852550	SALK 0751
C 558	9.2	43.8	49	1	AA500776	AA500776	vg01b11.r		C 631	9	42.9	36	8	BH853541	BH853541	SALK 0771
C 559	9.2	43.8	49	2	BF203474	BF203474	601865731		C 632	9	42.9	36	8	BZ764686	BZ764686	SALK 1261
C 560	9.2	43.8	49	6	C20872	C20872	HUMGS000493		C 633	9	42.9	36	9	DR43A15T	DR43A15T	Danio rer
C 561	9.2	43.8	49	8	AZ451557	AZ451557	1M0251C04		C 634	9	42.9	36	9	CG846682	CG846682	GSSI14 RPC
C 562	9.2	43.8	49	9	AX182587	AX182587	Danio rer		C 635	9	42.9	36	9	AG194334	AG194334	Pan trogl
C 563	9.2	43.8	49	9	CC889041	CC889041	SALK 1527		C 636	9	42.9	37	1	AA680722	AA680722	LmFtAm022
C 564	9.2	43.8	49	9	AG188180	AG188180	Pan trogl		C 637	9	42.9	37	1	AA112707	AA112707	zn70h11.s
C 565	9.2	43.8	50	1	AU103166	AU103166	AU103166		C 638	9	42.9	37	1	AA114088	AA114088	qa55g12.s
C 566	9.2	43.8	50	1	AU103852	AU103852	AU103852		C 639	9	42.9	37	1	AA1667553	AA1667553	fc41905.x
C 567	9.2	43.8	50	1	AU103860	AU103860	AU103860		C 640	9	42.9	37	1	AA233522	AA233522	zr30B02.r
C 568	9.2	43.8	50	1	AU103861	AU103861	AU103861		C 641	9	42.9	37	1	AA611583	AA611583	vo93b03.r
C 569	9.2	43.8	50	1	AU103862	AU103862	AU103862		C 642	9	42.9	37	2	BE407487	BE407487	601300314
C 570	9.2	43.8	50	1	AU106994	AU106994	AU106994		C 643	9	42.9	37	4	B7034112	B7034112	B7034112
C 571	9.2	43.8	50	1	AU107049	AU107049	AU107049		C 644	9	42.9	37	7	R70733	R70733	Yi46d12.r1
C 572	9.2	43.8	50	1	AU108052	AU108052	AU108052		C 645	9	42.9	37	7	T92129	T92129	ye02h11.r1
C 573	9.2	43.8	50	1	AU108092	AU108092	AU108092		C 646	9	42.9	37	8	AZ480603	AZ480603	1M0302F18
C 574	9.2	43.8	50	4	BM253047	BM253047	kf01 K P1		C 647	9	42.9	37	8	AZ658024	AZ658024	1M0534M03
C 575	9.2	43.8	50	5	BP134996	BP134996	BP134996		C 648	9	42.9	37	9	EX660247	EX660247	Arabidops
C 576	9.2	43.8	50	6	CB832519	CB832519	SWHmfCAV		C 649	9	42.9	38	1	AJ652144	AJ652144	AJ652144
C 577	9.2	43.8	50	6	CD028941	CD028941	mgns002xJ		C 650	9	42.9	38	7	N34814	N34814	Yy44c12.s1
C 578	9.2	43.8	50	8	BF791926	BF791926	SALK 0620		C 651	9	42.9	38	8	AZ483597	AZ483597	1M0409K20
C 579	9.2	43.8	50	9	BX225007	BX225007	Danio rer		C 652	9	42.9	38	8	AZ662729	AZ662729	1M0542C04
C 580	9.2	43.8	50	9	CR167367	CR167367	Forward s		C 653	9	42.9	38	8	AZ769958	AZ769958	1M0571G07
C 581	9.2	43.8	50	9	CR198849	CR198849	Reverse s		C 654	9	42.9	38	8	BH865421	BH865421	SALK 0984
C 582	9.2	43.8	50	9	TA130E07P	TA130E07P			C 655	9	42.9	38	9	DME547594	DME547594	Drosophil
C 583	9	42.9	21	8	AZ410517	AZ410517	1M0183M02		C 656	9	42.9	38	9	TA195B01P	TA195B01P	T. brucei
C 584	9	42.9	22	8	AZ309394	AZ309394	1M0013P22		C 657	9	42.9	38	1	AV851903	AV851903	AV851903
C 585	9	42.9	22	8	AZ479594	AZ479594	1M0300B22		C 658	9	42.9	39	8	AZ499836	AZ499836	1M0337C21
C 586	9	42.9	22	8	AZ812710	AZ812710	2M0079N03		C 659	9	42.9	39	9	CC887781	CC887781	SALK 1507
C 587	9	42.9	23	8	AZ361811	AZ361811	1M0106I08		C 660	9	42.9	40	1	AA769281	AA769281	nz33F09.s
C 588	9	42.9	23	8	AZ433756	AZ433756	1M0219J18		C 661	9	42.9	40	1	AA969885	AA969885	op59a10.s
C 589	9	42.9	23	8	AZ762598	AZ762598	1M0557I12		C 662	9	42.9	40	1	AI200247	AI200247	qf9re12.x
C 590	9	42.9	24	8	AZ489445	AZ489445	1M0321P09		C 663	9	42.9	40	1	AJ664162	AJ664162	AJ664162
C 591	9	42.9	24	8	AZ761439	AZ761439	1M0555G14		C 664	9	42.9	40	1	AA290676	AA290676	zt19e11.s
C 592	9	42.9	24	9	TA39F0751	TA39F0751			C 665	9	42.9	40	1	AV834221	AV834221	AV834221
C 593	9	42.9	25	8	AZ817511	AZ817511	2M0087G05		C 666	9	42.9	40	4	BM396033	BM396033	5009-0-15
C 594	9	42.9	27	1	AJ651227	AJ651227	AJ651227		C 667	9	42.9	40	7	D74285	D74285	CELK079A9F
C 595	9	42.9	27	1	AJ655548	AJ655548	AJ655548		C 668	9	42.9	40	7	H55146	H55146	CHR220085 C
C 596	9	42.9	27	8	AZ438274	AZ438274	1M0228H16		C 669	9	42.9	40	7	H87885	H87885	Yw16d04.r1
C 597	9	42.9	27	8	AZ603545	AZ603545	1M0422019		C 670	9	42.9	40	7	N91653	N91653	za20h02.r1
C 598	9	42.9	28	6	CF305592	CF305592	HDAl - 01-		C 671	9	42.9	40	7	R89723	R89723	ym99c12.r1
C 599	9	42.9	28	8	AZ810960	AZ810960	2M0076C23		C 672	9	42.9	40	8	BH251215	BH251215	SALK 0112
C 600	9	42.9	28	8	AZ835848	AZ835848	2M0130J14		C 673	9	42.9	40	8	BH909406	BH909406	SALK 0534
C 601	9	42.9	29	7	D21044	D21044	HUMGS02029		C 674	9	42.9	40	9	AJ600768	AJ600768	Arabidops
C 602	9	42.9	29	8	AZ610133	AZ610133	1M0435F16		C 675	9	42.9	41	1	AA737623	AA737623	oa52b06.s
C 603	9	42.9	29	8	BH901129	BH901129	SALK 0731		C 676	9	42.9	41	8	BZ354052	BZ354052	SALK 1225
C 604	9	42.9	30	8	AZ439292	AZ439292	1M0229F19		C 677	9	42.9	41	9	BX662958	BX662958	Arabidops
C 605	9	42.9	31	9	CR399375	CR399375	Arabidops		C 678	9	42.9	41	9	CR399139	CR399139	Arabidops
C 606	9	42.9	32	6	C01986	C01986	HUMGS000400		C 679	9	42.9	41	9	HSMC36D01	HSMC36D01	
C 607	9	42.9	32	8	AZ625072	AZ625072	1M0464I11		C 680	9	42.9	41	9	AB082397	AB082397	Drosophil
C 608	9	42.9	33	6	CD532323	CD532323	26K5 Arab		C 681	9	42.9	42	4	BI855685	BI855685	603383215

828	8.8	41.9	28	1	AL118404	AL118404 ue36c02.x	901	8.8	41.9	32	9	DR5N3T	AL738957	Danio rer
829	8.8	41.9	28	6	CF278412	CF278412 14ETL--04	902	8.8	41.9	32	9	TA207C02Q	AL475834	T. brucei
830	8.8	41.9	28	6	CF315658	CF315658 HD--04-K1	903	8.8	41.9	32	6	CF316372	HD--05-K0	
831	8.8	41.9	28	6	CF316663	CF316663 HD--06-A2	904	8.8	41.9	33	8	AZ785987	2M0030G18	
832	8.8	41.9	28	6	CF316792	CF316792 HD--06-D1	905	8.8	41.9	33	8	AZ822129	2M0095004	
833	8.8	41.9	28	6	CF317075	CF317075 HD--06-K0	906	8.8	41.9	33	8	BH856433	SALK_0797	
834	8.8	41.9	28	6	CF318998	CF318998 HD--10-J0	907	8.8	41.9	33	8	BH856436	SALK_0797	
835	8.8	41.9	28	6	CF327928	CF327928 NACL--02-	908	8.8	41.9	33	9	DR11H23T	Danio rer	
836	8.8	41.9	28	8	AQ073606	AQ073606 EP(2)2460	909	8.8	41.9	33	9	DR19P8T	Danio rer	
837	8.8	41.9	28	8	AQ257939	AQ257939 1M0363B22	910	8.8	41.9	33	9	DR19P8T	Danio rer	
838	8.8	41.9	28	8	BH864082	BH864082 SALK_0952	911	8.8	41.9	33	9	DR104T	Danio rer	
839	8.8	41.9	28	8	AG191782	AG191782 Pan trogl	912	8.8	41.9	33	9	DR43C9T	Danio rer	
840	8.8	41.9	29	6	CF316615	CF316615 HD--05-F1	913	8.8	41.9	33	9	DR43F16T	Danio rer	
841	8.8	41.9	29	6	CF316869	CF316869 HD--06-F1	914	8.8	41.9	33	9	DR43K14T	Danio rer	
842	8.8	41.9	29	6	CF317167	CF317167 HD--06-M0	915	8.8	41.9	33	9	TA152C04P	AL467190 T. brucei	
843	8.8	41.9	29	6	CF327123	CF327123 NACL--01-	916	8.8	41.9	33	9	TA193D02P	AL478361 T. brucei	
844	8.8	41.9	29	6	CF327275	CF327275 NACL--01-	917	8.8	41.9	33	9	CC883904	CC883904 SALK_1022	
845	8.8	41.9	29	7	HL5932	HL5932 Y127903.s1	918	8.8	41.9	33	9	CL670049	PR10161a	
846	8.8	41.9	29	9	CG724617	CG724617 1119082A0	919	8.8	41.9	34	4	BJ064029	BJ064029	
847	8.8	41.9	29	9	CG729336	CG729336 1119110H0	920	8.8	41.9	34	7	D19569	MUSGS00974	
848	8.8	41.9	30	1	AV833957	AV833957 AV833957	921	8.8	41.9	34	7	D19569	MUSGS00974	
849	8.8	41.9	30	6	CA794646	CA794646 Cac BL 11	922	8.8	41.9	34	8	AZ486062	1M0313P14	
850	8.8	41.9	30	6	CF301322	CF301322 7L5AF--06	923	8.8	41.9	34	8	BH846925	SALK_0119	
851	8.8	41.9	30	6	CF311738	CF311738 ABF--07-C	924	8.8	41.9	34	8	BZ761684	SALK_0750	
852	8.8	41.9	30	6	CF313400	CF313400 HD--01-I0	925	8.8	41.9	34	9	AJ596322	Arabidops	
853	8.8	41.9	30	6	CF314025	CF314025 HD--02-G0	926	8.8	41.9	34	9	AJ601221	Arabidops	
854	8.8	41.9	30	6	CF314237	CF314237 HD--02-K2	927	8.8	41.9	34	9	DMES45069	AJ601221 Arabidops	
855	8.8	41.9	30	6	CF314484	CF314484 HD--03-A1	928	8.8	41.9	34	9	TA48H05Q	AL456533 T. brucei	
856	8.8	41.9	30	6	CF316772	CF316772 HD--06-D0	929	8.8	41.9	35	1	AJ655516	AJ655516	
857	8.8	41.9	30	6	CF317266	CF317266 HD--06-O1	930	8.8	41.9	35	4	BI834797	B1834797 603090235	
858	8.8	41.9	30	6	CF317281	CF317281 HD--06-O1	931	8.8	41.9	35	8	AZ371114	1M0122J03	
859	8.8	41.9	30	6	CF337208	CF337208 JMT--07-J	932	8.8	41.9	35	8	AZ417198	1M0192H13	
860	8.8	41.9	30	8	AZ759753	AZ759753 1M0552O13	933	8.8	41.9	35	8	AZ511217	1M0356H11	
861	8.8	41.9	30	8	BX001445	BX001445 Arabidops	934	8.8	41.9	35	8	AZ610544	1M0435F24	
862	8.8	41.9	30	9	DR42M15T	DR42M15T	935	8.8	41.9	35	8	BH128269	BH128269	
863	8.8	41.9	30	9	DR43D1T	DR43D1T	936	8.8	41.9	35	8	BH846699	SALK_0098	
864	8.8	41.9	30	9	DR43K4T	DR43K4T	937	8.8	41.9	35	8	DR10P1T	DR10P1T	
865	8.8	41.9	30	9	TA272C09Q	TA272C09Q	938	8.8	41.9	35	9	DR7M21T	AL737949 Danio rer	
866	8.8	41.9	30	9	CG708764	CG708764 T. brucei	939	8.8	41.9	35	9	CL529717	Danio rer	
867	8.8	41.9	31	1	AA999756	AA999756 os93e04.s	940	8.8	41.9	36	4	BI761983	BI761983 603048930	
868	8.8	41.9	31	1	AI582089	AI582089 ar96c09.x	941	8.8	41.9	36	7	H97116	H97116 Yv89h06.r1	
869	8.8	41.9	31	1	AV845243	AV845243 AV845243	942	8.8	41.9	36	7	T64414	T64414 Yc48e08.s1	
870	8.8	41.9	31	6	CF313407	CF313407 HD--01-I1	943	8.8	41.9	36	7	T65804	T65804 Yc11h12.s1	
871	8.8	41.9	31	6	CF313473	CF313473 HD--01-J2	944	8.8	41.9	36	8	BH810737	BH810737 SALK_0511	
872	8.8	41.9	31	6	CF313764	CF313764 HD--02-A0	945	8.8	41.9	36	9	AL752038	Arabidops	
873	8.8	41.9	31	6	CF316529	CF316529 HD--05-N1	946	8.8	41.9	36	9	DR43H15T	AL981997 Danio rer	
874	8.8	41.9	31	6	CF319713	CF319713 HD--10-F0	947	8.8	41.9	36	9	DR43L19T	AL987312 Danio rer	
875	8.8	41.9	31	6	CF336854	CF336854 JMT--07-B	948	8.8	41.9	36	9	DR43M4T	Danio rer	
876	8.8	41.9	31	6	CF337032	CF337032 JMT--07-F	949	8.8	41.9	36	9	TA127A09P	AL462753 T. brucei	
877	8.8	41.9	31	6	CF337142	CF337142 JMT--07-H	950	8.8	41.9	36	9	CL213621	CL213621 W126B07 G	
878	8.8	41.9	31	8	AZ596685	AZ596685 1M0410A07	951	8.8	41.9	36	9	AG203210	Pan trogl	
879	8.8	41.9	31	8	AZ815238	AZ815238 2M0083B23	952	8.8	41.9	37	1	AA871389	AA871389 vq34g05.r	
880	8.8	41.9	31	8	AZ832018	AZ832018 2M0112B11	953	8.8	41.9	37	1	AA103225	AA103225 mo23g08.r	
881	8.8	41.9	31	9	DR1566T	DR1566T	954	8.8	41.9	37	1	AI565790	AI565790 tn20d12.x	
882	8.8	41.9	31	9	DR43B24T	DR43B24T	955	8.8	41.9	37	1	AA190625	AA190625 zp86e08.s	
883	8.8	41.9	31	9	DR43B2T	DR43B2T	956	8.8	41.9	37	1	AA231248	AA231248 mw38h11.r	
884	8.8	41.9	31	9	DR43J7T	DR43J7T	957	8.8	41.9	37	1	AA457896	AA457896 v7f3f10.r	
885	8.8	41.9	31	9	DR43O8T	DR43O8T	958	8.8	41.9	37	1	AA482567	AA482567 zt34e07.s	
886	8.8	41.9	31	9	DR48D10T	DR48D10T	959	8.8	41.9	37	1	AA625732	AA625732 ad10h09.s	
887	8.8	41.9	31	9	DR48K10T	DR48K10T	960	8.8	41.9	37	8	AZ460879	AZ460879 1M0266022	
888	8.8	41.9	31	9	CC887244	CC887244 SALK_1498	961	8.8	41.9	37	8	BH759504	BH759504 KG04663-s-5	
889	8.8	41.9	32	4	B1223057	B1223057 602942007	962	8.8	41.9	37	9	DR21K7T	DR21K7T	
890	8.8	41.9	32	6	CF313280	CF313280 HD--01-F1	963	8.8	41.9	38	1	AU008661	AU008661	
891	8.8	41.9	32	6	CF313422	CF313422 HD--01-I1	964	8.8	41.9	38	1	AV833104	AV833104	
892	8.8	41.9	32	6	CF313772	CF313772 HD--02-A1	965	8.8	41.9	38	4	BI453898	BI453898 603174776	
893	8.8	41.9	32	6	CF316885	CF316885 HD--06-F2	966	8.8	41.9	38	4	BJ082600	BJ082600	
894	8.8	41.9	32	8	AZ597602	AZ597602 1M0411P03	967	8.8	41.9	38	6	CF297975	CF297975 7LEAF--01	
895	8.8	41.9	32	8	AZ660571	AZ660571 1M0538C13	968	8.8	41.9	38	8	T73578	T73578 Yc36d06.s1	
896	8.8	41.9	32	8	AZ772645	AZ772645 1M0583N09	969	8.8	41.9	38	8	AZ346775	AZ346775 1M0082J08	
897	8.8	41.9	32	8	AZ779073	AZ779073 2M0014N20	970	8.8	41.9	38	8	AZ596174	AZ596174 1M0409115	
898	8.8	41.9	32	8	AZ989128	AZ989128 2M0272D24	971	8.8	41.9	38	8	BZ287177	SALK_0205	
899	8.8	41.9	32	9	DR1009T	DR1009T	972	8.8	41.9	38	9	DR43C7T	Danio rer	
900	8.8	41.9	32	9	DR14123T	DR14123T	973	8.8	41.9	38	9	DR48U2T	AL982936 Danio rer	


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974 8.8 41.9 38 9 CC885168
975 8.8 41.9 39 1 AU006742
976 8.8 41.9 39 4 BJ047458
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978 8.8 41.9 39 8 AZ416776
979 8.8 41.9 39 9 BX894937
980 8.8 41.9 39 9 DR1L3T
981 8.8 41.9 39 9 DR43P11T
982 8.8 41.9 39 9 DRJ31D02Q
983 8.8 41.9 39 9 CL661996
984 8.8 41.9 39 9 AG198761
985 8.8 41.9 40 1 AA666796
986 8.8 41.9 40 1 AA980528
987 8.8 41.9 40 1 AA983863
988 8.8 41.9 40 1 AI089080
989 8.8 41.9 40 1 AI140587
990 8.8 41.9 40 1 AI174290
991 8.8 41.9 40 1 AI208979
992 8.8 41.9 40 1 AI219362
993 8.8 41.9 40 1 AA199222
994 8.8 41.9 40 1 AV851328
995 8.8 41.9 40 1 AV967687
996 8.8 41.9 40 4 BI158571
997 8.8 41.9 40 4 BM394053
998 8.8 41.9 40 7 CO786949
999 8.8 41.9 40 8 AZ433386
1000 8.8 41.9 40 8 AZ438011

CC885168 SALK 1464
AU006742 AU006742
BJ047458 BJ047458
H26408 Y155c02.s1
AZ416776 IM0192J07
BX894937 Arabidopsis
AL741519 Danio rerio
AL987184 Danio rerio
AL492033 T. brucei
CL661996 PRI0140b
AG198761 Pan trogl
AA666796 vm67C05.s
AA980528 ua42d03.r
AA983863 op63a03.s
AI089080 cu8h08.s
AI140587 ow84eil.s
AI174290 am67b06.s
AI208979 qm29h02.x
AI219362 qg14e08.x
AA199222 mv43a11.r
AV851328 AV851328
AV967687 AV967687
BI158571 602922323
BM394053 50072-2-1
CO786949 BL287D_B0
AZ433386 IM0219A14
AZ438011 IM0226B20

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ALIGNMENTS

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RESULT 1
BX547835/c 34 bp DNA linear GSS 04-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-548F05-020587,
DEFINITION genomic survey sequence.
ACCESSION BX547835
VERSION BX547835.1 GI:32440655
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weisshaar, B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse Genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4
Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.
Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

```

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g40320. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

Location/Qualifiers

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/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-548F05-020587"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 61.9%; Score 13; DB 9; Length 34;
 Best Local Similarity 76.2%; Pred. No. 6.1e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGATGCCAGATTACTGGC 21

Db 22 AACGCATGCCAAGTAGTGAC 2

RESULT 2

DR10119T

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 38)

Humphray, S.J., Huckle, E. and Hunt, S.E.

Direct Submission

Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:

humquerry@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 10I19. 10I19 is

part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

Location/Qualifiers

1..38

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="DKEY-10I19"

/tissue_type="Testis"

/note="vector pIndigoBAC-536"

ORIGIN

Query Match 61.0%; Score 12.8; DB 9; Length 38;

Best Local Similarity 87.5%; Pred. No. 7.9e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTG 19


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Db      21 GCATCAAGCTTACTG 36

RESULT 3
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LOCUS
DEFINITION uc566g08.rl Soares mammary_gland NbMMG Mus musculus cDNA clone
IMAGE:1430654 5', similar to TR:Q27125 Q27125 CATHEPSIN B-LIKE
PROTEASE. ;, mRNA sequence.
ACCESSION A1182864
VERSION uc566g08.rl
KEYWORDS 37 bp mRNA linear EST 08-OCT-1998
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:914722
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 30.
Location/Qualifiers
1. .37
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1430654"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland NbMMG"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCAATCTGAAGTCGAGCGCGCGAATGTTTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Patima
Bonaldo."
ORIGIN
Query Match 60.0%; Score 12.6; DB 1; Length 37;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATCCAGATTACTG 19
|||||
Db 3 AGCACATCCACAGTACTG 21

RESULT 4
A1284041
LOCUS
DEFINITION qt72d04.xl NCI CGAP Eso2 Homo sapiens cDNA clone IMAGE:1960807 3'
similar to SW:PRPL_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO
;contains MSRI.t2 MSRI repetitive element ;, mRNA sequence.
ACCESSION A1284041
VERSION qt72d04.xl
KEYWORDS 37 bp mRNA linear EST 13-MAY-1999
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40Up from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1960807"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Eso2"
/note="Organ: esophagus; Vector: pCMV-SPORT6; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.1 kb. Life Technologies
catalog #: 11502-010"
ORIGIN
Query Match 60.0%; Score 12.6; DB 1; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGG 20
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Db 22 GCGCGCGCCAGGTTTCTGG 4

RESULT 5
A1561150/c
LOCUS
DEFINITION tg37a08.xl NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2210966 3'
similar to TR:O14975 O14975 VERY-LONG-CHAIN ACYL-COA SYNTHETASE. ;,
mRNA sequence.
ACCESSION A1561150
VERSION tg37a08.xl
KEYWORDS 37 bp mRNA linear EST 13-MAY-1999
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

```

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1275 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1
 POLYA=No.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2210966"
 /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP_Ut1"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN

Query Match 58.1%; Score 12.2; DB 1; Length 37;
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTAC 17
 Db 21 AGCGCATGCTGATTAC 5

RESULT 6

AG203065/c
 LOCUS 48 bp DNA linear GSS 06-MAR-2004
 DEFINITION Pan troglodytes DNA, clone: RP43-087A19.TJ, genomic survey sequence.
 AG203065
 VERSION GI:452335240
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM

REFERENCE 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE BAC end sequences of Library RP-43
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 48)
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE Direct Submission

JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/, Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
 PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACE3.6
 R.Site 1 : EcorI
 R.Site 2 : EcorI
 Location/Qualifiers

FEATURES

source

1..48
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-087A19.TJ"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 58.1%; Score 12.2; DB 9; Length 48;
 Best Local Similarity 82.4%; Pred. No. 1.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGGC 21
 Db 23 CATGCCGTGCTGCTGGC 7

RESULT 7

CG709763/c
 LOCUS 39 bp DNA linear GSS 20-OCT-2003
 DEFINITION 1119014G12.1EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.

ACCESSION CG709763
 VERSION CG709763.1 GI:37735669
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE 1 (bases 1 to 39)
 AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1119014 row: G column: 12
 Class: transposon-tagged.

FEATURES

source

1..39
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1119 - RescueMu Grid AA"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 57.1%; Score 12; DB 9; Length 39;
 Best Local Similarity 75.0%; Pred. No. 2.1e+05;

ORIGIN	LONRAGQ.									
Query Match	57.1%	Score 12;	DB 1;	Length 43;						
Best Local Similarity	75.0%;	Pred. No. 2.1e+05;								
Matches	15;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;	
Qy	2	GC	GATGCCAGATTACTGC	21						

```

ORIGIN
Query Match          57.1%; Score 12; DB 8; Length 43;
Best Local Similarity 75.0%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GCGCATGCCAGATTACTGGC 21
      | | | | | | | | | |
Db      28  GTGCATGCCAGATCGCOTGC 9

RESULT 10
BE907096
LOCUS
DEFINITION BE907096 45 bp mRNA linear EST 20-OCT-2000
601500842F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902555 5',
mRNA sequence.
ACCESSION BE907096
VERSION BE907096.1 GI:10400439
KEYWORDS EST.
SOURCE Homo sapiens (human)

```

```

ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 45)
JOURNAL        NIH-MGC http://mgc.nci.nih.gov/.
COMMENT        National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: ATCC
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: L1AM9705 row: d column: 12
                High quality sequence stop: 45.
FEATURES       Location/Qualifiers
                1..45
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3902555"
                /tissue_type="epithelioid carcinoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 70"
                /notes="Organ: Pancreas; Vector: pCMV-SPORT6; Site: 1; NotI;
                Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.1 Kb. Library constructed by Life
                Technologies."
ORIGIN
Query Match      57.1%; Score 12; DB 2; Length 45;
Best Local Similarity 75.0%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 AGCGCATGCCAGATTACTGG 20
      |||||
Db      5 AGTCATCGCAGATGCTGG 24

RESULT 11
CL423735      48 bp DNA linear GSS 16-MAR-2004
LOCUS         01S0749-01C1-F01 UniformMu MutAIL Library Zea mays genomic clone
DEFINITION    01S0749-01C1-F01, genomic survey sequence.
ACCESSION     CL423735
VERSION       CL423735.1 GI:45501779
KEYWORDS      GSS.
SOURCE        Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE     1 (bases 1 to 48)
AUTHORS       Latschew.S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE         Sequence tagged transposon insertions from the UniformMu maize
                population
JOURNAL        Unpublished (2003)
COMMENT        Contact: Donald R. McCarty
                Plant Molecular and Cellular Biology Program
                University of Florida
                PO 110690 Gainesville, FL 32611-0690, USA
                Tel: 352-392-1928 x322
                Email: drm@ufl.edu
                Sequence flanking probable Mu insertion site in UniformMu
                line: 01S0749-01, Primer set: C
                Class: transposon insertion site.
FEATURES       Location/Qualifiers
                1..48
                /organism="Zea mays"
                /mol_type="genomic DNA"

```

```

/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0749-01C1-F01"
/clone_lib="UniformMu MutAIL Library"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
ORIGIN
Query Match      57.1%; Score 12; DB 9; Length 48;
Best Local Similarity 75.0%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 GCGCATGCCAGATTACTGGC 21
      |||||
Db      4 GCGCATGCCAGGTAATGGGC 23

RESULT 12
AUI02389/c      50 bp mRNA linear EST 28-JAN-2004
LOCUS         AUI02389 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION    AUI02389 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION     AUI02389
VERSION       AUI02389.1 GI:13551909
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 50)
AUTHORS       Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
                Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
                Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
                Diverse transcriptional initiation revealed by fine, large-scale
                mapping of mRNA start sites
TITLE          EMBL Rep. 2 (5), 388-393 (2001)
JOURNAL        21270072
MEDLINE        11375929
COMMENT        Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: yusuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                Sugano,S. Construction and characterization of a full
                length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                149-156 (1997).
FEATURES       Location/Qualifiers
                1..50
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="ADSH01565"
                /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      57.1%; Score 12; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AGCGCATGCCAGATTACTGGC 21
      |||||
Db      34 AGCCGCTGCTGATCNCITGGC 14

RESULT 13
TA329D01Q

```

LOCUS TA329D01Q 36 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 329d01, reverse sequence,
 genomic survey sequence.
 ACCESSION AL492403
 VERSION AL492403.1 GI:11868665
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Trypanosoma brucei
 Trypanosomatidae; Kinetoplastida; Trypanosomatidae;
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
 Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
 Melville S.E., Rajandream M.A. and Barrell B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The V + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsavedetigr.org
 DETAILS OF T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 FEATURES
 source
 1. .36
 Location/Qualifiers
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="329d01"
 ORIGIN
 Query Match 56.2%; Score 11.8; DB 9; Length 36;
 Best Local Similarity 86.7%; Pred. No. 2.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 GCGCATGCCAGATTA 16
 |||||
 Db 19 GCCCATGCCAGACTA 33
 RESULT 14
 CR358600/c
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-729F02-025222,
 genomic survey sequence.
 ACCESSION CR358600
 VERSION CR358600.1 GI:45541522
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.
 TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 MEDLINE 22755829
 PUBMED 12874060
 REFERENCE 2
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weisshaar, B.

TTITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 MEDLINE 23117147
 PUBMED 14756321
 REFERENCE 3
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
 Weisshaar, B.
 TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050
 REFERENCE 4 (bases 1 to 44)
 AUTHORS Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 COMMENT This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 TSK6. Details on the protocols used for generation of the sequence
 are described in References 1-3. The sequences are generated at the
 MPI for Plant Breeding Research in the context of the GABI-Kat
 project. GABI-Kat is part of the German Plant Genomics program
 designated 'GABI'. Information on line availability can be found
 at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
 FEATURES
 source
 1. .44
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-729F02-025222"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (Ti) which were transformed with the T-DNA from
 vector pGAB1 (GenBank accession number: AY529716). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."
 ORIGIN
 Query Match 56.2%; Score 11.8; DB 9; Length 44;
 Best Local Similarity 86.7%; Pred. No. 2.7e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 AGCGCATGCCAGATT 15
 |
 Db 18 ATCGCATGCCACATT 4
 RESULT 15
 CG711376/c
 LOCUS 1119021B09.x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
 DEFINITION survey sequence.
 ACCESSION CG711376
 VERSION CG711376.1 GI:37737282
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

EST.	
KEYWORDS	
SOURCE	Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM	Magnaporthe grisea
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
REFERENCE	1 (bases 1 to 31)
AUTHORS	Ebbols,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,C.,

Bhatterai, K. and Dean, R.A.
 Expressed sequence tags from the rice blast fungus, Magnaporthe
 grisea
 Unpublished (2002)
 Contact: Ebbole DJ
 Department of Plant Pathology & Microbiology
 Texas A&M University
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
 Tel: 979 845 4831
 Fax: 979 845 6483
 Email: d-ebbole@tamu.edu
 Chromatogram file of this sequence is available, see contact
 person;

PCR Primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgmt009 row: B column: 10
 Seq primer: T3

FEATURES

source

```
1. .31
/organism="Magnaporthe grisea"
/mol_type="mrna"
/strain="4091-5-8 X 4136-4-3"
/db_xref="taxon:148305"
/clone="mgmt009xB10"
/sex="Mat1-2 and Mat1-1 mixed culture"
/cell_type="mixed sexual development"
/dev_stage="asci, ascospores, perithecia, mycelium"
/clone_lib="Mated culture"
/note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI;
Two mating types were co-cultivated over a filter paper on
oatmeal agar medium. After three days at 25 C plates were
transferred to 21 C. Perithecia with asci and ascospores
formed at the beginning of the third week. Material was
collected by scraping tissue from the filter paper.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimmed according to the
alignment, otherwise sequence quality was assessed using
phredPhrap version 991019 and trimmed according to phd
files (0.05) and for vector segs."
```

ORIGIN

```
Query Match      55.2%; Score 11.6; DB 6; Length 31;
Best Local Similarity 77.8%; Pred. No. 3.2e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 4 GCATGCCAGATTACTGCG 21
   |||||
Db 26 GCATGCCAGTGTACATGC 9
```

```
RESULT 19
AZ828889 LOCUS
DEFINITION 2M0106L07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0106L07 F, genomic survey sequence.
ACCESSION AZ828889
VERSION AZ828889.1 GI:12998797
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

```

```
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL Unpublished (2000)
 CONTACT: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0106 row: L column: 07
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 32.

FEATURES

source

```
1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0106L07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ORIGIN

```
Query Match      55.2%; Score 11.6; DB 8; Length 32;
Best Local Similarity 77.8%; Pred. No. 3.2e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 GCGCATGCCAGATTACTG 19
   |||||
Db 1 GCGAATGCCAGTCACTG 18
```

```
RESULT 20
AZ471345 LOCUS
DEFINITION 1M0285I119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0285I19 R, genomic survey sequence.
ACCESSION AZ471345
VERSION AZ471345.1 GI:10629470
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

```

```
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL Unpublished (2000)
 CONTACT: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0285 row: 1 column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 41.
 Location/Qualifiers
 1. 41
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0285119"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 55.2%; Score 11.6; DB 8; Length 41;
 Best Local Similarity 77.8%; Pred. No. 3.4e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGGC 21
 |||||
 Db 20 GTATGGCAGAAACTGGC 37

RESULT 21
 TA92F10Q/c
 LOCUS
 DEFINITION
 T. brucei sheared genomic DNA clone 92f10, reverse sequence, genomic survey sequence.
 ACCESSION
 AL462451
 VERSION
 AL462451.1 GI:11862749
 KEYWORDS
 GSS.
 SOURCE
 Trypanosoma brucei
 ORGANISM
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 42)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1. 42
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="92f10"

ORIGIN
 Query Match 55.2%; Score 11.6; DB 9; Length 42;
 Best Local Similarity 77.8%; Pred. No. 3.4e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGGC 21
 |||||
 Db 23 GCAGCCAGATAGGGGC 6

RESULT 22
 AZ503905
 LOCUS
 DEFINITION
 1M0343E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0343E20 R, genomic survey sequence.
 ACCESSION
 AZ503905
 VERSION
 AZ503905.1 GI:10685221
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Chordata; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 49)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0343 row: E column: 20
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 49.
 Location/Qualifiers
 1. 49
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0343E20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.2%; Score 11.6; DB 8; Length 49;
Best Local Similarity 77.8%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGCC 21
|||||

Db 14 GCCTGCTGGTTACTGCC 31
|||||

RESULT 23
AB082362
LOCUS Drosophila melanogaster DNA, clone:1(2)SH2 1052, genomic survey
DEFINITION sequence.
ACCESSION AB082362
VERSION AB082362.1 GI:23307398
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
AUTHORS Oh,S.W., Kingsley,T., Shin,H.H., Zheng,Z., Chen,H.W., Chen,X., Wang,H., Ruan,P., Moody,M. and Hou,S.X.
TITLE A p-element insertion screen identified mutations in 455 novel essential genes in Drosophila

JOURNAL Genetics 163 (1), 195-201 (2003)
MEDLINE 22474228
PUBMED 12586707
REFERENCE 2 (bases 1 to 50)
AUTHORS Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2002) Suan Oh, The Laboratory of Immunobiology, National Institutes of Health, National Cancer Institute, Frederick, 1050 Boyles st., Frederick, Maryland 21702-1201, USA (E-mail:ohsuan@mail.ncifcrf.gov, Tel:1-301-846-7314, Fax:1-301-846-6145)

FEATURES
source Location/Qualifiers
1..50
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="1(2)SH2 1052"

ORIGIN

Query Match 55.2%; Score 11.6; DB 9; Length 50;
Best Local Similarity 73.7%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AGCGATCCGATTACTG 19
|||||

Db 32 AGACTGGCCATTACTG 50
|||||

RESULT 24
BX651219/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-55SH12-021706,
DEFINITION genomic survey sequence.
ACCESSION BX651219
VERSION BX651219.1 GI:37607607
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weishaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
MEDLINE 14682050
PUBMED
REFERENCE 4 (bases 1 to 31)
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT It indicates an insertion close to or within gene At3g48830. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source

1..31
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-55SH12-021706"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 54.3%; Score 11.4; DB 9; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.1e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.3%; Score 11.4; DB 8; Length 41;
Best Local Similarity 92.3%; Pred. No. 4.3e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCCAGATTACTG 19
| | | | |
Db 23 TGCCATATTACTG 35

RESULT 28

AZ369672

LOCUS

DEFINITION MW10120E21F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0120E21 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0120 row: E column: 21
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 47.

Location/Qualifiers
1. 47
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0120E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"

FEATURES

source

1. 47
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0120E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.3%; Score 11.4; DB 8; Length 47;
Best Local Similarity 71.4%; Pred. No. 4.4e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGCG 21
| | | | |
Db 7 ATCGCGTGCACACAGACTGTC 27

RESULT 29

CL302431

LOCUS

DEFINITION CL302431 G058B11 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone G058B11, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

On Jun 30, 2004 this sequence version replaced gi:42743260.
Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
USCEO gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=G058B11', ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
1' Inhouse Sequence Identifier: 17086
Class: Gene Trap.

Location/Qualifiers
1. 48
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G058B11"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129S6/SvEvTac] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"

FEATURES

source

1. 48
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G058B11"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129S6/SvEvTac] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"

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ORIGIN
Query Match      54.3%; Score 11.4; DB 9; Length 48;
Best Local Similarity 71.4%; Pred. No. 4.4e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
    ||||| ||||| ||||| |||||
Db 3 AGTGGATCTCACATTTCTGGC 23

RESULT 30
AUI04945
LOCUS AUI04945 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI04945 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION HRC05721, mRNA sequence.
VERSION AUI04945
KEYWORDS AUI04945.1 GI:13554466
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J.,
Hata.H., Ota.T., Isoqai.T., Tanaka.T., Morishita,S., Okubo,K.,
Sakaki.Y., Nakamura.Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PubMed 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HRC05721"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      54.3%; Score 11.4; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 4.4e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
    ||||| ||||| ||||| |||||
Db 27 AGCGCTGCGAGCAGATGGC 47

RESULT 31
AA641303/c
LOCUS AA641303 34 bp mRNA linear EST 27-OCT-1997
DEFINITION nr78d09.s1 NCI CGAP Pr24 Homo sapiens cDNA clone IMAGE:1174097 3,
similar to TR:G440389 G440389 EPSILON-COP. ; mRNA sequence.
ACCESSION AA641303
VERSION AA641303.1 GI:2566553
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 34)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..34
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1174097"
/tissue_type="invasive tumor (cell line)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI CGAP Pr24"
/note="Organ: prostate; Vector: Bluescript SK-; Site:1:
EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Invasive prostate tumor cell line (HPV
immortalized). 5' adaptor sequence: 5' GAATTCGGCAGAG 3'
3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
Average insert size: 1.0 kb."

ORIGIN
Query Match      53.3%; Score 11.2; DB 1; Length 34;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTAC 17
    ||||| ||||| |||||
Db 33 GCGCTGCCACATTGC 18

RESULT 32
AUI040922/c
LOCUS AUI040922 35 bp mRNA linear EST 04-DEC-1998
DEFINITION J0820609 3', mRNA sequence.
ACCESSION AUI040922
VERSION AUI040922.1 GI:3955087
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 35)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Ko.M.S.H., Kitchen,J.R., Wang,X., Threat,T.A., Sun,T.,
DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Lim,M.K. and
Doi,H.
Systematic analyses of genes expressed in 4-cell mouse embryo (The
ERATO/Doi Project at Wayne State University)
Unpublished (1998)
Contact: Hirofumi Doi
Doi Biosymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bioa.jst.go.jp.
Location/Qualifiers
1..35
source
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"

```

```

/db_xref="taxon:10090"
/clone="J0820609"
/dev_stages="four-cell-embryo"
/clone_lib="Mouse four-cell-embryo cDNA"

ORIGIN
Query Match      53.3%; Score 11.2; DB 1; Length 35;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGCG 21
    ||| ||||| |||||
Db 16 ATGTCAGATCACTGAC 1

RESULT 33
AU040926/c
LOCUS AU040926 35 bp mRNA linear EST 04-DEC-1998
DEFINITION AU040926 Mouse four-cell-embryo cDNA Mus musculus cDNA clone
ACCESSION J0820609 3', mRNA sequence.
VERSION AU040926
KEYWORDS AU040926.1 GI:3955091
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
AUTHORS Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T.,
Depalma, G.E., Liang, Y., Kargul, G.J., Sharara, R., Lim, M.K. and
Doi, H.
TITLE Systematic analyses of genes expressed in 4-cell mouse embryo (The
JOURNAL ERATO/Doi Project at Wayne State University)
COMMENT Unpublished (1998)
Contact: Hirofumi Doi
Doi Biosymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdo@bioa.jst.go.jp.

FEATURES
source
1. .35
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0820609"
/dev_stages="four-cell-embryo"
/clone_lib="Mouse four-cell-embryo cDNA"

ORIGIN
Query Match      53.3%; Score 11.2; DB 1; Length 35;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGCG 21
    ||| ||||| |||||
Db 16 ATGTCAGATCACTGAC 1

RESULT 34
DR4J11T
LOCUS DR4J11T 35 bp DNA linear GSS 27-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-4J11, genomic survey sequence.
ACCESSION AL736749
VERSION AL736749.1 GI:21350789
KEYWORDS GSS
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 35)
AUTHORS Humphray, S.J., Huckle, E. and Hunt, S.E.

```

```

Direct Submission
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
hnmquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 4J11. 4J11 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
source
1. .35
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-4J11"
/tissue type="Testis"
/note="vector pIndigoBAC-536"

ORIGIN
Query Match      53.3%; Score 11.2; DB 9; Length 35;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
    ||||| ||||| |||||
Db 20 GCATGCCAGCTTATTG 35

RESULT 35
AZ821751/c
LOCUS AZ821751 37 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0094H09R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0094H09 R, genomic survey sequence.
ACCESSION AZ821751
VERSION AZ821751.1 GI:12991659
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: H column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
source
1. .37
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0094H09"
/sex="Male"
/lab hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 37;
 Best Local Similarity 81.2%; Pred. No. 5.4e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGATGCCAGATTA 16
 |||||
 Db 16 AGGAATGCCAGATTA 1

RESULT 36
 AL760654/c
 LOCUS
 DEFINITION 40 bp DNA linear GSS 01-APR-2004
 Arabidopsis thaliana T-DNA flanking sequence GK-200F07-014483,
 genomic survey sequence.
 ACCESSION AL760654
 VERSION AL760654.1 GI:21499948
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)
 MEDLINE 22753829
 PUBMED 12874060

REFERENCE 2
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 MEDLINE 23117147
 PUBMED 14756321

REFERENCE 3
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
 Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 MEDLINE 14682050
 PUBMED 14756321

REFERENCE 4
 (bases 1 to 40)
 Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.
 Direct Submission
 Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion close to or within gene At3g14440.
 Details on the protocols used for generation of the sequence are
 described in References 1-3. The sequences are generated at the MPI
 for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated
 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
 source

Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-200F07-014483"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (Ti) which were transformed with the T-DNA from
 vector PAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 40;
 Best Local Similarity 81.2%; Pred. No. 5.4e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCATGCCAGATTACT 18
 |||||
 Db 34 CGCTTGGCGTTACT 19

RESULT 37
 AZ471345/c
 LOCUS
 DEFINITION 41 bp DNA linear GSS 04-OCT-2000
 1M0285119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0285119 R, genomic survey sequence.

ACCESSION AZ471345
 VERSION AZ471345.1 GI:10629470
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 41)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0285 row: 1 column: 19
 Seq primer: CACACAGGAAACAGTCATGACC
 Class: plasmid ends
 High quality sequence stop: 41.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0285119"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

FEATURES
 source

Location/Qualifiers
 1..41
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0285119"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 41;
Best Local Similarity 81.2%; Pred. No. 5.5e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGGC 21
||||| ||| |||
Db 39 ATGCCAGTTTCTGCC 24

RESULT 38
CA853264/c
LOCUS
DEFINITION 32 bp mRNA linear EST 01-AUG-2003
B06C01.5, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 32)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers

FEATURES

source
1..32
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clones="B06C01"
/tissue_type="Roots"
/dev_stages="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="vector: phluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

ORIGIN

Unpublished (2000)

Query Match 52.4%; Score 11; DB 6; Length 32;
Best Local Similarity 73.7%; Pred. No. 6.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCGCATCCAGATTACTGGC 20
||||| ||| ||| |||
Db 21 GTGGTCGAGATTATCGG 3

RESULT 39

AJ746715

LOCUS

DEFINITION 41 bp mRNA linear EST 07-JUL-2004

AJ746715

clone ap03_6_D02, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)

Sus scrofa

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

AUTHORS

Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.

and Dixon, L.

development of a porcine cDNA microarray

Unpublished (2004)

CONTACT: Hopwood PA

Dept. of Preclinical Veterinary Sciences

Royal School for Veterinary Studies

Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM

Sequencing was performed by ARK genomics. This clone is available

from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,

UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES

source

1..41

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="ap03_6_D02"

/tissue_type="muscle"

/cell_type="macrophage"

/clone_lib="muscle - muscle minus alveolar macrophage"

ORIGIN

Query Match 52.4%; Score 11; DB 1; Length 41;

Best Local Similarity 73.7%; Pred. No. 6.9e+05;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GCGATGCCAGATTACTGGC 21

||||| ||| ||| |||

Db 12 CGCACCCAGCTTCTGTC 30

RESULT 40

AZ447897/c

LOCUS

DEFINITION 43 bp DNA linear GSS 04-OCT-2000

clone UUGC1M0245G17 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Search completed: November 23, 2004, 22:21:20
Job time : 1059.82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 378.157 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21
Sequence: 1 tcgcgtacgggtctaatgacgc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	21	100.0	21	6	BD181363	BD181363	A method
c 2	21	100.0	21	6	BD181378	BD181378	A method
	21	100.0	21	6	AX523943	AX523943	Sequence
3	21	100.0	21	6	AX524841	AX524841	Sequence
4	21	100.0	21	6	AX524856	AX524856	Sequence
c 5	21	100.0	21	6	BD227377	BD227377	Secreted
c 6	13.6	64.8	29	6	AX752106	AX752106	Sequence
7	12.8	61.0	30	6	AX295474	AX295474	Sequence
8	12.6	60.0	20	6	AX290841	AX290841	Sequence
9	12.6	60.0	24	6	BD260345	BD260345	Methods.
10	12.6	60.0	26	6	AX044290	AX044290	Sequence
11	12.6	60.0	26	6	AR168721	AR168721	Sequence
12	12.6	60.0	31	6	AR047950	AR047950	Sequence
13	12.6	60.0	33	6	AR334533	AR334533	Sequence
c 14	12.6	60.0	38	6	AR335779	AR335779	Sequence
c 15	12.6	60.0	38	6	AR336409	AR336409	Sequence
c 16	12.6	60.0	38	6	AR455837	AR455837	Sequence
17	12.6	60.0	38	6	AX219207	AX219207	Sequence
c 18	12.6	60.0	38	6	AX219231	AX219231	Sequence
c 19	12.6	60.0	38	6	AX219231	AX219231	Sequence

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c	21	12.6	38	6	AX424618 Sequence
c	22	12.6	38	6	AX424731 Sequence
c	23	12.6	38	6	AX581188 Sequence
c	24	12.6	38	6	AX581359 Sequence
c	25	12.6	42	6	AX5234 Sequence 5
26	12.4	59.0	20	6	AX295733 Sequence
27	12.4	59.0	24	6	AX291100 Sequence
28	12.4	59.0	34	6	AX464504 Sequence
29	12.4	59.0	38	6	AR046887 Sequence
30	12.4	59.0	38	6	IS3939 Sequence 16
31	12.4	59.0	38	6	AX220204 Sequence
32	12.2	58.1	20	6	AR314417 Sequence
33	12.2	58.1	21	6	AR364921 Sequence
34	12.2	58.1	22	6	AX392054 Sequence
c	35	12.2	32	6	AX755148 Sequence
c	36	12.2	32	6	AX755156 Sequence
37	12.2	58.1	37	6	AX351239 Sequence
38	12.2	58.1	37	6	AX581788 Sequence
39	12.2	58.1	37	6	AX581793 Sequence
40	12.2	58.1	37	6	AX581826 Sequence
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c	42	12.2	41	6	AR238615 Sequence
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c	46	12.2	29	6	AR474494 Sequence
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c	48	12.2	29	6	AX260008 Sequence
c	49	12.2	29	6	AX262370 Sequence
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c	57	12.2	38	6	AR332572 Sequence
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c	61	12.2	38	6	AX580628 Sequence
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63	12.2	57.1	45	6	BD096959 Delivery
64	11.8	56.2	15	6	BD208648 Enzymatic
65	11.8	56.2	21	6	BD014023 Plant gen
c	66	11.8	28	6	AS6797 Sequence 5
c	67	11.8	29	6	BD198088 Method an
68	11.6	55.2	20	6	E30564 Neurogesi
69	11.6	55.2	20	6	AR268852 Sequence
c	70	11.6	20	6	AX295529 Sequence
c	71	11.6	24	6	AX290896 Sequence
c	72	11.6	24	6	AX291942 Sequence
c	73	11.6	25	6	BD225557 Assay for
74	11.6	55.2	26	6	BD260282 Methods.
75	11.6	55.2	26	6	BD260303 Methods.
76	11.6	55.2	26	6	AX044227 Sequence
77	11.6	55.2	26	6	AX044248 Sequence
c	78	11.6	36	6	BD259716 Regulatio
c	79	11.6	36	6	BD259812 Regulatio
80	11.6	55.2	37	6	AR492124 Sequence
81	11.6	55.2	37	6	AX581783 Sequence
82	11.6	55.2	37	6	AX581844 Sequence
83	11.6	55.2	37	6	BD095159 Novel met
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c	85	11.6	38	6	AR334672 Sequence
c	86	11.6	38	6	AR334753 Sequence
c	87	11.6	38	6	AR334978 Sequence
c	88	11.6	38	6	AR334994 Sequence
c	89	11.6	38	6	AR335787 Sequence
c	90	11.6	38	6	AR336048 Sequence
c	91	11.6	38	6	AX219110 Sequence
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C 239	11	52.4	38	6	AR334792	AR334792 Sequence	C 312	11	52.4	38	6	AX219600	AX219600 Sequence
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C 243	11	52.4	38	6	AR334886	AR334886 Sequence	C 316	11	52.4	38	6	AX219685	AX219685 Sequence
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C 245	11	52.4	38	6	AR334926	AR334926 Sequence	C 318	11	52.4	38	6	AX219712	AX219712 Sequence
C 246	11	52.4	38	6	AR334958	AR334958 Sequence	C 319	11	52.4	38	6	AX219718	AX219718 Sequence
C 247	11	52.4	38	6	AR334973	AR334973 Sequence	C 320	11	52.4	38	6	AX219736	AX219736 Sequence
C 248	11	52.4	38	6	AR335053	AR335053 Sequence	C 321	11	52.4	38	6	AX219768	AX219768 Sequence
C 249	11	52.4	38	6	AR335059	AR335059 Sequence	C 322	11	52.4	38	6	AX219770	AX219770 Sequence
C 250	11	52.4	38	6	AR335101	AR335101 Sequence	C 323	11	52.4	38	6	AX219864	AX219864 Sequence
C 251	11	52.4	38	6	AR335155	AR335155 Sequence	C 324	11	52.4	38	6	AX222552	AX222552 Sequence
C 252	11	52.4	38	6	AR335186	AR335186 Sequence	C 325	11	52.4	38	6	AX222732	AX222732 Sequence
C 253	11	52.4	38	6	AR335196	AR335196 Sequence	C 326	11	52.4	38	6	AX222801	AX222801 Sequence
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C 256	11	52.4	38	6	AR335279	AR335279 Sequence	C 329	11	52.4	38	6	AX222863	AX222863 Sequence
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C 260	11	52.4	38	6	AR335816	AR335816 Sequence	C 333	11	52.4	38	6	AX222914	AX222914 Sequence
C 261	11	52.4	38	6	AR335824	AR335824 Sequence	C 334	11	52.4	38	6	AX222940	AX222940 Sequence
C 262	11	52.4	38	6	AR335844	AR335844 Sequence	C 335	11	52.4	38	6	AX222993	AX222993 Sequence
C 263	11	52.4	38	6	AR335851	AR335851 Sequence	C 336	11	52.4	38	6	AX228295	AX228295 Sequence
C 264	11	52.4	38	6	AR336019	AR336019 Sequence	C 337	11	52.4	38	6	AX228350	AX228350 Sequence
C 265	11	52.4	38	6	AR336039	AR336039 Sequence	C 338	11	52.4	38	6	AX228362	AX228362 Sequence
C 266	11	52.4	38	6	AR336085	AR336085 Sequence	C 339	11	52.4	38	6	AX228463	AX228463 Sequence
C 267	11	52.4	38	6	AR336116	AR336116 Sequence	C 340	11	52.4	38	6	AX228493	AX228493 Sequence
C 268	11	52.4	38	6	AR336127	AR336127 Sequence	C 341	11	52.4	38	6	AX228499	AX228499 Sequence
C 269	11	52.4	38	6	AR336189	AR336189 Sequence	C 342	11	52.4	38	6	AX273539	AX273539 Sequence
C 270	11	52.4	38	6	AR336231	AR336231 Sequence	C 343	11	52.4	38	6	AX273543	AX273543 Sequence
C 271	11	52.4	38	6	AR336250	AR336250 Sequence	C 344	11	52.4	38	6	AX273564	AX273564 Sequence
C 272	11	52.4	38	6	AR336267	AR336267 Sequence	C 345	11	52.4	38	6	AX273594	AX273594 Sequence
C 273	11	52.4	38	6	AR336279	AR336279 Sequence	C 346	11	52.4	38	6	AX273615	AX273615 Sequence
C 274	11	52.4	38	6	AR336308	AR336308 Sequence	C 347	11	52.4	38	6	AX273619	AX273619 Sequence
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C 305	11	52.4	38	6	AX219382	AX219382 Sequence	C 378	11	52.4	38	6	AX424913	AX424913 Sequence
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C 385	11	52.4	38	6	AX581157	Sequence	C 458	10.6	50.5	18	6	BD250577	Identific
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C 387	11	52.4	38	6	AX581242	Sequence	C 460	10.6	50.5	18	6	AR293681	Sequence
C 388	11	52.4	38	6	AX581278	Sequence	C 461	10.6	50.5	18	6	AX498002	Sequence
C 389	11	52.4	38	6	AX581286	Sequence	C 462	10.6	50.5	19	6	CO799895	Sequence
C 390	11	52.4	38	6	AX581302	Sequence	C 463	10.6	50.5	20	6	AX295232	Sequence
C 391	11	52.4	38	6	AX581352	Sequence	C 464	10.6	50.5	20	6	AX296546	Sequence
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C 393	11	52.4	38	6	AX581446	Sequence	C 466	10.6	50.5	22	6	AX922710	Sequence
C 394	11	52.4	38	6	AX581446	Sequence	C 467	10.6	50.5	24	6	AX56684	Sequence
C 395	11	52.4	40	6	AR095875	Sequence	C 468	10.6	50.5	24	6	BD260387	Methods.
C 396	11	52.4	40	6	AR167230	Sequence	C 469	10.6	50.5	24	6	AR261951	Sequence
C 397	11	52.4	40	6	AR361064	Sequence	C 470	10.6	50.5	24	6	AX044332	Sequence
C 398	11	52.4	40	6	AX767184	Sequence	C 471	10.6	50.5	24	6	AX181781	Sequence
C 399	11	52.4	40	6	AX767190	Sequence	C 472	10.6	50.5	24	6	AX290523	Sequence
C 400	11	52.4	42	6	AR007099	Sequence	C 473	10.6	50.5	24	6	AX290599	Sequence
C 401	11	52.4	42	6	AR034923	Sequence	C 474	10.6	50.5	24	6	AX291913	Sequence
C 402	11	52.4	42	6	AR111123	Sequence	C 475	10.6	50.5	24	6	BD077184	Method an
C 403	11	52.4	42	6	I75039	Sequence	C 476	10.6	50.5	26	6	BD260268	Methods.
C 404	11	52.4	44	6	BD086796	Sequence	C 477	10.6	50.5	26	6	BD260289	Methods.
C 405	11	52.4	44	6	AX752645	Sequence	C 478	10.6	50.5	26	6	BD260331	Methods.
C 406	11	52.4	44	6	AX752646	Sequence	C 479	10.6	50.5	26	6	BD260385	Methods.
C 407	11	52.4	50	6	AX952578	Sequence	C 480	10.6	50.5	26	6	BD260386	Methods.
C 408	11	52.4	50	6	BD199105	Method an	C 481	10.6	50.5	26	6	BD260395	Methods.
C 409	10.8	51.4	17	6	AR096607	Sequence	C 482	10.6	50.5	26	6	BD260396	Methods.
C 410	10.8	51.4	19	6	AR065350	Sequence	C 483	10.6	50.5	26	6	BD260398	Methods.
C 411	10.8	51.4	20	6	AR653528	Sequence	C 484	10.6	50.5	26	6	BD260399	Methods.
C 412	10.8	51.4	23	6	AX443621	Sequence	C 485	10.6	50.5	26	6	BD260400	Methods.
C 413	10.8	51.4	24	6	AX446991	Sequence	C 486	10.6	50.5	26	6	BD260401	Methods.
C 414	10.8	51.4	24	6	CO797626	Sequence	C 487	10.6	50.5	26	6	BD260402	Methods.
C 415	10.8	51.4	25	6	AX447603	Sequence	C 488	10.6	50.5	26	6	BD260403	Methods.
C 416	10.8	51.4	25	6	BD177071	Standard	C 489	10.6	50.5	26	6	BD260404	Methods.
C 417	10.8	51.4	27	6	BD207836	Enzymatic	C 490	10.6	50.5	26	6	BD260405	Methods.
C 418	10.8	51.4	27	6	BD208021	Enzymatic	C 491	10.6	50.5	26	6	AX044213	Sequence
C 419	10.8	51.4	27	6	AR185827	Sequence	C 492	10.6	50.5	26	6	AX044234	Sequence
C 420	10.8	51.4	27	6	AR191116	Sequence	C 493	10.6	50.5	26	6	AX044276	Sequence
C 421	10.8	51.4	27	6	AR191317	Sequence	C 494	10.6	50.5	26	6	AX044330	Sequence
C 422	10.8	51.4	29	6	BD199461	Method an	C 495	10.6	50.5	26	6	AX044331	Sequence
C 423	10.8	51.4	29	6	BD200040	Method an	C 496	10.6	50.5	26	6	AX044340	Sequence
C 424	10.8	51.4	29	6	BD252904	Regulatio	C 497	10.6	50.5	26	6	AX044341	Sequence
C 425	10.8	51.4	29	6	E11596	PCR primer	C 498	10.6	50.5	26	6	AX044342	Sequence
C 426	10.8	51.4	30	6	AR117368	Sequence	C 499	10.6	50.5	26	6	AX044343	Sequence
C 427	10.8	51.4	31	6	AR205147	Sequence	C 500	10.6	50.5	26	6	AX044344	Sequence
C 428	10.8	51.4	31	6	AR223351	Sequence	C 501	10.6	50.5	26	6	AX044345	Sequence
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C 431	10.8	51.4	34	6	AX068354	Sequence	C 504	10.6	50.5	26	6	AX044348	Sequence
C 432	10.8	51.4	34	6	AX357130	Sequence	C 505	10.6	50.5	26	6	AX044349	Sequence
C 433	10.8	51.4	34	6	AR056608	Sequence	C 506	10.6	50.5	26	6	AX044350	Sequence
C 434	10.8	51.4	36	6	AR114366	Sequence	C 507	10.6	50.5	26	6	AX322870	Sequence
C 435	10.8	51.4	36	6	AX058554	Sequence	C 508	10.6	50.5	28	6	AX109831	Sequence
C 436	10.8	51.4	36	6	AX063667	Sequence	C 509	10.6	50.5	29	6	AR456133	Sequence
C 437	10.8	51.4	37	6	CO802201	Sequence	C 510	10.6	50.5	30	6	AR481875	Sequence
C 438	10.8	51.4	37	6	AX776244	Sequence	C 511	10.6	50.5	30	6	AX792877	Sequence
C 439	10.8	51.4	38	6	AR045842	Sequence	C 512	10.6	50.5	30	6	BD103629	Method an
C 440	10.8	51.4	38	6	I52894	Sequence	C 513	10.6	50.5	31	6	E41691	Process for
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C 442	10.8	51.4	38	6	AR331074	Sequence	C 515	10.6	50.5	31	6	AX117935	Sequence
C 443	10.8	51.4	38	6	AR333021	Sequence	C 516	10.6	50.5	31	6	AX248288	Sequence
C 444	10.8	51.4	38	6	AX273974	Sequence	C 517	10.6	50.5	31	6	BD070102	Modified
C 445	10.8	51.4	38	6	AX424644	Sequence	C 518	10.6	50.5	31	6	AX236535	Sequence
C 446	10.8	51.4	38	6	AR080416	Sequence	C 519	10.6	50.5	32	6	AR256595	Sequence
C 447	10.8	51.4	39	6	AR092540	Sequence	C 520	10.6	50.5	34	6	AX938055	Sequence
C 448	10.8	51.4	39	6	AR122895	Sequence	C 521	10.6	50.5	35	6	BD209507	Enzymatic
C 449	10.8	51.4	39	6	AR123550	Sequence	C 522	10.6	50.5	36	6	BD259738	Regulatio
C 450	10.8	51.4	39	6	AR148367	Sequence	C 523	10.6	50.5	36	6	BD259739	Regulatio
C 451	10.8	51.4	39	6	AX484526	Sequence	C 524	10.6	50.5	36	6	BD259768	Regulatio
C 452	10.8	51.4	43	6	A05538	Oligonucleo	C 525	10.6	50.5	36	6	BD259773	Regulatio
C 453	10.8	51.4	45	6	AR001631	Sequence	C 526	10.6	50.5	36	6	BD259834	Regulatio
C 454	10.8	51.4	45	6	I09088	Sequence	C 527	10.6	50.5	36	6	BD259835	Regulatio
C 455	10.8	51.4	45	6	AR365316	Sequence	C 528	10.6	50.5	36	6	BD259864	Regulatio
C 456	10.8	51.4	45	6			C 529	10.6	50.5	36	6	BD259869	Regulatio
C 457	10.8	51.4	45	6			C 530	10.6	50.5	36	6		

C 531	10.6	50.5	36	6	BD259894	BD259894 Regulation	C 604	10.6	50.5	38	6	AR336224	AR336224 Sequence
C 532	10.6	50.5	37	6	I69247	I69247 Sequence 51	C 605	10.6	50.5	38	6	AR336243	AR336243 Sequence
C 533	10.6	50.5	37	6	AR253845	AR253845 Sequence	C 606	10.6	50.5	38	6	AR336260	AR336260 Sequence
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DEFINITION A method for determination of a nucleic acid using a control.
ACCESSION BD181363
VERSION BD181363.1 GI:30792281
KEYWORDS JP 2002335981-A/2.
SOURCE synthetic construct
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REFERENCE 1 (bases 1 to 21)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 2 26-NOV-2002;
COMMENT F HOFFMANN LA ROCHE AG
OS Artificial Sequence
EN JP 2002335981-A/2
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,
PC C12N15/00
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ACCESSION AX523943
VERSION AX523943.1 GI:25168874
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ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
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FEATURES Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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ACCESSION BD181378
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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 17 26-NOV-2002;
COMMENT F HOFFMANN LA ROCHE AG
PN JP 2002335981-A/17
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/69,G01N33/50,G01N33/53,G01N33/566,G01N33/58,
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ACCESSION AX523943
VERSION AX523943.1 GI:25168874
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: EP 1236804-A 2 04-SEP-2002;
FEATURES Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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DEFINITION Sequence 2 from Patent EP1236805.
ACCESSION AX524841
VERSION AX524841.1 GI:25169935
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 2 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
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ACCESSION AX524856
VERSION AX524856.1 GI:25169950
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 17 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
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DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION BD227377
VERSION BD227377.1 GI:33037147
KEYWORDS JP 2002522062-A/138.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A.C., Evans,C.,
Merberg,D., Treacy,M., Agostino,M.J., Ii,R.J.S., Spaulding,V.,
Wong,G.G., Clark,H.F. and Fechtel,K.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2002522062-A 138 23-JUL-2002;
GENETICS INSTITUTE INC
COMMENT OS Artificial Sequence
PN JP 2002522062-A/138
PD 23-JUL-2002
PF 13-AUG-1999 JP 2000565001
PR 14-AUG-1998 US 60/096622,17-AUG-1998 US 60/096815 PR
04-SEP-1998 US 60/099229,23-OCT-1998 US 60/105368 PR
08-JAN-1999 US 60/115234,12-FEB-1999 US 60/119931 PR
18-FEB-1999 US 60/120575,30-APR-1999 US 60/132020 PR
11-AUG-1999 US 60/148424
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COLLINS
PI RACIE,
PI CHERYL EVANS,DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,
PI ROBERT J STEININGER II,VIKKI SPAULDING,GORDON G WONG,HILARY F
PI CLARK,
PI KIM FECHTEL
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
PC A61P7/00,
PC A61P7/02,A61P7/04,A61P7/06,A61P13/00,A61P29/00,A61P35/00, PC
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PC A61P43/00,A61P43/00,C07K14/47,C12N5/10,C12P21/02,G01N33/15, PC
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DEFINITION Sequence 5 from Patent WO03035876.
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VERSION AX752106.1 GI:32134216
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

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REFERENCE 1 Hepacivirus.
AUTHORS Krebs,A., John,M., Schuppan,D., Limmer,S. and Kreutzner,R.
TITLE Use of a double strand ribonucleic acid for treating an infection with a positive-strand rna-virus
JOURNAL Patent: WO 03035876-A 5 01-MAY-2003;
Ribopharma AG (DE)
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DEFINITION Sequence 7236 from Patent WO0179548.
ACCESSION AX295474
VERSION AX295474.1 GI:17057163
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7236 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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/mol_type="unassigned DNA"
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/note="Hypothetical Probe Sequence"
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Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CGGTACGGTCTAATGACCG 21
Db 2 CGGTCTGGTCTAGTGACGG 20
RESULT 9
LOCUS AX290841 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 2603 from Patent WO0179548.
ACCESSION AX290841
VERSION AX290841.1 GI:17052524
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 2603 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
Location/Qualifiers

source 1. .24
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
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Query Match 60.0%; Score 12.6; DB 6; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CGGTACGGTCTAATGACCG 21
Db 2 CGGTCTGGTCTAGTGACGG 20
RESULT 10
LOCUS BD260345 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods.
ACCESSION BD260345
VERSION BD260345.1 GI:33070115
KEYWORDS JP 2002542803-A/102.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Windass,J.D., Heaney,S.P., Renwick,A., Whitcombe,D.M., Little,S., Gibson,N.J., Theaker,J. and Stanger,C.P.
TITLE Methods
JOURNAL Patent: JP 2002542803-A 102 17-DEC-2002;
SYNGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002542803-A/102
PD 17-DEC-2002
PF 26-APR-2000 JP 2000615395
PR 30-APR-1999 GB 9910100.8,13-MAR-2000 GB 0006004.6 PR
31-MAR-2000 GB 0007901.2
PI JOHN DAVID WINDASS,STEPHEN PAUL HEANEY,ANNABEL RENWICK, PI
DAVID MARK WHITCOMBE,STEPHEN LITTLE,NEIL JAMES GIBSON,JANE PI
THEAKER.
PI CAROLE PATRICIA STANGER
PC Cl2N15/09,C07K14/37,C12O1/68,G01N33/566,G01N33/569,C12N15/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
FT source 1. .26
/organism="Artificial Sequence".
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 CGGTACGGTCTAATGACC 20
Db 2 CGGTATGGTCAATGACC 20
RESULT 11
LOCUS AX044290 26 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 102 from Patent WO0066773.
ACCESSION AX044290
VERSION AX044290.1 GI:11343168
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

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REFERENCE
AUTHORS      Windas,J.D., Heaney,S.P., Renwick,A., Whitcombe,D.M., Little,S.,
              Gibson,N.J., Theaker,J. and Stanger,C.P.
TITLE        Method of detection of cytochrome b mutations in funghi leading to
              resistance against anti-fungal agents
JOURNAL      Patent: WO 0066773-A 102 09-NOV-2000;
              ZENECA LIMITED (GB)
FEATURES
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Primer"

ORIGIN
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Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15, Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGACC 20
    ||||| ||||| |||||
Db 2 CGTGTATGCTCAATGAGC 20

RESULT 12
LOCUS      AR168721 31 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6287866.
ACCESSION AR168721
VERSION AR168721.1 GI:17904788
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Mukerji,P., Lemmel,S.A., Leonard,A.Eun.-Yeong. and Chaudhary,S.
TITLE .beta.-casein expressing constructs
JOURNAL Patent: US 6287866-A 17 11-SEP-2001;
FEATURES
source     Location/Qualifiers
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              /mol_type="unassigned DNA"

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Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15, Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGCGTACGGTCTAATGACCG 21
    ||||| ||||| |||||
Db 12 GAGTACTGTCTCATGAGCG 30

RESULT 13
LOCUS      AR047950 33 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 29 from patent US 5820866.
ACCESSION AR047950
VERSION AR047950.1 GI:5970293
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kappler,J.W. and Marrack,P.
TITLE Product and process for T cell regulation
JOURNAL Patent: US 5820866-A 29 13-OCT-1998;
FEATURES
source     Location/Qualifiers
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              /mol_type="unassigned DNA"

ORIGIN

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AR336409					
ACCESSION	AR336409.1	GI:33722217			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 38)				
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 13811 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1..38				
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	/mol_type="unassigned RNA"				
ORIGIN					
Query Match	60.0%; Score 12.6; DB 6; Length 38;				
Best Local Similarity	75.0%; Pred. No. 1e+05;				
Matches	15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
QY	1 TCGGTACGGTCTAATGACC 20				
Dd	35 TCGNTTCGGCCTAACGGCC 16				
RESULT 17					
LOCUS	AR455837 38 bp DNA linear PAT 20-FEB-2004				
DEFINITION	Sequence 83 from patent US 6686154.				
ACCESSION	AR455837				
VERSION	AR455837.1 GI:42690729				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 38)				
AUTHORS	Nock,S. and Kassner,P.D.				
TITLE	Screening of phage displayed peptides without clearing of the cell culture				
JOURNAL	Patent: US 6686154-A 83 03-FEB-2004;				
FEATURES	Location/Qualifiers				
source	1..38				
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QY	2 CGGTACGGTCTAATGACC 20				
Dd	12 CGCGACATTGTTAATGACC 30				
RESULT 18					
LOCUS	AX219207/c 38 bp RNA linear PAT 07-SEP-2001				
DEFINITION	Sequence 4649 from Patent WO0159103.				
ACCESSION	AX219207				
VERSION	AX219207.1 GI:15546931				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Blatt,L., McSwiggen,J. and Chowrira,B.M.				
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression				
JOURNAL	Patent: WO 0159103-A 4649 16-AUG-2001;				
	RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)				
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AR336409					
ACCESSION	AR336409.1	GI:33722217			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 38)				
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 13811 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1..38				
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Query Match	60.0%; Score 12.6; DB 6; Length 38;				
Best Local Similarity	75.0%; Pred. No. 1e+05;				
Matches	15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
QY	1 TCGGTACGGTCTAATGACC 20				
Dd	35 TCGNTTCGGCCTAACGGCC 16				
RESULT 17					
LOCUS	AR455837 38 bp DNA linear PAT 20-FEB-2004				
DEFINITION	Sequence 83 from patent US 6686154.				
ACCESSION	AR455837				
VERSION	AR455837.1 GI:42690729				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 38)				
AUTHORS	Nock,S. and Kassner,P.D.				
TITLE	Screening of phage displayed peptides without clearing of the cell culture				
JOURNAL	Patent: US 6686154-A 83 03-FEB-2004;				
FEATURES	Location/Qualifiers				
source	1..38				
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	/mol_type="genomic DNA"				
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Query Match	60.0%; Score 12.6; DB 6; Length 38;				
Best Local Similarity	78.9%; Pred. No. 1e+05;				
Matches	15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
QY	2 CGGTACGGTCTAATGACC 20				
Dd	12 CGCGACATTGTTAATGACC 30				
RESULT 18					
LOCUS	AX219207/c 38 bp RNA linear PAT 07-SEP-2001				
DEFINITION	Sequence 4649 from Patent WO0159103.				
ACCESSION	AX219207				
VERSION	AX219207.1 GI:15546931				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Blatt,L., McSwiggen,J. and Chowrira,B.M.				
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression				
JOURNAL	Patent: WO 0159103-A 4649 16-AUG-2001;				
	RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)				
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AX351248					
ACCESSION	AX351248	GI:18616596			
VERSION	AX351248.1				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Nock,S. and Kassner,P.D.				
TITLE	Screening of phage displayed peptides without clearing of the cell culture				
JOURNAL	Patent: WO 0194950-A 83 13-DEC-2001;				
FEATURES	Location/Qualifiers				
source	1..38				
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modified_base					

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/organism="synthetic construct"
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/db_xref="taxon:32630"
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ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2  CGCGTACGGTCTTAATGACC 20
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Db  12  CGCGGACATTGTAATGACC 30

RESULT 21
AX424618/c
LOCUS      AX424618          38 bp      RNA          linear          PAT 18-JUN-2002
DEFINITION Sequence 2954 from Patent WO0188124.
ACCESSION  AX424618
VERSION     AX424618.1  GI:21528000
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
           Randi, A.M.
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 2954 22-NOV-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   source
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           /note="n stands for inosine"

ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGCGTACGGTCTTAATGACC 20
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Db  35  TCGCNTTCGGCCTAACGGCC 16

RESULT 22
AX424731/c
LOCUS      AX424731          38 bp      RNA          linear          PAT 18-JUN-2002
DEFINITION Sequence 3067 from Patent WO0188124.
ACCESSION  AX424731
VERSION     AX424731.1  GI:21528113
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
           Randi, A.M.
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 3067 22-NOV-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   source
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misc_feature 31
           /note="n stands for inosine"

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ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGCGTACGGTCTTAATGACC 20
    ||||| ||||| ||||| |||||
Db  35  TCGCNTTCGGCCTAACGGCC 16

RESULT 23
AX581188/c
LOCUS      AX581188          38 bp      RNA          linear          PAT 10-JAN-2003
DEFINITION Sequence 3026 from Patent WO0211674.
ACCESSION  AX581188
VERSION     AX581188.1  GI:27652998
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
           and Grupe, A.
TITLE      Method and reagent for the inhibition of calcium activated chloride
           channel-1 (clca-1)
JOURNAL    Patent: WO 0211674-A 3026 14-FEB-2002;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
           Thompson, James (US)
FEATURES   source
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           /note="Enzymatic Nucleic Acid"
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ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGCGTACGGTCTTAATGACC 20
    ||||| ||||| ||||| |||||
Db  35  TCGCNTTCGGCCTAACGGCC 16

RESULT 24
AX581359/c
LOCUS      AX581359          38 bp      RNA          linear          PAT 10-JAN-2003
DEFINITION Sequence 3197 from Patent WO0211674.
ACCESSION  AX581359
VERSION     AX581359.1  GI:27653169
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
           and Grupe, A.
TITLE      Method and reagent for the inhibition of calcium activated chloride
           channel-1 (clca-1)
JOURNAL    Patent: WO 0211674-A 3197 14-FEB-2002;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
           Thompson, James (US)
FEATURES   source
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modified_base 31 /mod_base=i
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
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Db 35 TCGCNTTCGGCTTAACGGCC 16

RESULT 25
LOCUS A65234 42 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 5 from Patent WO9735011.
ACCESSION A65234
VERSION A65234.1 GI:4531029
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Silvestrini, M.C., Cutruzzola, F., Ciabatti, Ilaria, Zennaro, E.,
Visco, C., Discepolo and Massimo.
TITLE RECOMBINANT PROCESS FOR THE PRODUCTION IN PSEUDOMONAS PUTIDA OF THE
CYTOCHROME C551 OF PSEUDOMONAS AERUGINOSA
JOURNAL Patent: WO 9735011-A 5 25-SEP-1997;
MINI RICERCA SCIENIT TECNOLOG (IT)
COMMENT Other publication IT M1960515 19970915.
FEATURES
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/db_xref="taxon:32644"

ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 42;
Best Local Similarity 78.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
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Db 37 GCGTACGGTTTCATCAGG 19

RESULT 26
LOCUS AX295733 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 7495 from Patent WO0179548.
ACCESSION AX295733
VERSION AX295733.1 GI:17057422
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7495 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN
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Best Local Similarity 92.9%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAAT 16
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Db 2 GCGCACGGTCTAAT 15

RESULT 27
LOCUS AX291100 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 2862 from Patent WO0179548.
ACCESSION AX291100
VERSION AX291100.1 GI:17052783
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 2862 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAAT 16
    ||| ||| ||| ||| |||
Db 2 GCGCACGGTCTAAT 15

RESULT 28
LOCUS AX464504 34 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 39 from Patent EP1219635.
ACCESSION AX464504
VERSION AX464504.1 GI:21899300
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Couture, F., Hamel, J., Brodeur, B.R. and Martin, D.
TITLE Chlamydia pneumoniae antigens
JOURNAL Patent: EP 1219635-A 39 03-JUL-2002;
SHIRE BIOCHEM INC. (CA)
FEATURES
source 1..34
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 34;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGTACGGTCTAATG 17
    ||| ||| ||| ||| |||
Db 21 CGTACGGTCTAAGG 34

RESULT 29
Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AR046887 AR046887 38 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1680 from patent US 5817796.
DEFINITION AR046887
ACCESSION AR046887
VERSION AR046887.1 GI:5968352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2',5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 1680 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GTACGGTCTAATGA 18
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Db 2 GTACGGTCTAATGA 15

RESULT 30
I53939 I53939 38 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 1680 from patent US 5646042.
DEFINITION I53939
ACCESSION I53939
VERSION I53939.1 GI:2475142
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1680 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GTACGGTCTAATGA 18
|||||
Db 2 GTACGGTCTAATGA 15

RESULT 31
AX220204 AX220204 38 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 5646 from Patent WO0159103.
DEFINITION AX220204
ACCESSION AX220204
VERSION AX220204.1 GI:15547928
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,I., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 5646 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
source 1..38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 ACGGTCTAATGACC 20
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Db 24 AAGGTCTAATGACC 37

RESULT 32
AR314417 AR314417 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 4954 from patent US 6559294.
DEFINITION AR314417
ACCESSION AR314417
VERSION AR314417.1 GI:31707843
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 4954 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CGCGTACGGTCTAATGA 18
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Db 2 CGCGTACGGTCTAATGA 18

RESULT 33
AR364921 AR364921 21 bp DNA linear PAT 03-SEP-2003
LOCUS Sequence 8 from patent US 5451502.
DEFINITION AR364921
ACCESSION AR364921
VERSION AR364921.1 GI:34428117
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS George,A.L. Jr.
TITLE Restriction amplification assay
JOURNAL Patent: US 5451502-A 8 19-SEP-1995;
FEATURES Location/Qualifiers
source 1..21
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/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db
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5 TCGCATAGGTCGAATG 21

RESULT 34
AX392054
LOCUS linear PAT 23-MAR-2002
DEFINITION Sequence 13 from Patent WO0215920.
ACCESSION AX392054
VERSION AX392054.1 GI:19700558
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Ward,S.B., Bavik,C.B., Cork,M.B. and Tazi-Ahmini,R.B.
TITLE Treatment of hyperproliferative diseases
JOURNAL Patent: WO 0215920-A 13 28-FEB-2002;
THE UNIVERSITY OF SHEFFIELD (GB)
FEATURES
source
1..22
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/db_xref="taxon:32630"
/note="Primer"

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Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 2 GCTACGGTCTTAATGAC 18

RESULT 35
AX755148/c
LOCUS linear PAT 23-JUN-2003
DEFINITION Sequence 29 from Patent WO03025003.
ACCESSION AX755148
VERSION AX755148.1 GI:32167628
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van
Wely,C.A.
TITLE Vaccines
JOURNAL Patent: WO 03025003-A 29 27-MAR-2003;
GLAXO GROUP LIMITED (GB)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 17 TCGGGCGGCTCTTAATG 1

RESULT 36
AX755156/c
LOCUS linear PAT 23-JUN-2003
DEFINITION Sequence 37 from Patent WO03025003.
ACCESSION AX755156
VERSION AX755156.1 GI:32167636
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van
Wely,C.A.
TITLE Vaccines
JOURNAL Patent: WO 03025003-A 37 27-MAR-2003;
GLAXO GROUP LIMITED (GB)
FEATURES
source
1..32
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

ORIGIN
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Best Local Similarity 73.7%; Pred. No. 1.7e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db 12 CGCGGACATTSTGATGACC 30

RESULT 38
AX581788
LOCUS linear PAT 10-JAN-2003
DEFINITION Sequence 3626 from Patent WO0211674.
ACCESSION AX581788
VERSION AX581788.1 GI:27653598
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 112.708 Seconds
(without alignments)
978.085 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21
Sequence: 1 tcgcgtacggtctaatgacgc 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	13.6	64.8	29	3	AAAI6755 Human sec
C 3	13.4	63.8	25	9	ACI09445 Human mic
C 4	13.2	62.9	25	9	ACI88862 Human mic
C 5	13.2	62.9	25	9	ACI88824 Human mic
C 6	13.2	62.9	35	2	AAV61559 Adaptor N
C 7	13.2	62.9	37	6	ACN31831 WNV minus
C 8	13.2	62.9	39	2	AAV61560 Adaptor N
C 9	13.2	61.0	25	9	ACI71602 Human mic
C 10	12.8	61.0	25	9	ACI71017 Human mic
C 11	12.8	61.0	30	10	ADDI12949 HCV NS3 p
C 12	12.6	60.0	20	6	AB195516 Capture o
C 13	12.6	60.0	24	6	AB187602 Capture o
C 14	12.6	60.0	24	6	AB187603 Capture o
C 15	12.6	60.0	25	9	ACI25753 Human mic
C 16	12.6	60.0	25	9	ACK18838 Human mic
C 17	12.6	60.0	25	9	ACI56057 Human mic
C 18	12.6	60.0	25	9	ACK18839 Human mic
C 19	12.6	60.0	26	4	AAAC97127 Cytochrom
C 20	12.6	60.0	31	3	AAZ50914 PCR primer
C 21	12.6	60.0	33	2	AAAT04264 Primer #2

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23	12.6	60.0	36	8	ACD66384	Acid66384 Anti-HCV
24	12.6	60.0	37	6	ACN19551	Acn19551 WNV Zinz
25	12.6	60.0	37	6	ACN31602	Acn31602 WNV minus
26	12.6	60.0	37	6	ACN19001	Acn19001 WNV Zinz
27	12.6	60.0	37	8	ACA07993	Acad07993 Necrosis
28	12.6	60.0	38	4	ABK04673	Abk04673 Human NOG
29	12.6	60.0	38	4	ABK04649	Abk04649 Human NOG
30	12.6	60.0	38	6	ABQ72447	Abq72447 PCR prime
31	12.6	60.0	38	6	ABK20307	Abk20307 Human ERG
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34	12.6	60.0	38	6	ABK58826	Abk58826 Human CLC
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38	12.6	60.0	38	6	ACN30373	Acn30373 WNV minus
39	12.6	60.0	38	6	ACN29690	Acn29690 WNV minus
40	12.6	60.0	38	6	ACN27931	Acn27931 WNV minus
41	12.6	60.0	38	6	ACN29837	Acn29837 WNV minus
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43	12.6	60.0	38	6	ACN17833	Acn17833 WNV Inoz
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45	12.6	60.0	38	6	ACN29870	Acn29870 WNV minus
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53	12.6	60.0	38	12	ADM61630	Adm61630 Hepatitis
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57	12.4	59.0	24	6	AB188120	Abi88120 Capture o
58	12.4	59.0	32	12	ADH36452	Adh36452 Human pur
59	12.4	59.0	34	6	ABQ92506	Abq92506 C. pneumo
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61	12.2	58.1	20	2	AAAX95628	Aax95628 PCR prime
62	12.2	58.1	25	9	ACI17482	Ac117482 Human mic
63	12.2	58.1	25	9	ACI27184	Ac127184 Human mic
64	12.2	58.1	25	9	ACI28438	Ac128438 Human mic
65	12.2	58.1	25	9	ACI36708	Ac136708 Human mic
66	12.2	58.1	32	10	ACC69881	Acc69881 HIV-1 pla
67	12.2	58.1	32	10	ACC69889	Acc69889 HIV-1 pla
68	12.2	58.1	32	12	ADH56317	Adh56317 Retroviri
69	12.2	58.1	34	12	ADN00529	Adn00529 Anti-apol
70	12.2	58.1	34	12	ADM98149	Adm98149 Anti-apol
71	12.2	58.1	37	6	ABQ72438	Abq72438 PCR prime
72	12.2	58.1	37	6	ABK59293	Abk59293 Human CLC
73	12.2	58.1	37	6	ABK59255	Abk59255 Human CLC
74	12.2	58.1	37	6	ABK59260	Abk59260 Human CLC
75	12.2	58.1	37	6	ACN31660	Acn31660 WNV minus
76	12.2	58.1	40	12	ADH56313	Adh56313 A. thalia
77	12.2	58.1	41	3	AAZ48334	Aaz48334 Primer sp
78	12.2	58.1	41	4	AAH45154	Aah45154 Human pro
79	12.2	58.1	20	10	ADK66022	Adk66022 Standardi
80	12.2	58.1	21	2	AAAX32506	Aax32506 GAPDH cDN
81	12.2	58.1	23	9	ADA22715	Ada22715 Human GAP
82	12.2	58.1	25	9	ACK22315	Ack22315 Human mic
83	12.2	58.1	25	9	ACI03832	Ac103832 Human mic
84	12.2	58.1	25	9	ACK16701	Ack16701 Human mic
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86	12.2	58.1	25	9	ACI68761	Ac168761 Human mic
87	12.2	58.1	25	9	ACI03833	Ac103833 Human mic
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89	12.2	58.1	29	4	AAI70164	Aai70164 Human uro
90	12.2	58.1	29	5	AAH43542	Aah43542 Primer 12
91	12.2	58.1	29	5	AAF87256	Aaf87256 Fusion pr
92	12.2	58.1	32	3	AAAC5266	Aac5266 GAPDH dow
93	12.2	58.1	32	3	AAZ36904	Aaz36904 PCR prime
94	12.2	58.1	36	6	ABX01948	Abx01948 HCV hamme

c 95	12	57.1	36	6	ABX02182	Abx02182 HCV hamme	c 168	11.6	55.2	25	9	ACI00796	AcI00796 Human mic
c 96	12	57.1	36	6	ABX02155	Abx02155 HCV hamme	c 169	11.6	55.2	25	9	ACI88245	AcI88245 Human mic
c 97	12	57.1	36	6	ABX02284	Abx02284 HCV hamme	c 170	11.6	55.2	26	4	AAC97085	Aac97085 Cytochrom
c 98	12	57.1	37	6	ABX59280	Abx59280 Human CLC	c 171	11.6	55.2	26	4	AAC97064	Aac97064 Cytochrom
99	12	57.1	37	6	ACN19032	Acn19032 WNV Zinz	c 172	11.6	55.2	32	12	ADOS9622	Ados9622 HCV RNA p
100	12	57.1	37	6	ACN30898	Acn30898 WNV minus	c 173	11.6	55.2	32	12	ADOS9629	Ados9629 HCV RNA p
101	12	57.1	37	6	ACN18814	Acn18814 WNV Zinz	c 174	11.6	55.2	32	12	ADOS9633	Ados9633 HCV RNA p
102	12	57.1	37	6	ACN18893	Acn18893 WNV Zinz	c 175	11.6	55.2	32	12	ADOS9625	Ados9625 HCV RNA p
103	12	57.1	37	6	ACN19198	Acn19198 WNV Zinz	c 176	11.6	55.2	32	12	ADOS9628	Ados9628 HCV RNA p
104	12	57.1	37	6	ACN30720	Acn30720 WNV minus	c 177	11.6	55.2	32	12	ADOS9635	Ados9635 HCV RNA p
105	12	57.1	37	6	ACN19979	Acn19979 WNV Zinz	c 178	11.6	55.2	32	12	ADOS9632	Ados9632 HCV RNA p
106	12	57.1	37	6	ACN31491	Acn31491 WNV minus	c 179	11.6	55.2	32	12	ADOS9624	Ados9624 HCV RNA p
107	12	57.1	37	6	ACN31195	Acn31195 WNV minus	c 180	11.6	55.2	32	12	ADOS9630	Ados9630 HCV RNA p
108	12	57.1	37	6	ACN31240	Acn31240 WNV minus	c 181	11.6	55.2	32	12	ADOS9634	Ados9634 HCV RNA p
109	12	57.1	37	8	ACA08151	ACA08151 Necrosis	c 182	11.6	55.2	32	12	ADOS9636	Ados9636 HCV RNA p
110	12	57.1	37	11	ADL52699	Adl52699 Human NOG	c 183	11.6	55.2	32	12	ADOS9623	Ados9623 HCV RNA p
111	12	57.1	37	11	ADL54425	Adl54425 Human IKK	c 184	11.6	55.2	32	12	ADOS9627	Ados9627 HCV RNA p
112	12	57.1	37	11	ADL73501	Adl73501 Human PCR	c 185	11.6	55.2	32	12	ADOS9631	Ados9631 HCV RNA p
c 113	12	57.1	37	11	ADL73524	Adl73524 Human PCR	c 186	11.6	55.2	32	12	ADOS9626	Ados9626 HCV RNA p
c 114	12	57.1	38	6	ABX58095	Abx58095 Human CLC	c 187	11.6	55.2	34	8	ACA10065	ACA10065 Necrosis
c 115	12	57.1	38	6	ACN27173	Acn27173 WNV minus	c 188	11.6	55.2	35	2	AAV61557	Aav61557 Adaptor N
c 116	12	57.1	38	6	ACN16487	Acn16487 WNV Hamme	c 189	11.6	55.2	36	12	ADI59444	Adi59444 Incozyme s
c 117	12	57.1	38	6	ACN27061	Acn27061 WNV minus	c 190	11.6	55.2	37	5	AAH41019	Aah41019 PCR prime
c 118	12	57.1	38	6	ACN27710	Acn27710 WNV minus	c 191	11.6	55.2	37	6	ABK59250	Abk59250 Human CLC
c 119	12	57.1	38	6	ACN16340	Acn16340 WNV Hamme	c 192	11.6	55.2	37	6	ABK59311	Abk59311 Human CLC
c 120	12	57.1	38	6	ACN16340	Acn16340 WNV Hamme	c 193	11.6	55.2	37	6	ACN31481	Acn31481 WNV minus
c 121	12	57.1	38	6	ACN16550	Acn16550 WNV Hamme	c 194	11.6	55.2	37	6	ACN30995	Acn30995 WNV minus
c 122	12	57.1	38	6	ACN16547	Acn16547 WNV Hamme	c 195	11.6	55.2	37	6	ACN31582	Acn31582 WNV minus
c 123	12	57.1	38	6	ACD51020	Acn51020 HBV hamme	c 196	11.6	55.2	37	6	ACN30780	Acn30780 WNV minus
c 124	12	57.1	38	11	ADL53578	Adl53578 Human IKK	c 197	11.6	55.2	37	6	ACN31436	Acn31436 WNV minus
c 125	12	57.1	38	11	ADL56069	Adl56069 Human PCR	c 198	11.6	55.2	37	6	ACN37009	Acn37009 WNV enzym
c 126	12	57.1	38	11	ADL55761	Adl55761 Human PCR	c 199	11.6	55.2	37	6	ACN31816	Acn31816 WNV minus
c 127	12	57.1	38	12	ADM60741	Adm60741 Hepatitis	c 200	11.6	55.2	37	6	ACN31773	Acn31773 WNV minus
c 128	12	57.1	45	2	AAx83991	Aax83991 Mouse pro	c 201	11.6	55.2	37	11	ADL54295	Adl54295 Human IKK
c 129	12	57.1	50	8	ABZ68287	Abz68287 Nucleotid	c 202	11.6	55.2	38	4	ABK04734	Abk04734 Human NOG
c 130	12	57.1	50	10	ADD31953	Add31953 BBP-Bix a	c 203	11.6	55.2	38	4	ABK04713	Abk04713 Human NOG
c 131	11.8	56.2	15	3	AAZ64070	Aaz64070 Substrate	c 204	11.6	55.2	38	4	ABK04626	Abk04626 Human NOG
c 132	11.8	56.2	15	6	ABX01123	Abx01123 Hepatitis	c 205	11.6	55.2	38	4	ABK05250	Abk05250 Human NOG
c 133	11.8	56.2	17	8	ACD59069	Acn59069 HCV DNaz	c 206	11.6	55.2	38	4	ABK05292	Abk05292 Human NOG
c 134	11.8	56.2	17	12	AD183905	Adi83905 HCV DNaz	c 207	11.6	55.2	38	4	ABK04552	Abk04552 Human NOG
c 135	11.8	56.2	25	9	ACI98341	AcI98341 Human mic	c 208	11.6	55.2	38	4	ABK04620	Abk04620 Human NOG
c 136	11.8	56.2	25	9	ACI36939	AcI36939 Human mic	c 209	11.6	55.2	38	4	ABK04722	Abk04722 Human NOG
c 137	11.8	56.2	25	9	ACI28871	AcI28871 Human mic	c 210	11.6	55.2	38	4	ABK04634	Abk04634 Human NOG
c 138	11.8	56.2	25	9	ACI09444	AcI09444 Human mic	c 211	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
c 139	11.8	56.2	25	9	ACI20469	AcI20469 Human mic	c 212	11.6	55.2	38	4	ABK04662	Abk04662 Human NOG
c 140	11.8	56.2	25	9	ACI32881	AcI32881 Human mic	c 213	11.6	55.2	38	4	ABL47651	AbI47651 Human GRI
c 141	11.8	56.2	25	9	ACI87003	AcI87003 Human mic	c 214	11.6	55.2	38	4	ABL47726	AbI47726 Human GRI
c 142	11.8	56.2	28	2	AAI38250	Aat38250 Y. pestis	c 215	11.6	55.2	38	6	ABK20206	Abk20206 Human ERG
c 143	11.8	56.2	29	2	AAAI7888	Aaai7888 Human TIE	c 216	11.6	55.2	38	6	ABK20037	Abk20037 Human ERG
c 144	11.8	56.2	34	9	ACC83715	Acc83715 Fragile X	c 217	11.6	55.2	38	6	ABK20037	Abk20037 Human ERG
c 145	11.8	56.2	38	6	ACN16238	Acn16238 WNV Hamme	c 218	11.6	55.2	38	6	ABK20238	Abk20238 Human ERG
c 146	11.8	56.2	38	8	ACD51219	Acn51219 HBV hamme	c 219	11.6	55.2	38	6	ABK19972	Abk19972 Human ERG
c 147	11.8	56.2	38	12	ADM60838	Adm60838 Hepatitis	c 220	11.6	55.2	38	6	ABK19972	Abk19972 Human ERG
c 148	11.6	55.2	20	3	AAZ55942	Aaz55942 Xenopus l	c 221	11.6	55.2	38	6	ABK20342	Abk20342 Human ERG
c 149	11.6	55.2	20	6	ABI95571	Abi95571 Capture o	c 222	11.6	55.2	38	6	ABK20287	Abk20287 Human ERG
c 150	11.6	55.2	24	6	ABI87712	Abi87712 Capture o	c 223	11.6	55.2	38	6	ABK58983	Abk58983 Human CLC
c 151	11.6	55.2	24	6	ABI89805	Abi89805 Capture o	c 224	11.6	55.2	38	6	ABK58564	Abk58564 Human CLC
c 152	11.6	55.2	24	6	ABI89804	Abi89804 Capture o	c 225	11.6	55.2	38	6	ABK58622	Abk58622 Human CLC
c 153	11.6	55.2	24	6	ABI87713	Abi87713 Capture o	c 226	11.6	55.2	38	6	ACN17225	Acn17225 WNV Inozy
c 154	11.6	55.2	25	3	AAZ47402	Aaz47402 Forward P	c 227	11.6	55.2	38	6	ACN16832	Acn16832 WNV Inozy
c 155	11.6	55.2	25	9	ACK27505	Ack27505 Human mic	c 228	11.6	55.2	38	6	ACN17021	Acn17021 WNV Inozy
c 156	11.6	55.2	25	9	ACK09489	Ack09489 Human mic	c 229	11.6	55.2	38	6	ACN17078	Acn17078 WNV Inozy
c 157	11.6	55.2	25	9	ACI77375	AcI77375 Human mic	c 230	11.6	55.2	38	6	ACN18453	Acn18453 WNV Inozy
c 158	11.6	55.2	25	9	ACI72460	AcI72460 Human mic	c 231	11.6	55.2	38	6	ACN128674	Acn128674 WNV minus
c 159	11.6	55.2	25	9	ACI53846	AcI53846 Human mic	c 232	11.6	55.2	38	6	ACN17229	Acn17229 WNV Inozy
c 160	11.6	55.2	25	9	ACI77677	AcI77677 Human mic	c 233	11.6	55.2	38	6	ACN17823	Acn17823 WNV Inozy
c 161	11.6	55.2	25	9	ACI88863	AcI88863 Human mic	c 234	11.6	55.2	38	6	ACN18346	Acn18346 WNV Inozy
c 162	11.6	55.2	25	9	ACI00797	AcI00797 Human mic	c 235	11.6	55.2	38	6	ACN29827	Acn29827 WNV minus
c 163	11.6	55.2	25	9	ACI07794	AcI07794 Human mic	c 236	11.6	55.2	38	6	ACN18161	Acn18161 WNV Inozy
c 164	11.6	55.2	25	9	ACK07040	Ack07040 Human mic	c 237	11.6	55.2	38	6	ACN18372	Acn18372 WNV Inozy
c 165	11.6	55.2	25	9	ACI46353	AcI46353 Human mic	c 238	11.6	55.2	38	6	ACN28510	Acn28510 WNV minus
c 166	11.6	55.2	25	9	ACI33578	AcI33578 Human mic	c 239	11.6	55.2	38	6	ACN28957	Acn28957 WNV minus
c 167	11.6	55.2	25	9	ACK00389	Ack00389 Human mic	c 240	11.6	55.2	38	6	ACN30573	Acn30573 WNV minus

C 241	11.6	55.2	38	6	ACN16944	Acn16944	WNV Inozoy	314	11.4	54.3	20	2	AAQ45350	Aaq45350	PCR prime
C 242	11.6	55.2	38	6	ACN18309	Acn18309	WNV Inozoy	C 315	11.4	54.3	22	6	ABL31902	Ab131902	Human CYP
C 243	11.6	55.2	38	6	ACN18573	Acn18573	WNV Inozoy	316	11.4	54.3	23	8	ABV75861	Abv75861	Arabidops
C 244	11.6	55.2	38	6	ACN17194	Acn17194	WNV Inozoy	317	11.4	54.3	23	9	ABZ81234	Abz81234	Arabidops
C 245	11.6	55.2	38	6	ACN28445	Acn28445	WNV minus	318	11.4	54.3	23	10	ADH35553	Adh35553	H+ -ATPas
C 246	11.6	55.2	38	6	ACN30165	Acn30165	WNV minus	319	11.4	54.3	23	10	ADL18214	Adl18214	H+ -ATPas
C 247	11.6	55.2	38	6	ACN18467	Acn18467	WNV Inozoy	C 320	11.4	54.3	24	6	ABQ08710	Abq08710	Oligonuc1
C 248	11.6	55.2	38	6	ACN18695	Acn18695	WNV Inozoy	321	11.4	54.3	24	6	ABQ02374	Abq02374	Oligonuc1
C 249	11.6	55.2	38	6	ACN28523	Acn28523	WNV minus	322	11.4	54.3	24	6	ABQ08669	Abq08669	Oligonuc1
C 250	11.6	55.2	38	6	ACN29692	Acn29692	WNV minus	C 323	11.4	54.3	24	6	ABQ08669	Abq08669	Oligonuc1
C 251	11.6	55.2	38	6	ACN29037	Acn29037	WNV minus	324	11.4	54.3	24	6	ABQ08669	Abq08669	Oligonuc1
C 252	11.6	55.2	38	6	ACN28657	Acn28657	WNV minus	C 325	11.4	54.3	25	9	ACI156633	Ac156633	Human mic
C 253	11.6	55.2	38	6	ACN29459	Acn29459	WNV minus	326	11.4	54.3	25	9	ACK10586	Ack10586	Human mic
C 254	11.6	55.2	38	6	ACN29488	Acn29488	WNV minus	327	11.4	54.3	25	9	ACI189575	Ac189575	Human mic
C 255	11.6	55.2	38	6	ACN30357	Acn30357	WNV minus	328	11.4	54.3	25	9	ACI189575	Ac189575	Human mic
C 256	11.6	55.2	38	6	ACN18644	Acn18644	WNV Inozoy	C 329	11.4	54.3	25	9	ACI171603	Ac171603	Human mic
C 257	11.6	55.2	38	6	ACN29655	Acn29655	WNV Inozoy	C 330	11.4	54.3	25	9	ACK04317	Ack04317	Human mic
C 258	11.6	55.2	38	6	ACN29671	Acn29671	WNV minus	331	11.4	54.3	25	9	ACI134741	Ac134741	Human mic
C 259	11.6	55.2	38	6	ACN17594	Acn17594	WNV Inozoy	332	11.4	54.3	25	9	ACK04457	Ack04457	Human mic
C 260	11.6	55.2	38	6	ACN29252	Acn29252	WNV minus	C 333	11.4	54.3	25	9	ACK21465	Ack21465	Human mic
C 261	11.6	55.2	38	6	ACN17438	Acn17438	WNV Inozoy	C 334	11.4	54.3	25	9	ACI69299	Ac169299	Human mic
C 262	11.6	55.2	38	6	ACN17890	Acn17890	WNV Inozoy	C 335	11.4	54.3	25	9	ACH61541	Ach61541	DNA targe
C 263	11.6	55.2	38	6	ACN16983	Acn16983	WNV Inozoy	C 336	11.4	54.3	25	9	ACH54299	Ach54299	DNA targe
C 264	11.6	55.2	38	8	ACA07403	Acn07403	Necrosis	C 337	11.4	54.3	25	9	ACH56738	Ach56738	DNA targe
C 265	11.6	55.2	38	8	ACA07408	Acn07408	Necrosis	C 338	11.4	54.3	26	6	ABT11741	Abt11741	Drosophil
C 266	11.6	55.2	38	8	ACA07040	Acn07040	Necrosis	339	11.4	54.3	27	8	ABT17185	Abt17185	Transcrip
C 267	11.6	55.2	38	8	ACA07037	Acn07037	Necrosis	C 340	11.4	54.3	27	8	ABT17185	Abt17185	Transcrip
C 268	11.6	55.2	38	8	ABZ66597	Abz66597	Human HIV	341	11.4	54.3	27	10	ADC60797	Adc60797	Cis eleme
C 269	11.6	55.2	38	8	ACD52161	Acn52161	HBV inozoy	C 342	11.4	54.3	27	10	ADC60796	Adc60796	Cis eleme
C 270	11.6	55.2	38	8	ACD52955	Acn52955	HBV inozoy	C 343	11.4	54.3	27	10	ADF48566	Adf48566	Cis-eleme
C 271	11.6	55.2	38	8	ACD52428	Acn52428	HBV inozoy	344	11.4	54.3	27	10	ADF48566	Adf48566	Cis-eleme
C 272	11.6	55.2	38	8	ACD52650	Acn52650	HBV inozoy	C 345	11.4	54.3	28	3	AAA64500	Aaa64500	PCR prime
C 273	11.6	55.2	38	8	ACD52433	Acn52433	HBV inozoy	346	11.4	54.3	34	2	AAAX91910	Aax91910	Porphorym
C 274	11.6	55.2	38	8	ACD52468	Acn52468	HBV inozoy	C 347	11.4	54.3	36	9	ADA50300	Ada50300	Human PCR
C 275	11.6	55.2	38	8	ACD53061	Acn53061	HBV inozoy	C 348	11.4	54.3	37	2	AAAT60208	Aat60208	Synthetic
C 276	11.6	55.2	38	11	ADL53906	Adl53906	Human IKK	349	11.4	54.3	38	6	ACN28511	Acn28511	WNV minus
C 277	11.6	55.2	38	11	ADL5242	Adl5242	Human PTG	350	11.4	54.3	42	2	AAQ28514	Aaq28514	Hypercalc
C 278	11.6	55.2	38	11	ADL5357	Adl5357	Human PTG	351	11.4	54.3	43	2	AAV34727	Aav34727	Recombina
C 279	11.6	55.2	38	11	ADL52170	Adl52170	Human NOG	352	11.4	54.3	43	2	AAV24315	Aav24315	Primer pP
C 280	11.6	55.2	38	11	ADL53903	Adl53903	Human IKK	C 353	11.2	53.3	17	10	ADB44420	Adb44420	Tumour su
C 281	11.6	55.2	38	11	ADL54002	Adl54002	Human IKK	C 354	11.2	53.3	17	10	ACC51692	Acc51692	Human tum
C 282	11.6	55.2	38	11	ADL75463	Adl75463	Human PTG	C 355	11.2	53.3	18	10	ADE15211	Adel15211	Beer spoi
C 283	11.6	55.2	38	11	ADL54079	Adl54079	Human IKK	C 356	11.2	53.3	18	10	AAH50337	Aah50337	Bacterial
C 284	11.6	55.2	38	11	ADL52085	Adl52085	Human PTG	C 357	11.2	53.3	19	4	AAH50337	Aah50337	Bacterial
C 285	11.6	55.2	38	11	ADL75413	Adl75413	Human PTG	358	11.2	53.3	20	2	AAZ05198	Aaz05198	PCR prime
C 286	11.6	55.2	38	11	ADL52329	Adl52329	Human NOG	359	11.2	53.3	20	10	ADG20440	Adg20440	Aegilops
C 287	11.6	55.2	38	11	ADL52336	Adl52336	Human NOG	C 360	11.2	53.3	20	12	ADJ85254	Adj85254	Nucleic a
C 288	11.6	55.2	38	11	ADL52390	Adl52390	Human NOG	C 361	11.2	53.3	20	12	ADP44289	Adp44289	Human TEK
C 289	11.6	55.2	38	11	ADL75406	Adl75406	Human PTG	C 362	11.2	53.3	20	12	ADG20446	Adg20446	Aegilops
C 290	11.6	55.2	38	11	ADL52232	Adl52232	Human NOG	C 363	11.2	53.3	22	10	ADP44211	Adp44211	Human TEK
C 291	11.6	55.2	38	11	ADL56628	Adl56628	Human PKR	C 364	11.2	53.3	24	6	ABA99700	Aba99700	M. cerevi
C 292	11.6	55.2	38	11	ADL75325	Adl75325	Human PTG	C 365	11.2	53.3	25	9	ACI159270	Ac159270	Human mic
C 293	11.6	55.2	38	11	ADL54181	Adl54181	Human IKK	C 366	11.2	53.3	25	9	ACI134915	Ac134915	Human mic
C 294	11.6	55.2	38	11	ADL75218	Adl75218	Human PTG	C 367	11.2	53.3	25	9	ACI11940	Ac111940	Human mic
C 295	11.6	55.2	38	11	ADL52262	Adl52262	Human NOG	C 368	11.2	53.3	25	9	ACI26782	Ac126782	Human mic
C 296	11.6	55.2	38	11	ADL52304	Adl52304	Human NOG	C 369	11.2	53.3	25	9	ACI44103	Ac144103	Human mic
C 297	11.6	55.2	38	11	ADL75228	Adl75228	Human PTG	C 370	11.2	53.3	25	9	ACI72293	Ac172293	Human mic
C 298	11.6	55.2	38	11	ADL75251	Adl75251	Human PTG	C 371	11.2	53.3	25	9	ACI75169	Ac175169	Human mic
C 299	11.6	55.2	38	11	ADM54971	Adm54971	NCH riboz	C 372	11.2	53.3	25	9	ACI36189	Ac136189	Human mic
C 300	11.6	55.2	38	11	ADM55046	Adm55046	NCH riboz	C 373	11.2	53.3	25	9	ACK21477	Ack21477	Human mic
C 301	11.6	55.2	38	12	ADM61550	Adm61550	Hepatitis	C 374	11.2	53.3	25	9	ACI02089	Ac102089	Human mic
C 302	11.6	55.2	38	12	ADM61757	Adm61757	Hepatitis	C 375	11.2	53.3	25	9	ACI01027	Ac101027	Human mic
C 303	11.6	55.2	38	12	ADM61430	Adm61430	Hepatitis	C 376	11.2	53.3	25	9	ACI30581	Ac130581	Human mic
C 304	11.6	55.2	38	12	ADM61435	Adm61435	Hepatitis	C 377	11.2	53.3	25	9	ACI09687	Ac109687	Human mic
C 305	11.6	55.2	38	12	ADM61316	Adm61316	Hepatitis	C 378	11.2	53.3	25	9	ACI34418	Ac134418	Human mic
C 306	11.6	55.2	38	12	ADM61470	Adm61470	Hepatitis	C 379	11.2	53.3	25	9	ACK22045	Ack22045	Human mic
C 307	11.6	55.2	38	12	ADM61702	Adm61702	Hepatitis	C 380	11.2	53.3	25	9	ACI75771	Ac175771	Human mic
C 308	11.6	55.2	39	2	AAV61558	Aav61558	Adaptor N	C 381	11.2	53.3	25	9	ACI71016	Ac171016	Human mic
C 309	11.6	55.2	39	2	AAZ31574	Aaz31574	PCR prime	C 382	11.2	53.3	25	9	ACK28588	Ack28588	Human mic
C 310	11.6	55.2	39	12	ADG16984	Adg16984	Anti-salm	C 383	11.2	53.3	25	9	ACK28589	Ack28589	Human mic
C 311	11.6	55.2	47	4	AAZ933008	Aaz933008	Infectiou	C 384	11.2	53.3	25	9	ACH51172	Ach51172	DNA targe
C 312	11.4	54.3	15	3	AAZ64069	Aaz64069	Substrate	C 385	11.2	53.3	25	9	ACH59775	Ach59775	DNA targe
C 313	11.4	54.3	15	6	ABX01122	Abx01122	Hepatitis	C 386	11.2	53.3	25	9	ACH60780	Ach60780	DNA targe

c 387	11.2	53.3	25	9	ACH60892	AcH60892 DNA targe	460	11	52.4	24	10	ADC57939	Adc57939 Human PRO
388	11.2	53.3	25	10	ABZ84510	Abz84510 Toxicology	461	11	52.4	24	10	ADC55303	Adc55303 Human PRO
389	11.2	53.3	28	2	AAT73081	Aat73081 UI snRNA	462	11	52.4	24	10	ADC12170	Adc12170 Human PRO
c 390	11.2	53.3	28	12	ADOL1376	Adol1376 Single mu	463	11	52.4	24	10	ADC56592	Adc56592 Human PRO
c 391	11.2	53.3	28	12	ADOL1426	Adol1426 Single mu	464	11	52.4	24	10	ADC07647	Adc07647 Human PRO
c 392	11.2	53.3	29	6	ABQ82513	Abq82513 Promoter	465	11	52.4	24	10	ADC11637	Adc11637 Human PRO
c 393	11.2	53.3	30	10	ADC83961	Adc83961 Human pap	466	11	52.4	24	10	ADC14759	Adc14759 Novel hum
c 394	11.2	53.3	30	10	ADF43834	Adf43834 HPV 39 de	467	11	52.4	24	10	ADD08291	Add08291 Human sec
c 395	11.2	53.3	31	2	AAT35700	Aat35700 3' VK pri	468	11	52.4	24	10	ADC82116	Adc82116 Human PRO
c 396	11.2	53.3	31	2	AAx62513	Aax62513 Granule b	469	11	52.4	24	10	AD007758	Ad007758 Human PRO
c 397	11.2	53.3	34	3	AAA62282	Aaa62282 Sample ol	470	11	52.4	24	10	ADC82649	Adc82649 Human PRO
c 398	11.2	53.3	37	6	ABK59294	Abk59294 Human CLC	471	11	52.4	24	10	ADD008829	Add008829 Human sec
c 399	11.2	53.3	37	6	ACN19390	Acn19390 WNV Zinz	472	11	52.4	24	10	ADD007078	Add007078 Human PRO
c 400	11.2	53.3	37	6	ACN30875	Acn30875 WNV minus	473	11	52.4	24	10	ADC833325	Adc833325 Human PRO
c 401	11.2	53.3	37	6	ACN19673	Acn19673 WNV Zinz	474	11	52.4	24	10	AD62014	Ad62014 Plasmodiu
c 402	11.2	53.3	37	6	ACN18820	Acn18820 WNV Zinz	c 475	11	52.4	24	10	AD62015	Ad62015 Plasmodiu
c 403	11.2	53.3	37	6	ACN30634	Acn30634 WNV minus	476	11	52.4	24	10	AD55432	Ad55432 Human PRO
c 404	11.2	53.3	37	6	ACN31064	Acn31064 WNV minus	477	11	52.4	24	10	AD56390	Ad56390 Human PRO
c 405	11.2	53.3	37	6	ACN31914	Acn31914 WNV minus	478	11	52.4	24	10	AD554828	Ad554828 Human PRO
c 406	11.2	53.3	37	6	ACN30941	Acn30941 WNV minus	479	11	52.4	24	10	AD56390	Ad56390 Human PRO
c 407	11.2	53.3	37	6	ACN31346	Acn31346 WNV minus	480	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 408	11.2	53.3	37	8	ACA08020	AcA08020 Necrosis	481	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 409	11.2	53.3	38	10	ADC46944	Adc46944 Primer fo	482	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 410	11.2	53.3	38	10	AD626449	Ad626449 Primer fo	483	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 411	11.2	53.3	40	2	AAx782114	Aax782114 Interleuk	484	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 412	11.2	53.3	40	6	ABZ21788	Abz21788 Human ery	485	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 413	11.2	53.3	40	6	ABZ21789	Abz21789 Human ery	486	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 414	11.2	53.3	45	4	AAx13391	Aax13391 Alanine s	487	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 415	11.2	53.3	45	4	AAx13391	Aax13391 Alanine s	488	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 416	11.2	53.3	50	6	ABZ06239	Abz06239 Human leu	489	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 417	11	52.4	16	3	AAx47286	Aax47286 C-myc pro	490	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 418	11	52.4	17	2	AAx75296	Aax75296 Mouse fit	491	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 419	11	52.4	17	2	AAx75297	Aax75297 Mouse fit	492	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 420	11	52.4	20	2	AAx96177	Aax96177 PCR prime	493	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 421	11	52.4	20	3	AAZ72519	Aaz72519 Human bia	c 494	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 422	11	52.4	21	12	ADN92428	Adn92428 Pancreat	c 495	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 423	11	52.4	22	6	AB159233	Ab159233 Antisense	496	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 424	11	52.4	22	12	ADP86451	Adp86451 Mouse GAP	c 497	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 425	11	52.4	23	4	AAZ07923	Aaz07923 Human G-P	c 498	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 426	11	52.4	24	2	AAQ92089	Aaq92089 Human rec	c 499	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 427	11	52.4	24	2	AAx35284	Aax35284 PCR prime	500	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 428	11	52.4	24	3	AAx58316	Aax58316 Human PRO	c 501	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 429	11	52.4	24	5	AAx17470	Aax17470 P. vivax	c 502	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 430	11	52.4	24	5	AAx17470	Aax17470 P. vivax	c 503	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 431	11	52.4	24	6	ABK87485	Abk87485 Synthetic	c 504	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 432	11	52.4	24	6	ABK87486	Abk87486 Synthetic	505	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 433	11	52.4	24	6	ABQ03239	Abq03239 Oligonuc	506	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 434	11	52.4	24	6	ABQ79141	Abq79141 Primer #1	507	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 435	11	52.4	24	8	ACA64474	AcA64474 Novel hum	c 508	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 436	11	52.4	24	8	ABX80933	Abx80933 Human sec	c 509	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 437	11	52.4	24	8	ACD44442	AcD44442 Human PRO	c 510	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 438	11	52.4	24	8	ABX79613	Abx79613 Human sec	511	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 439	11	52.4	24	8	ACA93634	AcA93634 Novel hum	512	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 440	11	52.4	24	8	ABX81316	Abx81316 Human sec	c 513	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 441	11	52.4	24	8	ACA93132	AcA93132 Novel hum	c 514	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 442	11	52.4	24	8	ABX17216	Abx17216 Human PRO	c 515	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 443	11	52.4	24	9	ACA68071	AcA68071 Novel hum	516	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 444	11	52.4	24	9	ACA88520	AcA88520 Human sec	c 517	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 445	11	52.4	24	9	ACD82027	AcD82027 Human PRO	c 518	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 446	11	52.4	24	9	ADA37970	Ada37970 Human PRO	c 519	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 447	11	52.4	24	9	ADA21656	Ada21656 Human sec	c 520	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 448	11	52.4	24	9	ADA10443	Ada10443 Human PRO	c 521	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 449	11	52.4	24	9	ADA10443	Ada10443 Human PRO	c 522	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 450	11	52.4	24	9	ADA28095	Ada28095 Human PRO	c 523	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 451	11	52.4	24	9	ADA94675	Ada94675 Human PRO	c 524	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 452	11	52.4	24	9	ADA38900	Ada38900 Human PRO	c 525	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 453	11	52.4	24	9	ADA93021	Ada93021 Human PRO	c 526	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 454	11	52.4	24	9	ACH65588	Ach65588 Human PRO	c 527	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 455	11	52.4	24	9	ADA22582	Ada22582 Human sec	c 528	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 456	11	52.4	24	9	ACD39578	AcD39578 Human PRO	c 529	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 457	11	52.4	24	9	ADA06748	Ada06748 Human sec	c 530	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 458	11	52.4	24	9	ADA39441	Ada39441 Human PRO	c 531	11	52.4	24	10	AD626449	Ad626449 Novel hum
c 459	11	52.4	24	9	ADB96467	Adb96467 Human PRO	c 532	11	52.4	24	10	AD626449	Ad626449 Novel hum

C 533	11	52.4	36	6	ABX02836	Abx02836 HCV hamme	C 606	11	52.4	38	4	ABK05210	Abk05210 Human NOG
C 534	11	52.4	36	6	ABX02270	Abx02270 HCV hamme	C 607	11	52.4	38	4	ABK04785	Abk04785 Human NOG
C 535	11	52.4	36	6	ABX02731	Abx02731 HCV hamme	C 608	11	52.4	38	4	ABK04953	Abk04953 Human NOG
C 536	11	52.4	36	6	ABX02408	Abx02408 HCV hamme	C 609	11	52.4	38	4	ABK05212	Abk05212 Human NOG
C 537	11	52.4	36	6	ABX02198	Abx02198 HCV hamme	C 610	11	52.4	38	4	ABK03884	Abk03884 Human NOG
C 538	11	52.4	36	6	ABX02402	Abx02402 HCV hamme	C 611	11	52.4	38	4	ABK05178	Abk05178 Human NOG
C 539	11	52.4	36	6	ABX02026	Abx02026 HCV hamme	C 612	11	52.4	38	4	ABK08311	Abk08311 Human CD2
C 540	11	52.4	36	6	ABX02602	Abx02602 HCV hamme	C 613	11	52.4	38	4	ABK03825	Abk03825 Human NOG
C 541	11	52.4	36	6	ABX02319	Abx02319 HCV hamme	C 614	11	52.4	38	4	ABK04543	Abk04543 Human NOG
C 542	11	52.4	36	6	ABX01863	Abx01863 HCV hamme	C 615	11	52.4	38	4	ABK05160	Abk05160 Human NOG
C 543	11	52.4	36	6	ABX02404	Abx02404 HCV hamme	C 616	11	52.4	38	4	ABK08344	Abk08344 Human CD2
C 544	11	52.4	36	6	ABX02705	Abx02705 HCV hamme	C 617	11	52.4	38	4	ABK04527	Abk04527 Human NOG
C 545	11	52.4	36	6	ABX02219	Abx02219 HCV hamme	C 618	11	52.4	38	4	ABK04580	Abk04580 Human NOG
C 546	11	52.4	36	8	ACD56262	AcD56262 HBV enzym	C 619	11	52.4	38	4	ABK04691	Abk04691 Human NOG
C 547	11	52.4	36	8	ACD56358	AcD56358 HBV enzym	C 620	11	52.4	38	4	ABK04765	Abk04765 Human NOG
C 548	11	52.4	36	12	ADI59388	Adi59388 Inozyme s	C 621	11	52.4	38	4	ABK08356	Abk08356 Human CD2
C 549	11	52.4	36	12	ADI59408	Adi59408 Inozyme s	C 622	11	52.4	38	4	ABK04566	Abk04566 Human NOG
C 550	11	52.4	36	12	ADI59410	Adi59410 Inozyme s	C 623	11	52.4	38	4	ABK04583	Abk04583 Human NOG
C 551	11	52.4	36	12	ADI59425	Adi59425 Inozyme s	C 624	11	52.4	38	4	ABK04646	Abk04646 Human NOG
C 552	11	52.4	36	12	ADI59437	Adi59437 Inozyme s	C 625	11	52.4	38	4	ABK08260	Abk08260 Human CD2
C 553	11	52.4	36	12	ADI59396	Adi59396 Inozyme s	C 626	11	52.4	38	4	ABK08382	Abk08382 Human CD2
C 554	11	52.4	36	12	ADI59457	Adi59457 Inozyme s	C 627	11	52.4	38	4	ABK05112	Abk05112 Human NOG
C 555	11	52.4	37	3	Az64928	Aaz64928 RPI motif	C 628	11	52.4	38	4	ABK07994	Abk07994 Human CD2
C 556	11	52.4	37	6	ABX03427	Abx03427 Ribozyme	C 629	11	52.4	38	4	ABK08174	Abk08174 Human CD2
C 557	11	52.4	37	6	ABK59352	AbK59352 Human CLC	C 630	11	52.4	38	4	ABK08243	Abk08243 Human CD2
C 558	11	52.4	37	6	ABK59388	AbK59388 Human CLC	C 631	11	52.4	38	4	ABK04529	Abk04529 Human NOG
C 559	11	52.4	37	6	ABK59340	AbK59340 Human CLC	C 632	11	52.4	38	4	ABK04985	Abk04985 Human NOG
C 560	11	52.4	37	6	ACN18985	Acn18985 WNV Zinzzy	C 633	11	52.4	38	4	ABK05127	Abk05127 Human NOG
C 561	11	52.4	37	6	ACN18992	Acn18992 WNV Zinzzy	C 634	11	52.4	38	4	ABK08277	Abk08277 Human CD2
C 562	11	52.4	37	6	ACN31308	Acn31308 WNV minus	C 635	11	52.4	38	4	ABK08316	Abk08316 Human CD2
C 563	11	52.4	37	6	ACN19493	Acn19493 WNV Zinzzy	C 636	11	52.4	38	4	ABK03855	Abk03855 Human NOG
C 564	11	52.4	37	6	ACN19321	Acn19321 WNV Zinzzy	C 637	11	52.4	38	4	ABK04698	Abk04698 Human NOG
C 565	11	52.4	37	6	ACN19329	Acn19329 WNV Zinzzy	C 638	11	52.4	38	4	ABK04824	Abk04824 Human NOG
C 566	11	52.4	37	6	ACN19323	Acn19323 WNV Zinzzy	C 639	11	52.4	38	4	ABK05306	Abk05306 Human NOG
C 567	11	52.4	37	6	ACN19355	Acn19355 WNV Zinzzy	C 640	11	52.4	38	4	ABK08435	Abk08435 Human CD2
C 568	11	52.4	37	6	ACN19418	Acn19418 WNV Zinzzy	C 641	11	52.4	38	4	ABK04862	Abk04862 Human NOG
C 569	11	52.4	37	6	ACN19889	Acn19889 WNV Zinzzy	C 642	11	52.4	38	4	ABK04963	Abk04963 Human NOG
C 570	11	52.4	37	6	ACN31939	Acn31939 WNV minus	C 643	11	52.4	38	4	ABK05042	Abk05042 Human NOG
C 571	11	52.4	37	6	ACN19246	Acn19246 WNV Zinzzy	C 644	11	52.4	38	4	ABK08305	Abk08305 Human CD2
C 572	11	52.4	37	6	ACN19519	Acn19519 WNV Zinzzy	C 645	11	52.4	38	4	ABL47584	AbL47584 Human GRI
C 573	11	52.4	37	6	ACN37010	Acn37010 WNV enzym	C 646	11	52.4	38	4	ABL47630	AbL47630 Human GRI
C 574	11	52.4	37	6	ACN31978	Acn31978 WNV minus	C 647	11	52.4	38	4	ABL47555	AbL47555 Human GRI
C 575	11	52.4	37	6	ACN31928	Acn31928 WNV minus	C 648	11	52.4	38	4	ABL47620	AbL47620 Human GRI
C 576	11	52.4	37	6	ACN31151	Acn31151 WNV minus	C 649	11	52.4	38	4	ABL47500	AbL47500 Human GRI
C 577	11	52.4	37	6	ACN31700	Acn31700 WNV minus	C 650	11	52.4	38	4	ABL47479	AbL47479 Human GRI
C 578	11	52.4	37	6	ACN30899	Acn30899 WNV minus	C 651	11	52.4	38	4	ABL47551	AbL47551 Human GRI
C 579	11	52.4	37	8	ACA10034	AcA10034 Necrosis	C 652	11	52.4	38	4	ABL47475	AbL47475 Human GRI
C 580	11	52.4	37	8	ACA08160	AcA08160 Necrosis	C 653	11	52.4	38	4	ABL47530	AbL47530 Human GRI
C 581	11	52.4	37	8	ACA08072	AcA08072 Necrosis	C 654	11	52.4	38	6	ABQ72443	AbQ72443 PCR prime
C 582	11	52.4	37	8	ACA07927	AcA07927 Necrosis	C 655	11	52.4	38	6	ABQ72448	AbQ72448 PCR prime
C 583	11	52.4	37	11	ADL75687	AdL75687 Human PTG	C 656	11	52.4	38	6	ABK19546	AbK19546 Human ERG
C 584	11	52.4	37	11	ADL52737	AdL52737 Human NOG	C 657	11	52.4	38	6	ABK20611	AbK20611 Human ERG
C 585	11	52.4	37	11	ADL54427	AdL54427 Human IKK	C 658	11	52.4	38	6	ABK20602	AbK20602 Human ERG
C 586	11	52.4	37	11	ADL5730	AdL5730 Human PTG	C 659	11	52.4	38	6	ABK20586	AbK20586 Human ERG
C 587	11	52.4	37	11	ADL54222	AdL54222 Human IKK	C 660	11	52.4	38	6	ABK20090	AbK20090 Human ERG
C 588	11	52.4	37	11	ADL73674	AdL73674 Human PKR	C 661	11	52.4	38	6	ABK20145	AbK20145 Human ERG
C 589	11	52.4	37	11	ADL75675	AdL75675 Human PTG	C 662	11	52.4	38	6	ABK20161	AbK20161 Human ERG
C 590	11	52.4	37	12	ADM64239	Adm64239 Hepatitis	C 663	11	52.4	38	6	ABK20303	AbK20303 Human ERG
C 591	11	52.4	37	12	ADM64143	Adm64143 Hepatitis	C 664	11	52.4	38	6	ABK19639	AbK19639 Human ERG
C 592	11	52.4	37	12	ADI92342	Adi92342 Anti-HCV	C 665	11	52.4	38	6	ABK20081	AbK20081 Human ERG
C 593	11	52.4	38	4	AAH96508	Aah96508 Human Chk	C 666	11	52.4	38	6	ABK20415	AbK20415 Human ERG
C 594	11	52.4	38	4	AAH96651	Aah96651 Human Chk	C 667	11	52.4	38	6	ABK20181	AbK20181 Human ERG
C 595	11	52.4	38	4	AAH96621	Aah96621 Human Chk	C 668	11	52.4	38	6	ABK20216	AbK20216 Human ERG
C 596	11	52.4	38	4	AAH96520	Aah96520 Human Chk	C 669	11	52.4	38	6	ABK20559	AbK20559 Human ERG
C 597	11	52.4	38	4	AAH96453	Aah96453 Human Chk	C 670	11	52.4	38	6	ABK19485	AbK19485 Human ERG
C 598	11	52.4	38	4	ABK04658	AbK04658 Human NOG	C 671	11	52.4	38	6	ABK20075	AbK20075 Human ERG
C 600	11	52.4	38	4	ABK04965	AbK04965 Human NOG	C 672	11	52.4	38	6	ABK20275	AbK20275 Human ERG
C 601	11	52.4	38	4	ABK05131	AbK05131 Human NOG	C 673	11	52.4	38	6	ABK20379	AbK20379 Human ERG
C 602	11	52.4	38	4	ABK05154	AbK05154 Human NOG	C 674	11	52.4	38	6	ABK20563	AbK20563 Human ERG
C 603	11	52.4	38	4	ABK05066	AbK05066 Human NOG	C 675	11	52.4	38	6	ABK20267	AbK20267 Human ERG
C 604	11	52.4	38	4	ABK05101	AbK05101 Human NOG	C 676	11	52.4	38	6	ABK20126	AbK20126 Human ERG
C 605	11	52.4	38	4	ABK04871	AbK04871 Human NOG	C 677	11	52.4	38	6	ABK20391	AbK20391 Human ERG

C 679	11	52.4	38	6	ABK20483	Abk20483 Human ERG	C 752	11	52.4	38	6	ACN18355	Acn18355 WNV Inozy
C 680	11	52.4	38	6	ABK20593	Abk20593 Human ERG	C 753	11	52.4	38	6	ACN29005	Acn29005 WNV minus
C 681	11	52.4	38	6	ABK20087	Abk20087 Human ERG	C 754	11	52.4	38	6	ACN29142	Acn29142 WNV minus
C 682	11	52.4	38	6	ABK20244	Abk20244 Human ERG	C 755	11	52.4	38	6	ACN30123	Acn30123 WNV minus
C 683	11	52.4	38	6	ABK58122	Abk58122 Human CLC	C 756	11	52.4	38	6	ACN30260	Acn30260 WNV minus
C 684	11	52.4	38	6	ABK58769	Abk58769 Human CLC	C 757	11	52.4	38	6	ACN30315	Acn30315 WNV minus
C 685	11	52.4	38	6	ABK58447	Abk58447 Human CLC	C 758	11	52.4	38	6	ACN16816	Acn16816 WNV Inozy
C 686	11	52.4	38	6	ABK58819	Abk58819 Human CLC	C 759	11	52.4	38	6	ACN17288	Acn17288 WNV Inozy
C 687	11	52.4	38	6	ABK58411	Abk58411 Human CLC	C 760	11	52.4	38	6	ACN18040	Acn18040 WNV Inozy
C 688	11	52.4	38	6	ABK58709	Abk58709 Human CLC	C 761	11	52.4	38	6	ACN27900	Acn27900 WNV minus
C 689	11	52.4	38	6	ABK59011	Abk59011 Human CLC	C 762	11	52.4	38	6	ACN27910	Acn27910 WNV minus
C 690	11	52.4	38	6	ABK58560	Abk58560 Human CLC	C 763	11	52.4	38	6	ACN28558	Acn28558 WNV minus
C 691	11	52.4	38	6	ABK58624	Abk58624 Human CLC	C 764	11	52.4	38	6	ACN29274	Acn29274 WNV minus
C 692	11	52.4	38	6	ABK58913	Abk58913 Human CLC	C 765	11	52.4	38	6	ACN29354	Acn29354 WNV minus
C 693	11	52.4	38	6	ABK58753	Abk58753 Human CLC	C 766	11	52.4	38	6	ACN29677	Acn29677 WNV minus
C 694	11	52.4	38	6	ABK58832	Abk58832 Human CLC	C 767	11	52.4	38	6	ACN30104	Acn30104 WNV minus
C 695	11	52.4	38	6	ABK58745	Abk58745 Human CLC	C 768	11	52.4	38	6	ACN30273	Acn30273 WNV minus
C 696	11	52.4	38	6	ABK58745	Abk58745 Human CLC	C 769	11	52.4	38	6	ACN16820	Acn16820 WNV Inozy
C 697	11	52.4	38	6	ABK58485	Abk58485 Human CLC	C 770	11	52.4	38	6	ACN17460	Acn17460 WNV Inozy
C 698	11	52.4	38	6	ABK58667	Abk58667 Human CLC	C 771	11	52.4	38	6	ACN18547	Acn18547 WNV Inozy
C 699	11	52.4	38	6	ACN16957	Acn16957 WNV Inozy	C 772	11	52.4	38	6	ACN26565	Acn26565 WNV minus
C 700	11	52.4	38	6	ACN17961	Acn17961 WNV Inozy	C 773	11	52.4	38	6	ACN27006	Acn27006 WNV minus
C 701	11	52.4	38	6	ACN18702	Acn18702 WNV Inozy	C 774	11	52.4	38	6	ACN28084	Acn28084 WNV minus
C 702	11	52.4	38	6	ACN26995	Acn26995 WNV minus	C 775	11	52.4	38	6	ACN28733	Acn28733 WNV minus
C 703	11	52.4	38	6	ACN28105	Acn28105 WNV minus	C 776	11	52.4	38	6	ACN28773	Acn28773 WNV minus
C 704	11	52.4	38	6	ACN28136	Acn28136 WNV minus	C 777	11	52.4	38	6	ACN29740	Acn29740 WNV minus
C 705	11	52.4	38	6	ACN28157	Acn28157 WNV minus	C 778	11	52.4	38	6	ACN30310	Acn30310 WNV minus
C 706	11	52.4	38	6	ACN28240	Acn28240 WNV minus	C 779	11	52.4	38	6	ACN30517	Acn30517 WNV minus
C 707	11	52.4	38	6	ACN28476	Acn28476 WNV minus	C 780	11	52.4	38	6	ACN30588	Acn30588 WNV minus
C 708	11	52.4	38	6	ACN28689	Acn28689 WNV minus	C 781	11	52.4	38	6	ACN15616	Acn15616 WNV Hamme
C 709	11	52.4	38	6	ACN29388	Acn29388 WNV minus	C 782	11	52.4	38	6	ACN15956	Acn15956 WNV Hamme
C 710	11	52.4	38	6	ACN29477	Acn29477 WNV minus	C 783	11	52.4	38	6	ACN17088	Acn17088 WNV Inozy
C 711	11	52.4	38	6	ACN17601	Acn17601 WNV Inozy	C 784	11	52.4	38	6	ACN17550	Acn17550 WNV Inozy
C 712	11	52.4	38	6	ACN18460	Acn18460 WNV Inozy	C 785	11	52.4	38	6	ACN18481	Acn18481 WNV Inozy
C 713	11	52.4	38	6	ACN18571	Acn18571 WNV Inozy	C 786	11	52.4	38	6	ACN28044	Acn28044 WNV minus
C 714	11	52.4	38	6	ACN26148	Acn26148 WNV minus	C 787	11	52.4	38	6	ACN28074	Acn28074 WNV minus
C 715	11	52.4	38	6	ACN26491	Acn26491 WNV minus	C 788	11	52.4	38	6	ACN28260	Acn28260 WNV minus
C 716	11	52.4	38	6	ACN28227	Acn28227 WNV minus	C 789	11	52.4	38	6	ACN28612	Acn28612 WNV minus
C 717	11	52.4	38	6	ACN28248	Acn28248 WNV minus	C 790	11	52.4	38	6	ACN29159	Acn29159 WNV minus
C 718	11	52.4	38	6	ACN28336	Acn28336 WNV minus	C 791	11	52.4	38	6	ACN30301	Acn30301 WNV minus
C 719	11	52.4	38	6	ACN28714	Acn28714 WNV minus	C 792	11	52.4	38	6	ACN15754	Acn15754 WNV Hamme
C 720	11	52.4	38	6	ACN28832	Acn28832 WNV minus	C 793	11	52.4	38	6	ACN15808	Acn15808 WNV Inozy
C 721	11	52.4	38	6	ACN28890	Acn28890 WNV minus	C 794	11	52.4	38	6	ACN17155	Acn17155 WNV minus
C 722	11	52.4	38	6	ACN28896	Acn28896 WNV minus	C 795	11	52.4	38	6	ACN27977	Acn27977 WNV minus
C 723	11	52.4	38	6	ACN29186	Acn29186 WNV minus	C 796	11	52.4	38	6	ACN27460	Acn27460 WNV minus
C 724	11	52.4	38	6	ACN29258	Acn29258 WNV minus	C 797	11	52.4	38	6	ACN28190	Acn28190 WNV minus
C 725	11	52.4	38	6	ACN30266	Acn30266 WNV Hamme	C 798	11	52.4	38	6	ACN28200	Acn28200 WNV minus
C 726	11	52.4	38	6	ACN16287	Acn16287 WNV Inozy	C 799	11	52.4	38	6	ACN28828	Acn28828 WNV minus
C 727	11	52.4	38	6	ACN16916	Acn16916 WNV Inozy	C 800	11	52.4	38	6	ACN28862	Acn28862 WNV minus
C 728	11	52.4	38	6	ACN18442	Acn18442 WNV Inozy	C 801	11	52.4	38	6	ACN29056	Acn29056 WNV minus
C 729	11	52.4	38	6	ACN28317	Acn28317 WNV minus	C 802	11	52.4	38	6	ACN29365	Acn29365 WNV minus
C 730	11	52.4	38	6	ACN28845	Acn28845 WNV minus	C 803	11	52.4	38	6	ACN29395	Acn29395 WNV minus
C 731	11	52.4	38	6	ACN29129	Acn29129 WNV minus	C 804	11	52.4	38	6	ACN30263	Acn30263 WNV minus
C 732	11	52.4	38	6	ACN15795	Acn15795 WNV Hamme	C 805	11	52.4	38	6	ACN30263	Acn30263 WNV Inozy
C 733	11	52.4	38	6	ACN16946	Acn16946 WNV Inozy	C 806	11	52.4	38	6	ACN17108	Acn17108 WNV Inozy
C 734	11	52.4	38	6	ACN26710	Acn26710 WNV minus	C 807	11	52.4	38	6	ACN17324	Acn17324 WNV Inozy
C 735	11	52.4	38	6	ACN27240	Acn27240 WNV minus	C 808	11	52.4	38	6	ACN17380	Acn17380 WNV Inozy
C 736	11	52.4	38	6	ACN27890	Acn27890 WNV minus	C 809	11	52.4	38	6	ACN17509	Acn17509 WNV Inozy
C 737	11	52.4	38	6	ACN27940	Acn27940 WNV minus	C 810	11	52.4	38	6	ACN17711	Acn17711 WNV Inozy
C 738	11	52.4	38	6	ACN28391	Acn28391 WNV minus	C 811	11	52.4	38	6	ACN17894	Acn17894 WNV Inozy
C 739	11	52.4	38	6	ACN28563	Acn28563 WNV minus	C 812	11	52.4	38	6	ACN18041	Acn18041 WNV Inozy
C 740	11	52.4	38	6	ACN28588	Acn28588 WNV minus	C 813	11	52.4	38	6	ACN27999	Acn27999 WNV minus
C 741	11	52.4	38	6	ACN28599	Acn28599 WNV minus	C 814	11	52.4	38	6	ACN29957	Acn29957 WNV minus
C 742	11	52.4	38	6	ACN29103	Acn29103 WNV minus	C 815	11	52.4	38	6	ACN17485	Acn17485 WNV Inozy
C 743	11	52.4	38	6	ACN29501	Acn29501 WNV minus	C 816	11	52.4	38	6	ACN17578	Acn17578 WNV Inozy
C 744	11	52.4	38	6	ACN30440	Acn30440 WNV minus	C 817	11	52.4	38	6	ACN17764	Acn17764 WNV Inozy
C 745	11	52.4	38	6	ACN16780	Acn16780 WNV Inozy	C 818	11	52.4	38	6	ACN17937	Acn17937 WNV Inozy
C 746	11	52.4	38	6	ACN16875	Acn16875 WNV Inozy	C 819	11	52.4	38	6	ACN18052	Acn18052 WNV Inozy
C 747	11	52.4	38	6	ACN17072	Acn17072 WNV Inozy	C 820	11	52.4	38	6	ACN18201	Acn18201 WNV Inozy
C 748	11	52.4	38	6	ACN17627	Acn17627 WNV Inozy	C 821	11	52.4	38	6	ACN18216	Acn18216 WNV Inozy
C 749	11	52.4	38	6	ACN17717	Acn17717 WNV Inozy	C 822	11	52.4	38	6	ACN26930	Acn26930 WNV minus
C 750	11	52.4	38	6	ACN17925	Acn17925 WNV Inozy	C 823	11	52.4	38	6	ACN28373	Acn28373 WNV minus
C 751	11	52.4	38	6	ACN18329	Acn18329 WNV Inozy	C 824	11	52.4	38	6	ACN28406	Acn28406 WNV minus

C 825	11	52.4	38	6	ACN28443	ACn28443	WNV minus	C 898	11	52.4	38	8	ACA07471	ACA07471	Necrosis
C 826	11	52.4	38	6	ACN28810	ACn28810	WNV minus	C 899	11	52.4	38	8	ACA07599	ACA07599	Necrosis
C 827	11	52.4	38	6	ACN28885	ACn28885	WNV minus	C 900	11	52.4	38	8	ACA07377	ACA07377	Necrosis
C 828	11	52.4	38	6	ACN29256	ACn29256	WNV minus	C 901	11	52.4	38	8	ACA07332	ACA07332	Necrosis
C 829	11	52.4	38	6	ACN29922	ACn29922	WNV minus	C 902	11	52.4	38	8	ACA07457	ACA07457	Necrosis
C 830	11	52.4	38	6	ACN29953	ACn29953	WNV minus	C 903	11	52.4	38	8	ACA07558	ACA07558	Necrosis
C 831	11	52.4	38	6	ACN30579	ACn30579	WNV minus	C 904	11	52.4	38	8	ACA06952	ACA06952	Necrosis
C 832	11	52.4	38	6	ACN30579	ACn30579	WNV minus	C 905	11	52.4	38	8	ACA06968	ACA06968	Necrosis
C 833	11	52.4	38	6	ACN17136	ACn17136	WNV Inoxy	C 906	11	52.4	38	8	ACA07582	ACA07582	Necrosis
C 834	11	52.4	38	6	ACN17634	ACn17634	WNV Inoxy	C 907	11	52.4	38	8	ACA07274	ACA07274	Necrosis
C 835	11	52.4	38	6	ACN17918	ACn17918	WNV Inoxy	C 908	11	52.4	38	8	ACA07171	ACA07171	Necrosis
C 836	11	52.4	38	6	ACN18084	ACn18084	WNV Inoxy	C 909	11	52.4	38	8	ACA06902	ACA06902	Necrosis
C 837	11	52.4	38	6	ACN28708	ACn28708	WNV minus	C 910	11	52.4	38	8	ACA07132	ACA07132	Necrosis
C 838	11	52.4	38	6	ACN28738	ACn28738	WNV minus	C 911	11	52.4	38	8	ACA07486	ACA07486	Necrosis
C 839	11	52.4	38	6	ACN28907	ACn28907	WNV minus	C 912	11	52.4	38	8	ACA07208	ACA07208	Necrosis
C 840	11	52.4	38	6	ACN29169	ACn29169	WNV minus	C 913	11	52.4	38	8	ACA07211	ACA07211	Necrosis
C 841	11	52.4	38	6	ACN29180	ACn29180	WNV minus	C 914	11	52.4	38	8	ACA07386	ACA07386	Necrosis
C 842	11	52.4	38	6	ACN29563	ACn29563	WNV minus	C 915	11	52.4	38	8	ACA07091	ACA07091	Necrosis
C 843	11	52.4	38	6	ACN30084	ACn30084	WNV minus	C 916	11	52.4	38	8	ACA07247	ACA07247	Necrosis
C 844	11	52.4	38	6	ACN16310	ACn16310	WNV Hamme	C 917	11	52.4	38	8	ACA07263	ACA07263	Necrosis
C 845	11	52.4	38	6	ACN17199	ACn17199	WNV Inoxy	C 918	11	52.4	38	8	ACA07568	ACA07568	Necrosis
C 846	11	52.4	38	6	ACN17556	ACn17556	WNV Inoxy	C 919	11	52.4	38	8	ACD52556	ACD52556	HBV inoxy
C 847	11	52.4	38	6	ACN17661	ACn17661	WNV Inoxy	C 920	11	52.4	38	8	ACD52259	ACD52259	HBV inoxy
C 848	11	52.4	38	6	ACN18473	ACn18473	WNV Inoxy	C 921	11	52.4	38	8	ACD52146	ACD52146	HBV inoxy
C 849	11	52.4	38	6	ACN29017	ACn29017	WNV minus	C 922	11	52.4	38	8	ACD52647	ACD52647	HBV inoxy
C 850	11	52.4	38	6	ACN29109	ACn29109	WNV minus	C 923	11	52.4	38	8	ACD51846	ACD51846	HBV inoxy
C 851	11	52.4	38	6	ACN29662	ACn29662	WNV minus	C 924	11	52.4	38	8	ACD51853	ACD51853	HBV inoxy
C 852	11	52.4	38	6	ACN29849	ACn29849	WNV minus	C 925	11	52.4	38	8	ACD52059	ACD52059	HBV inoxy
C 853	11	52.4	38	6	ACN30114	ACn30114	WNV minus	C 926	11	52.4	38	8	ACD52884	ACD52884	HBV inoxy
C 854	11	52.4	38	6	ACN30291	ACn30291	WNV minus	C 927	11	52.4	38	8	ACD53068	ACD53068	HBV inoxy
C 855	11	52.4	38	6	ACN30347	ACn30347	WNV minus	C 928	11	52.4	38	8	ACD51000	ACD51000	HBV hamme
C 856	11	52.4	38	6	ACN15696	ACn15696	WNV Hamme	C 929	11	52.4	38	8	ACD52977	ACD52977	HBV inoxy
C 857	11	52.4	38	6	ACN16680	ACn16680	WNV Hamme	C 930	11	52.4	38	8	ACD50914	ACD50914	HBV hamme
C 858	11	52.4	38	6	ACN17566	ACn17566	WNV Inoxy	C 931	11	52.4	38	8	ACD51754	ACD51754	HBV inoxy
C 859	11	52.4	38	6	ACN17785	ACn17785	WNV Inoxy	C 932	11	52.4	38	8	ACD52661	ACD52661	HBV inoxy
C 860	11	52.4	38	6	ACN18063	ACn18063	WNV Inoxy	C 933	11	52.4	38	8	ACD50997	ACD50997	HBV hamme
C 861	11	52.4	38	6	ACN18465	ACn18465	WNV Inoxy	C 934	11	52.4	38	8	ACD51642	ACD51642	HBV hamme
C 862	11	52.4	38	6	ACN28121	ACn28121	WNV minus	C 935	11	52.4	38	8	ACD52243	ACD52243	HBV inoxy
C 863	11	52.4	38	6	ACN28284	ACn28284	WNV minus	C 936	11	52.4	38	8	ACD52637	ACD52637	HBV inoxy
C 864	11	52.4	38	6	ACN28574	ACn28574	WNV minus	C 937	11	52.4	38	8	ACD52664	ACD52664	HBV inoxy
C 865	11	52.4	38	6	ACN29324	ACn29324	WNV minus	C 938	11	52.4	38	8	ACD52673	ACD52673	HBV inoxy
C 866	11	52.4	38	6	ACN29616	ACn29616	WNV minus	C 939	11	52.4	38	8	ACD52981	ACD52981	HBV inoxy
C 867	11	52.4	38	6	ACN29697	ACn29697	WNV minus	C 940	11	52.4	38	8	ACD51940	ACD51940	HBV inoxy
C 868	11	52.4	38	6	ACN29765	ACn29765	WNV minus	C 941	11	52.4	38	8	ACD53074	ACD53074	HBV inoxy
C 869	11	52.4	38	6	ACN30340	ACn30340	WNV Hamme	C 942	11	52.4	38	8	ACD52268	ACD52268	HBV inoxy
C 870	11	52.4	38	6	ACN15599	ACn15599	WNV Hamme	C 943	11	52.4	38	8	ACD52343	ACD52343	HBV inoxy
C 871	11	52.4	38	6	ACN17500	ACn17500	WNV Inoxy	C 944	11	52.4	38	8	ACD52959	ACD52959	HBV inoxy
C 872	11	52.4	38	6	ACN17782	ACn17782	WNV Inoxy	C 945	11	52.4	38	8	ACD52460	ACD52460	HBV inoxy
C 873	11	52.4	38	6	ACN28162	ACn28162	WNV minus	C 946	11	52.4	38	8	ACD52646	ACD52646	HBV inoxy
C 874	11	52.4	38	6	ACN28211	ACn28211	WNV minus	C 947	11	52.4	38	8	ACD53152	ACD53152	HBV inoxy
C 875	11	52.4	38	6	ACN28291	ACn28291	WNV minus	C 948	11	52.4	38	8	ACD52548	ACD52548	HBV inoxy
C 876	11	52.4	38	6	ACN29165	ACn29165	WNV minus	C 949	11	52.4	38	8	ACD52775	ACD52775	HBV inoxy
C 877	11	52.4	38	6	ACN30093	ACn30093	WNV minus	C 950	11	52.4	38	8	ACD51858	ACD51858	HBV inoxy
C 878	11	52.4	38	6	ACN30562	ACn30562	WNV minus	C 951	11	52.4	38	8	ACD53141	ACD53141	HBV inoxy
C 879	11	52.4	38	6	ACN15580	ACn15580	WNV Hamme	C 952	11	52.4	38	11	ADL52282	ADL52282	Human NOG
C 880	11	52.4	38	6	ACN17256	ACn17256	WNV Inoxy	C 953	11	52.4	38	11	ADL53719	ADL53719	Human IKK
C 881	11	52.4	38	6	ACN17935	ACn17935	WNV Inoxy	C 954	11	52.4	38	11	ADL53750	ADL53750	Human IKK
C 882	11	52.4	38	6	ACN18449	ACn18449	WNV Inoxy	C 955	11	52.4	38	11	ADL53761	ADL53761	Human IKK
C 883	11	52.4	38	6	ACN18450	ACn18450	WNV Inoxy	C 956	11	52.4	38	11	ADL53913	ADL53913	Human IKK
C 884	11	52.4	38	6	ACN18506	ACn18506	WNV Inoxy	C 957	11	52.4	38	11	ADL54077	ADL54077	Human IKK
C 885	11	52.4	38	6	ACN28560	ACn28560	WNV minus	C 958	11	52.4	38	11	ADL75070	ADL75070	Human PTG
C 886	11	52.4	38	6	ACN28668	ACn28668	WNV minus	C 959	11	52.4	38	11	ADL52399	ADL52399	Human NOG
C 887	11	52.4	38	6	ACN28716	ACn28716	WNV minus	C 960	11	52.4	38	11	ADL74977	ADL74977	Human PTG
C 888	11	52.4	38	6	ACN29218	ACn29218	WNV minus	C 961	11	52.4	38	11	ADL75375	ADL75375	Human PTG
C 889	11	52.4	38	6	ACN29811	ACn29811	WNV minus	C 962	11	52.4	38	11	ADL52036	ADL52036	Human NOG
C 890	11	52.4	38	8	ACA07220	ACA07220	Necrosis	C 963	11	52.4	38	11	ADL52435	ADL52435	Human NOG
C 891	11	52.4	38	8	ACA07476	ACA07476	Necrosis	C 964	11	52.4	38	11	ADL53838	ADL53838	Human IKK
C 892	11	52.4	38	8	ACA07410	ACA07410	Necrosis	C 965	11	52.4	38	11	ADL75222	ADL75222	Human PTG
C 893	11	52.4	38	8	ACA07570	ACA07570	Necrosis	C 966	11	52.4	38	11	ADL52135	ADL52135	Human NOG
C 894	11	52.4	38	8	ACA07379	ACA07379	Necrosis	C 967	11	52.4	38	11	ADL52228	ADL52228	Human NOG
C 895	11	52.4	38	8	ACA06956	ACA06956	Necrosis	C 968	11	52.4	38	11	ADL52407	ADL52407	Human NOG
C 896	11	52.4	38	8	ACA07113	ACA07113	Necrosis	C 969	11	52.4	38	11	ADL53997	ADL53997	Human IKK
C 897	11	52.4	38	8	ACA07319	ACA07319	Necrosis	C 970	11	52.4	38	11	ADL54011	ADL54011	Human IKK

c 971 11 52.4 38 11 ADL54087
c 972 11 52.4 38 11 ADL53909
c 973 11 52.4 38 11 ADL53943
c 974 11 52.4 38 11 ADL54018
c 975 11 52.4 38 11 ADL54083
c 976 11 52.4 38 11 ADL54136
c 977 11 52.4 38 11 ADL56310
c 978 11 52.4 38 11 ADL52242
c 979 11 52.4 38 11 ADL52269
c 980 11 52.4 38 11 ADL53552
c 981 11 52.4 38 11 ADL54014
c 982 11 52.4 38 11 ADL75383
c 983 11 52.4 38 11 ADL52346
c 984 11 52.4 38 11 ADL56617
c 985 11 52.4 38 11 ADL75194
c 986 11 52.4 38 11 ADL75403
c 987 11 52.4 38 11 ADL52249
c 988 11 52.4 38 11 ADL53782
c 989 11 52.4 38 11 ADL54164
c 990 11 52.4 38 11 ADL54199
c 991 11 52.4 38 11 ADL55733
c 992 11 52.4 38 11 ADL56599
c 993 11 52.4 38 11 ADL75335
c 994 11 52.4 38 11 ADL75390
c 995 11 52.4 38 11 ADL52144
c 996 11 52.4 38 11 ADL53775
c 997 11 52.4 38 11 ADL75487
c 998 11 52.4 38 11 ADL54016
c 999 11 52.4 38 11 ADL56557
c1000 11 52.4 38 11 ADL56601

ALIGNMENTS

RESULT 1
ACI56056/c
ID ACI56056 standard; DNA; 25 BP.
XX
AC ACI56056;
XX
DT 13-OCT-2003 (first entry)
XX
Human microarray DNA oligonucleotide SEQ ID NO 56047.
XX
EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW Genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
Homo sapiens.
OS
US2003104410-A1.
PN
XX
05-JUN-2003.
XX
15-MAR-2002; 2002US-00098263.
XX
16-MAR-2001; 2001US-0276759P.
XX
(AFFY-) AFFYMETRIX INC.
PA
Mittmann MP;
PI
WPI; 2003-567953/53.
DR
XX
New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
PT
XX
Claim 1; SEQ ID NO 56047; 9pp; English.
PS
XX
The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its

CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 67.6%; Score 14.2; DB 9; Length 25;

Best Local Similarity 84.2%; Pred. NO. 5.1e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TCGCGTACGGTCTAATGAC 19

Db 24 TCGAACACGGTCTAATGAC 6

RESULT 2

AAAL6755/c

ID AAAL6755 standard; DNA; 29 BP.

XX AAAL6755;

XX 16-JUN-2000 (first entry)

XX Human secreted protein clone LL89_3 probe SEQ ID NO:218.

XX Human; secreted protein; immunostimulant; immunosuppressant; virucide;
KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;
KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
KW connective tissue disease; multiple sclerosis; erythematosis;
KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
KW insulin dependent diabetes mellitus; graft-versus-host-disease;
KW autoimmune inflammatory eye disease; allergy; hybridisation; probe; ss.

XX Homo sapiens.

XX WO200009552-A1.

XX 24-FEB-2000.

XX 13-AUG-1999; 99WO-US018298.

XX 14-AUG-1998; 98US-0096622P.

XX 17-AUG-1998; 98US-0096815P.

XX 04-SEP-1998; 98US-0099229P.

XX 23-OCT-1998; 98US-0105368P.

XX 08-JAN-1999; 99US-0115234P.

XX 12-FEB-1999; 99US-011931P.

XX 18-FEB-1999; 99US-0120575P.

XX 30-APR-1999; 99US-0132020P.

XX 11-AUG-1999; 99US-0148424P.

XX (GEMY) GENETICS INST INC.

PA

DR WPI; 1998-523164/45.
 XX Determination of gene expression levels - using combinations of different
 PT cDNA samples tagged with different PCR adaptors.
 XX
 XX Example 2; Page 10; 22pp; English.
 PS
 CC The present sequence represents an adaptor which was used in the method
 CC of the invention to determine the amount ratio between a cDNA coding for
 CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney
 CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-
 CC PCR). This method allows gene expression to be quantitatively determined,
 CC and because internal standards are not required to prepare a calibration
 CC curve, it is a quicker and less laborious process
 XX
 XX Sequence 35 BP; 8 A; 9 C; 9 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 62.9%; Score 13.2; DB 2; Length 35;
 Best Local Similarity 83.3%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 2 CGCGTACGGTCTAATGAC 19
 ||||| ||||| ||||| ||||| |||||
 DB 27 CGCGTACGGTCTAATGAC 10
 ||||| ||||| ||||| ||||| |||||
 RESULT 7
 ACN31831
 ID ACN31831 standard; RNA; 37 BP.
 AC ACN31831;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX
 DE WNV minus strand Zinzyne SEQ ID NO 31847.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.
 XX
 OS West Nile Virus.
 XX
 XX WO200268637-A2.
 FN
 XX
 XX 06-SEP-2002.
 PD
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX
 XX 20-OCT-2000; 2000US-024241P.
 PR
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 XX WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX Claim 24; SEQ ID NO 31847; 495pp; English.
 PS
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 37 BP; 13 A; 7 C; 12 G; 0 T; 5 U; 0 Other;
 SQ
 Query Match 62.9%; Score 13.2; DB 6; Length 37;
 Best Local Similarity 61.1%; Pred. No. 1.9e+03;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 2 CGCGTACGGTCTAATGAC 19
 ||||| ||||| ||||| ||||| |||||
 DB 18 CGAGUGAGGUCUAUGAC 35
 ||||| ||||| ||||| ||||| |||||
 RESULT 8
 AAV61560
 ID AAV61560 standard; DNA; 39 BP.
 XX
 XX AAV61560;
 AC
 XX 08-DEC-1998 (first entry)
 DT
 XX
 DE Adaptor NNNN-C1GSR (- strand).
 XX
 KW Adaptor; quantitate; amount ratio; liver; kidney; apolipoprotein;
 KW ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression;
 KW internal standard; calibration curve; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 XX EP870842-A2.
 FN
 XX 14-OCT-1998.
 PD
 XX 07-APR-1998; 98EP-00302726.
 PF
 XX 07-APR-1997; 97JP-00088495.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX Kato K;
 PI
 XX WPI; 1998-523164/45.
 DR
 XX Determination of gene expression levels - using combinations of different
 PT cDNA samples tagged with different PCR adaptors.
 PT
 XX Example 2; Page 10; 22pp; English.
 PS
 CC The present sequence represents an adaptor which was used in the method
 CC of the invention to determine the amount ratio between a cDNA coding for
 CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney
 CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-
 CC PCR). This method allows gene expression to be quantitatively determined,
 CC and because internal standards are not required to prepare a calibration
 CC curve, it is a quicker and less laborious process
 XX
 XX Sequence 39 BP; 9 A; 9 C; 9 G; 8 T; 0 U; 4 Other;
 SQ
 Query Match 62.9%; Score 13.2; DB 2; Length 39;
 Best Local Similarity 83.3%; Pred. No. 2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 2 CGCGTACGGTCTAATGAC 19
 ||||| ||||| ||||| ||||| |||||
 DB 13 CGCGTACGGTCTAATGAC 30
 ||||| ||||| ||||| ||||| |||||

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RESULT 9
ACI71602
ID ACI71602 standard; DNA; 25 BP.
XX AC
XX ACI71602;
XX AC
XX ACI71602;
XX DT 14-OCT-2003 (first entry)
XX DE
XX DE Human microarray DNA oligonucleotide SEQ ID NO 71593.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX OS
XX PN US2003104410-A1.
XX PN
XX PD 05-JUN-2003.
XX PD
XX PF 15-MAR-2002; 2002US-00098263.
XX PF
XX PR 16-MAR-2001; 2001US-0276759P.
XX PR
XX PA (AFFY-) AFFYMETRIX INC.
XX PA
XX PI Mittmann MP;
XX PI
XX DR WPI; 2003-567953/53.
XX DR
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 71593; 9pp; English.
XX PS
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX CC
XX SQ Sequence 25 BP; 5 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
XX SQ
Query Match 61.9%; Score 13; DB 9; Length 25;
Best Local Similarity 76.2%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCTACGGTCTAATGACCG 21
   |||||
DB 1 TCTCTACGGACTACCCACCG 21
   |||||

RESULT 10
ACI71017/c
ID ACI71017 standard; DNA; 25 BP.
XX AC
XX ACI71017;
XX AC
XX ACI71017;
XX DT 14-OCT-2003 (first entry)
XX DE
XX DE Human microarray DNA oligonucleotide SEQ ID NO 71008.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX OS
XX PN US2003104410-A1.
XX PN
XX PD 05-JUN-2003.
XX PD
XX PF 15-MAR-2002; 2002US-00098263.
XX PF
XX PR 16-MAR-2001; 2001US-0276759P.
XX PR
XX PA (AFFY-) AFFYMETRIX INC.
XX PA
XX PI Mittmann MP;
XX PI
XX DR WPI; 2003-567953/53.
XX DR
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 71008; 9pp; English.
XX PS
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX CC
XX SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;
XX SQ
Query Match 61.0%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGTACGGTCTAATGAC 19
   |||||
DB 20 CGTACGGTCAATGAC 5
   |||||

RESULT 11
ACI12949
ID ADD12949 standard; DNA; 30 BP.

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